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Geographical Gaps and Diversity in Deenanath Grass (*Pennisetum pedicellatum* Trin.) Germplasm Conserved at the ICRISAT Genebank

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The genebank at ICRISAT, India conserves 134 accessions of Deenanath grass (*Pennisetum pedicellatum* Trin.) from eight countries. A predicted probability map developed using FloraMap indicated 194 provinces in 21 countries of Asia and Africa as geographical gaps. All aceessions were annual and days to 50% flowering ranged from 43 to 109 days, number of total tillers/plant from 275 to 2,247 and number of productive tillers per plant from 114 to 1261. Accession IP 21821 produced maximum total tillers (2,247) and IP 21850 scored maximum (9) for forage yield potential. Early flowering (43 days) and high tillering (2,247) accessions of cluster 1 were considered as a promising source for early cuttings of green fodder. Mean diversity (H`) for quantitative traits (H`=0.591 $\pm$ 0.010) was higher than that for qualitative traits (H`=0.284 $\pm$ 0.089). Early flowering, high tillering habit and higher levels of resistance to downy mildew make the Deenanath grass important.

Key Words: Crop wild relative, Germplasm, Mapping, Probability, Variation

Introduction

Crop wild relatives (CWR) are important components of agro-ecosystems as potential gene contributors for breeding programs. When the levels of resistance to various biotic and abiotic stresses in cultivated germplasm are low or the range of genetic variability is narrow and selection pressure results in virulent biotypes of the pests and diseases, the discovery and incorporation of additional genes for resistance from wild species becomes key to sustain crop productivity. Despite their importance, compared to landraces wild species have not received due attention from germplasm collectors. World's genebanks are conserving only a fraction of the total genetic variability that exists in CWR and only a small proportion of conserved accessions have been characterized. The economic impacts of wild relatives in crop improvement have been towards increasing disease resistances in wheat (Malik *et al*., 2003), rice (Brar and Khush, 1997) and potato (Pavek and Corsini, 2001). They have also been used to raise the nutritional value of some crops, such as protein content in durum wheat (Kovacs *et al*., 1998), calcium content in potato (Bamberg and Hanneman, 2003) and provitamin A in tomato (Pan *et al*., 2000).

Pearl millet, an important crop of the semi-arid tropics (SAT), has immense potential for adaptation to extreme limits of agriculture and its importance is expected to increase under changing climate scenarios (Lane *et al*., 2007). The primary genepool of pearl millet includes cultivated *Pennisetum glaucum* ssp. *glaucum*, the wild progenitor *P. glaucum* ssp. *monodii* and the weedy form *P. glaucum* ssp. *stenostachyum*. Hanna (1989) reported the development of a stable male sterile cytoplasm A_4 from the ssp. *monodii*. *Pennisetum purpureum* (napier grass) is the only known species in the secondary genepool. It is a rhizomatous perennial, with desirable characters like resistance to most pests, vigorous growth and outstanding forage yield potential (Hanna, 1992). The tertiary genepool consists of the remainder of the wild *Pennisetum* species including *P. pedicellatum* Trin., also called as Deenanath grass. It is widely distributed in West Africa and India. It is known as a weed in grain sorghum crops in northern Australia. In north of Cameroon, it is an important weed in field crops (Schmelzer, 1997). *Pennisetum pedicellatum* is a profusely tillering annual with big fluffy inflorescences (Fig. 1). It is quick growing, luscious, leafy and thin-stemmed grass and grows well even on poor, eroded soils in areas receiving 500-1500 mm annual rainfall (Mukherjee *et al*., 1982). As a high yielding grass of a short duration, it fits in well in the small period left in between two arable crops. Usually, one cut is taken after 80-90 days of sowing. *P. pedicellatum* was also considered as an important source for higher levels of downy mildew resistance (Singh and Navi, 2000).

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Fig. 1. Plant of *Pennisetum pedicellatum*

To ensure the availability of large genetic diversity to the crop improvement programs, there is a need for collection, conservation, characterization, evaluation, documentation and distribution of plant genetic resources. The genetic variability accumulated over centuries is at risk, mainly due to replacement of landraces and wild relatives with improved varieties, climate change and concomitant natural catastrophes (droughts, floods, fire hazards etc.), human settlements, overgrazing, destruction of plant habitats for irrigation projects etc. (Upadhyaya and Gowda, 2009). Critical assessment of existing collections to identify geographical gaps, assess agronomic performance and launching germplasm collecting missions in the unexplored and under-explored areas is important to increase the variability. ICRISAT genebank being the world repository for the germplasm of its mandate crops and their wild relatives including pearl millet, assembled a total of 134 accessions of *P. pedicellatum* from India (57), Cameroon (56), Niger (14), Mali (3) and one each from Central African Republic, Mauritania, Tanzania and USA. Geographical distribution of any species is often scanty and patchy and makes it difficult to assess and map its occurrence in nature. In the present study, identified geographical gaps in *P. pedicellatum* germplasm assembled at ICRISAT genebank and evaluated to assess the diversity to enhance the utilization of germplasm in pearl millet improvement.

Materials and Methods

The present study was carried out with 134 accessions of *Pennisetum pedicellatum* assembled at ICRISAT genebank from eight countries. Passport data of the collection, particularly for information on precise location of collecting sites and corresponding geographic coordinates was updated verifying all records, collection reports and catalogs. Using the Microsoft Encarta®, an electronic atlas (MS Encarta Interactive World Atlas, 2000), geographic coordinates were retrieved to fill the gaps for accessions having location information and the accuracy of coordinates for 121 accessions was verified by plotting all accessions on political map. FloraMap, a GIS tool developed at Centro Internacional de Agricultura Tropical (CIAT) (Jones and Gladkov, 1999) was used to predict the probable areas of *P. pedicellatum* occurrence and identify geographical gaps in the collection. The basic input in the FloraMap software is the geographic coordinates (latitude and longitude) of the sampling site with a unique identifier (accessions number). The FloraMap system is based on calculating the probability that a climate record belongs to a multivariate normal distribution described by the climates at the collection points of a calibration set of organisms. With its user-friendly software linked to agroclimatic and other databases, biodiversity specialists can create maps showing the most likely distribution of any particular species in nature. FloraMap assigns climate data (monthly rainfall, minimum and maximum temperature, diurnal range in temperature) to each of the collection sites from the database provided along with the tool. Principal component analysis is used to reduce the dimensionality of this 36 dimensional dataset (set of 12 of the three variables) for each collection site and select first few components, which contribute to the maximum variation of the climatic characteristics. Also these few components are uncorrelated or orthogonal. Weights can be allocated to each of the three variables depending on the climate of the country/region. A probability density

function is calculated on these few uncorrelated variables to find out the probability of finding a location for the population. While working on the passport dataset equal weights were allocated to the three climatic variables (monthly rainfall, minimum and maximum temperature, diurnal range in temperature) and an exponential transformation with a power of 0.3 to 0.5 was applied to the monthly rainfall data. The probability map was generated and the probabilities greater than 70% were considered for interpretation and recommendation for germplasm collection. While estimating the probability of *P. pedicellatum* occurrence, multiple accessions with same coordinates were treated as single collection site. Collection sites or sampled sites were overlaid on the probability image and the provinces with high probability (>70%) areas, where no collection or few collections have been made, were identified. All the provinces identified were shown (shaded area) in the map along with the collection sites of past collections.

All the 134 accessions were characterized during 2007 rainy season under field conditions on ICRISAT farm (17^0 48'N) in alfisol-Patancheru Soil Series (Udic Rhodustolf) field at Patancheru (18^oN, 79^oE, 545 m above sea level, and 600 km away from sea), Andhra Pradesh, India. The seeds were germinated in small cups with red soil mix and seedlings having 2-4 leaves were transplanted after 10-15 days in a single row of 8-m length with a row to row distance of 100 cm and plant to plant distance of 75 cm within the row during July. Crop received a basal dose of DAP @ of 150 kg ha^{-1} and 100 kg urea as top dressing 20 days after transplanting. Life saving irrigation was provided. The crop was protected from weeds. For each accession, five representative plants were selected to record observations on days to 50% flowering, plant height (cm), total tillers (no.), productive tillers (no.), stem thickness (mm), leaf blade length (cm), leaf blade width (cm), panicle length (cm), panicle thickness (mm), panicle exsertion (cm), 1000-seed weight (g), stem color, leaf blade pubescence, leaf blade shape, leaf color, panicle shape, bristle length (on 1-9 score, 1 = smallest and 9 = longest), green fodder yield potential (on 1-9 score, 1 = poor and 9 = good), and seed shape and color (IBPGR and ICRISAT, 1993).

Data on agronomic traits were analyzed using Residual Maximum Likelihood (REML) method considering accessions as random (random model) in GenStat 12 (Patterson and Thompson, 1971). Balanced Linear Unbiased Predictors (BLUPs) were calculated for each accession and each trait (Schonfeld and Werner, 1986). Principal component analysis (PCA) was carried out using standardized data of 11 quantitative traits using GENSTAT 5.1. Cluster analysis according to Ward (1963) was performed using scores of first 10 principal components. The mean, range and variances were calculated for 11 agronomic characters among the clusters and the entire collection. The means for different traits were compared using the Newman-Keuls procedure (Keuls, 1952; Newman, 1939). Homogeneity of variances was tested by Leven's test (Leven, 1960). The Shannon-Weaver diversity index (H`) (Shannon and Weaver, 1949) was estimated for each of the nine qualitative traits and the 11 quantitative traits over all the accessions to measure and compare phenotypic diversity.

Results

Overlaying of collection sites on the predicted probability image developed using FloraMap revealed that the existing collections are only from few areas in the primary and secondary centers of diversity for pearl millet (Fig. 2). In addition, it also revealed that many high probability areas were found in Africa and Asia, where no collections have been made in the past. In addition, high predicted probability (>70%) areas were also detected in Laos, Myanmar and Thailand in Asia and Mozambique and Madagascar in Africa. The probability image identified 8 provinces in India, 10 provinces in Laos, 14 provinces in Myanmar, 3 provinces each in Nepal and Thailand in Asia as the important source regions. Similarly, a total of 156 provinces in 16 countries in Africa, mainly Mali (38 provinces), Burkina Faso (29 provinces) and Senegal (23 provinces) were found as the important source regions for *P. pedicellatum* germplasm and need exploration (Table 1).

About 50 per cent of accessions (67) produced green stems and remaining produced purple stems. Only three accessions (IP 21850, IP 21861 and IP 21846) produced stems of >7.5 mm thickness. Three accessions (IP 21849, IP 22072 and IP 21836) produced leaves longer than 50 cm. IP 21853 flowered late (in 106 days) and grew to a maximum height of 248 cm and found as the promising source for green fodder yield. IP 21853, IP 21861, IP 21850, IP 21849, IP 21862, IP 21845 and IP 21864 grew more than 230 cm. IP 21821 produced maximum total tillers (2247 tillers) followed by IP 21866 (1791), IP 22220 (1772), IP 22071 (1766), IP 22091 (1736). Only one accession (IP 21850) scored maximum (9) for forage

Table 1. Provinces with high probability for occurrence of *Pennisetum pedicellatum* in different countries

Country	Provinces identified
India	Andhra Pradesh, Bihar, Chattisgarh, Jharkhand, Karnataka, Maharashtra, Orissa and West Bengal
Laos	Oudomxay, Vientiane (Munic.), Bokeo, Luang Prabang, Vientiane 2, Khammouane, Savannakhet, Xiangkhouang, Vientiane and Sayabouri
Myanmar	Arakan (Rakhine), Bago (Pegu), Chin, Irrawaddy, Kachin, Kawthulei (Karen), Kayah, Magwe, Mandalay, Mon, Sagaing, Shan, Tenasserim and Yangon
Nepal	East, Central and West
Thailand	Central, Northern and Northeastern
Benin	Atakora and Borgou
Burkina Faso	Seno, Boulgou, Gourma, Bougouriba, Kadiogo, Kouritenga, Gnagna, Tapoa, Sourou, Ganzourgou, Namentenga, Sanguie, Comoe, Soum, Mou Houn, Yatenga, Poni, Nahouri, Zoundweogo, Kenedougou, Oubritenga, Houet, Sanmatenga, Passore, Bazega, Sissili, Boulkiemde, Bam and Kossi
Cameroon	Adamoua, Extreme-Nord and Nord
Chad	Ouaddai, Chari-Baguirmi, Mayo-Kebbi, Logone Orienta, Logone Occiden, Tandjile, Moyen-Chari, Salamat and Guera
Gambia	North Bank, Upper River, Maccarthy Island, Lower River and Western
Guinea	Kindia, Labe and Kankan
Guinea-Bissau	Gabu, Bafata, Bissau, Biombo, Oio and Cacheu
Madagascar	Antananarivo, Mahajanga and Toliary
Malawi	Southern
Mali	Niafunke, Goundam, Youvarou, Niono, Douentza, Sikasso, Macina, Tenenkou, Koro, Nara, Mopti, San, Nioro, Koutiala, Bandiagara, Bla, Segou, Djenne, Diema, Yelimane, Kadiolo, Kayes, Kolondieba, Bankass, Yorosso, Banamba, Dioila, Baraoueli, Kolokani, Koulikoro, Tominian, Kenieba, Bafoulabe, Bougouni, Yanfolila, Kita, Kati and Kangaba
Mauritania	Hodh ech Chargui, Hodh el Gharbi and Assaba
Mozambique	Nampula, Zambezia, Cabo Delgado, Manica, Sofala and Tete
Niger	Tillabery, Dosso, Zinder, Tahoua and Maradi
Nigeria	FCT, Yobe, Taraba, Borno, Sokoto, Katsina, Adamwara, Plateau, Kebbi, Kaduna, Niger, Jigawa, Bauchi and Kano
Senegal	Thies, Kebemer, Tivaouane, Bambey, Diourbel, Mbacke, Linguere, Foundiougne, Fatick, Bakel, Kolda, Mbour, Matam, Kedougou, Gossas, Kaffrine, Velingara, Kaolack, Nioro-Du-Rip, Tambacounda, Sedhiou, Bignona and Ziguinchor
Sudan	Equatoria, Upper Nile, Darfur, Bahr el Ghazal, Central and Kordufan

yield potential and 23 accessions scored 8 on a 1-9 scale, 1 being the poorest and 9 as the best. All accessions produced brown colored seed either with elliptical shape (123 accessions) or obovate (11 accessions) shape.

REML Analysis

Residual Maximum Likelihood (REML) indicated that genetic variance components were highly significant for all the traits indicating the considerable diversity in the collection (Table 2). All accessions were annual and completed life cycle in one season and days to flowering ranged from 43 to 109. Similarly, important traits like plant height (73-248 cm), number of total tillers/plant from (275 to 2247), leaf blade length (16-53 cm) and leaf blade width (1-2.3 cm), which contribute for fodder yield had shown large variation.

Cluster Analysis

Principal component analysis (PCA) carried out using standardized data of 11 quantitative traits captured 71% of total variation from first three principal components (PCs). A hierarchical cluster analysis conducted on the scores of these three PCs resulted in three clusters (Table 3). The accessions from Cameroon (15), India (14), Niger (13), Mali (2) and Mauritania (1) formed the first cluster with 45 accessions; accessions from Cameroon (26) and one accession each from India, Mali and Tanzania formed the second cluster having 29 accessions and accessions from India (42), Cameroon (15), and one accession each from Central African Republic, Niger and USA formed the third cluster with 60 accessions. Clustering of accessions revealed no effect of geographic origin on agronomic performance. Accessions in cluster 1 were highly diverse with high range of variation for days to 50% flowering, plant height, total tillers, stem thickness, panicle exsertion and 1000 seed weight. Accessions in cluster 3 showed high range of variation for leaf blade length and width and panicle length.

Means and Variances

Newman-Keuls test of significance for mean values indicated significant differences among the clusters for all characters except panicle exsertion (Table 2). Cluster 1 was found as the best source for early flowering and high tillering accessions, whereas cluster 2 was found as the good source for late flowering accessions, with tall thick stems long and broad leaves forming an important source of high fodder yield. Cluster 3 was found as promising for panicle and seed traits. Homogeneity of variances of all the traits were tested by Leven's test (Leven, 1960) and were heterogeneous for days to 50% flowering, plant height, productive tillers/plant, leaf blade width, panicle thickness and 1000-seed weight indicating significant differences among the clusters for these traits. Variances

Table 2. Range, mean and variances for different traits of *P. pedicellatum* germplasm assembled and evaluated at ICRISAT genebank

Trait	Entire collection	Cluster 1 (45)	Cluster 2 (29)	Cluster 3 (60)	F value	P	$\delta^2 g$
Range							
Days to 50% flowering.	43-109	43-109	88-107	72-103			
Plant height (cm)	73-248	73-218	192-248	124-217			
Total tillers (no.)	275-2247	500-2247	420-1248	275-1056			
Productive tillers (no.)	114-1261	223-1261	167-742	114-637			
Stem thickness (mm)	2.7-8	2.7-6.4	4.7-8.0	3.5-7			
Leaf blade length (cm)	16-53	16.4-41.7	35.4-53.0	24.5-51.7			
Leaf blade width (cm)	1-2.33	1.0-2.3	1.4-2.4	1.2-2.2			
Panicle length (cm)	10-20	10.4-17	10.4-17	12-20.4			
Panicle thickness (mm)	5-20	4.7-18.4	5-9.7	8.4-20			
Panicle exsertion (cm)	(-)6.7-3.7	(-)6.7-3.7	(-)4.4-3.7	(-)6-3			
1000-Seed weight (g)	0.2-2.1	0.2-2.1	0.3-1.2	0.4-2			
Mean[1]							
Days to 50% flowering.	89±1.0	79.2c	98.2a	92.8b			
Plant height (cm)	181±3.0	153.1c	221.1a	182.9b			
Total tillers (no.)	823±28.0	1095.0a	779.0b	639.5c			
Productive tillers (no.)	420±18.0	579.6a	336.9b	341.4bb			
Stem thickness (mm)	5.1±0.1	4.2c	5.9a	5.4b			
Leaf blade length (cm)	36±1.0	29.1c	41.3a	38.5b			
Leaf blade width (cm)	1.7±0.0	1.5b	1.8a	1.8a			
Panicle length (cm)	15±0.0	13.7b	14.4bb	15.9a			
Panicle thickness (mm)	11±0.0	11.4b	7.5c	13.2a			
Panicle exsertion (cm)	-0.3±0.2	0.2a	-0.1a	-0.8a			
1000-Seed weight (g)	1.1±0.1	1.0b	0.6c	1.5a			
Variance[2]							
Days to 50% flowering.	126.7	138.9	37.4	35.8	6.76	0.002	70.71**
Plant height (cm)	1122.5	993.4	234.4	291.5	9.32	0.0002	515.00**
Total tillers (no.)	104557.6	117690.9	45513.7	34707.4	2.83	0.063	64889.00**
Productive tillers (no.)	41966.9	52220.5	14540.9	19666.7	4.69	0.010	29505.00**
Stem thickness (mm)	1.2	0.8	1.0	0.6	1.45	0.238	0.67**
Leaf blade length (cm)	56.8	37.2	16.2	36.1	0.01	0.989	32.16**
Leaf blade width (cm)	0.1	0.1	0.1	0.1	6.56	0.002	0.05**
Panicle length (cm)	3.3	2.7	2.3	2.0	0.54	0.587	2.28**
Panicle thickness (mm)	14.8	15.6	1.4	10.2	14.02	<0.0001	10.09**
Panicle exsertion (cm)	4.9	4.7	4.7	4.8	1.77	0.175	4.70**
1000-Seed weight (g)	0.3	0.3	0.1	0.1	11.02	<0.0001	0.16**

[1] Means were tested using Newman-Keuls test. Means followed by different letters were significant at p=0.05;
[2] Variances were tested using Leven's test.

for days to 50% flowering, plant height, tillering, stem thickness, leaf blade length, panicle length and width and 1000-seed weight was high in cluster 1. Variance for leaf blade width was similar in all clusters and it was high for panicle exsertion in cluster 3.

Phenotypic Diversity

The Shannon-Weaver diversity index (H`) was calculated to compare phenotypic diversity for nine qualitative and 11 quantitative traits (Table 4). The diversity values (H`) were variable among traits. Among the qualitative traits, fodder yield potential had the highest diversity (H`= 0.696± 0.089) and among quantitative traits, stem thickness had the highest diversity (H`=0.632 ± 0.010). Mean diversity for quantitative traits (H`=0.591 ± 0.010) was higher than that for qualitative traits (H`=0.284 ± 0.089).

Discussion

Increasing the variability by launching germplasm collection missions in unexplored and under explored areas is essential to ensure the availability of large genetic variability to the crop improvement scientists. The activities of genetic resources for cultivated and wild relatives' germplasm are basically same. However, the collection strategy for CWR involve difficulties in identification of geographic distribution of species, precise location, time of maturity etc., which need to be gathered from different floras, herbaria, catalogs, literature and through correspondence. Because, the wild relatives are rather uncommon in natural vegetation and location data are often very old and not precise, it is not always feasible to follow the strategy recommended for the collection of cultivated species. The use of GIS tools to analyze of passport data and corresponding climate data to map the potential distribution of a species is a powerful method to assist germplasm collectors and genebank managers.

FloraMap, a GIS tool is very useful to know the geographical distribution of species and has been useful for identification of geographical gaps in the *P. pedicellatum* collection at ICRISAT genebank in the present study. The probability image developed using FloraMap has indicated a total of 38 provinces in five countries in Asia and a total of 156 provinces in 16 countries in Africa as the important source regions for *P. pedicellatum* germplasm and need exploration (Fig. 2) (Table 1). The probability map generated in the present study matched quite closely to the origin and dispersal of pearl millet supporting the prediction of *P. pedicellatum* occurrence in different regions (Appa

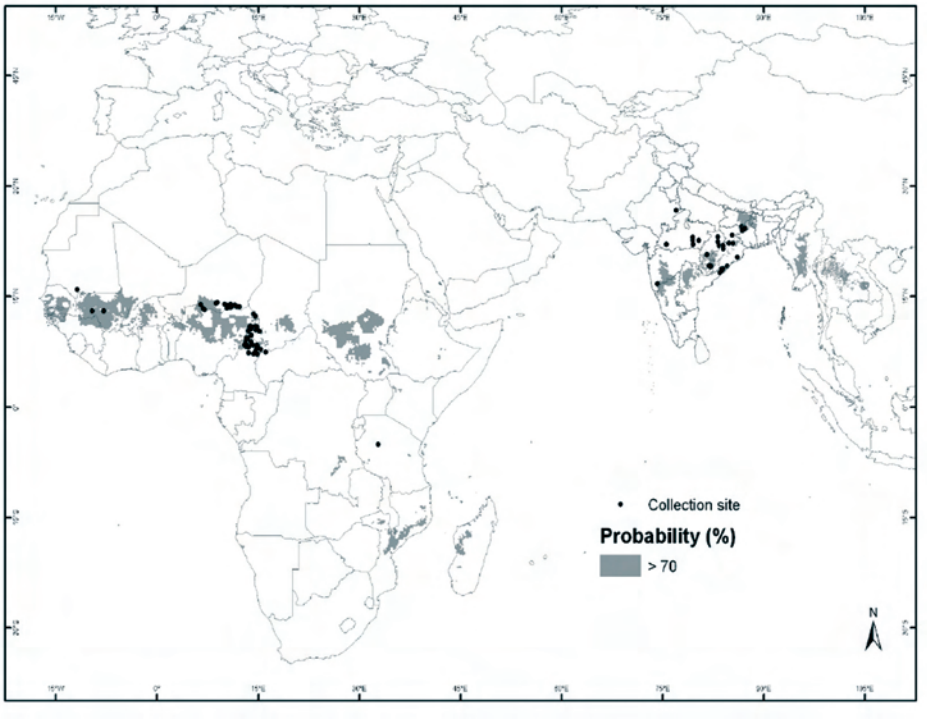

Fig. 2. Geographical distribution of *Pennisetum pedicellatum* collection at ICRISAT genebank and the high (>70%) probability areas of its occurrence (shaded area)

Table 3. Cluster wise *P. pedicellatum* accessions from different countries conserved at the ICRISAT genebank

Cluster No.	Country	IP No.
1	Cameroon	21811, 21812, 21813, 21814, 21816, 21817, 21820, 21821, 21822, 21824, 21832, 21834, 21858, 21859, 21860
	India	21795, 21805, 21806, 21863, 21881, 21883, 21884, 22071, 22074, 22075, 22082, 22085, 22091, 22220
	Mali	21866, 22088
	Mauritania	22148
	Niger	21867, 21868, 21869, 21870, 21871, 21872, 21873, 21874, 21875, 21876, 22092, 22094, 22095
2	Cameroon	21809, 21815, 21828, 21829, 21831, 21838, 21839, 21840, 21842, 21843, 21844, 21845, 21846, 21847, 21848, 21849, 21850, 21851, 21852, 21853, 21854, 21855, 21856, 21857, 21861, 21862
	India	21807
	Mali	21865
	Tanzania	21864
3	C. African Rep.	21803
	Cameroon	21810, 21818, 21819, 21823, 21825, 21826, 21827, 21830, 21833, 21835, 21836, 21837, 21841, 21941, 22090
	India	21789, 21790, 21791, 21792, 21793, 21794, 21796, 21797, 21798, 21799, 21800, 21801, 21802, 21804, 21808, 21877, 21878, 21879, 21880, 21882, 21885, 21886, 21887, 21888, 21889, 21890, 21891, 21892, 21893, 22072, 22073, 22076, 22077, 22078, 22079, 22080, 22081, 22083, 22084, 22086, 22087, 22219
	Niger	22093
	USA	22089

Table 4. Shannon-Weaver diversity (H`) for different traits in *P. pedicellatum* germplasm assembled and characterized at ICRISAT genebank

Trait	Diversity index (H`)
Qualitative traits	
Stem color	0.426
Leaf blade pubescence (P/A)	0.290
Leaf color	0.000
Leaf blade shape	0.375
Panicle shape	0.019
Bristle length (1-9 score)	0.625
FYP (1-9 score)	0.696
Seed shape	0.123
Seed color	0.000
Mean-qualitative traits	0.284
Se±	0.089
Quantitative traits	
Days to 50% flowering	0.589
Plant height (cm)	0.625
Total tillers (no.)	0.556
Productive tillers (no.)	0.563
Stem thickness (mm)	0.632
Leaf blade length (cm)	0.591
Leaf blade width (cm)	0.619
Panicle length (cm)	0.613
Panicle thickness (mm)	0.566
Panicle exsertion (cm)	0.611
1000-Seed weight (g)	0.534
Mean-quantitative traits	0.591
Se±	0.010
Mean-all traits	0.453
Se±	0.053

Rao and de Wet, 1999; Brunken, 1977). Schmelzer (1997) reported the occurrence of *P. pedicellatum* in parts of Cap Verdiane islands, Ethiopia, Tanzania, western and northern Australia. Though, the GIS tools provide precise cartographic representation of eco-geographic regions and of the germplasm collecting sites (Marilia *et al*., 2003), it is important to go through different flora and fauna, catalogs and literature for the distribution of species before embarking on actual germplasm collection. Generally, different species mature at different times. Therefore, the overall knowledge of CWR is essential to collect different species in one collection mission and make the collection mission a success.

Although resistance sources were identified in cultivated germplasm, their resistance could be overcome when the inoculum's levels are high. Singh and Navi (2000) screened 539 accessions of pearl millet wild relatives belonging to 12 species for resistance to downy mildew (*Sclerospora graminicola* (Sacc.) J. Schröt) at ICRISAT, Patancheru and reported that all (129) but two accessions of *P. pedicellatum* as completely free from the disease. Wild species are more important when they possess resistance to biotic and/or abiotic stresses in addition to traits of agronomic importance. Large variation observed for important traits in the *P. pedicellatum* collection is useful in crop improvement programs. Early flowering (43 days) and high tillering (maximum 2,247 total tillers) accessions of cluster 1 were considered as a promising source for early cuttings of green fodder. It can be used for short-term production only due to its poor regeneration capacity (Bhagavandoss *et al*., 1989). *P. pedicellatum* can stand several cuts a

year for green fodder and is generally used as cut-and-carry green forage at ear emergence but it can also be made into silage and hay (Schmelzer, 1997). It responds to nitrogen fertilization and grows well under mixed cropping with cowpea (*Vigna unguiculata*) or rice bean (*Vigna umbellata*) and thus provides optimum quality forage for dairy cattle (Mukerjee *et al*., 1982). On the other hand, Prasad *et al*. (1990) reported highest green fodder yield of 53.30 t/ha and 11.50 t dry fodder/ha by cross-sowing with cowpea. Shukla *et al*. (1988) reported 32.12 t fresh fodder and 6.08 t dry matter/ha by sowing on ridges.

There has been only limited exploitation of wild species in tertiary genepool of pearl millet due to cross incompatibility with the cultigens. Crosses between cultivated pearl millet and *P. pedicellatum* are difficult, but are sometimes possible by using special techniques. Inter-specific crosses usually result in high male and female sterility. Attempts to produce inter-specific hybrids between pearl millet and species of the tertiary genepool using conventional techniques were not successful (Dujardin and Hanna, 1989). If required, recent advances in biotechnology could be used to transfer useful traits from *P. pedicellatum* to cultivated pearl millet (Sharma and Ortiz, 2000). The availability of sources of resistance to downy mildew in the cultivated pearl millet may meet the present requirement, but for future needs of higher levels of resistance, we may have to depend on species of tertiary genepool, particularly on *P. pedicellatum*. Therefore, currently, the need in wild *Pennisetum* research is to adequately and systematically collect the *P. pedicellatum* germplasm representing all areas of its occurrence. When compared with other *Pennisetum* species, *P. pedicellatum* produces more tillers than that of ssp. *monodii*, and grows tall facilitating more green fodder yield in a short period. Of the 12 *Pennisetum* species screened for downy mildew, only *P. pedicellatum* had shown no downy mildew incidence in almost all accessions. In addition, *Pennisetum glaucum* ssp. *monodii* stems are weak and susceptible to lodging. Therefore, early flowering, high tillering habit, tallness and higher levels of resistance to downy mildew makes the *P. pedicellatum* important in future pearl millet research for fodder.

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Analysis of Unique Rice (*Oryza sativa* L.) Germplasm Accessions Using ISSR, SSR and Morphological Markers

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Rice is a major crop grown under all the conditions due to its adaptive nature. Present investigation of genetic diversity analysis was based on 46 selected unique germplasm (based on their morphological and biochemical properties) from IGKV, Raipur and 2 check varieties of rice. Diversity analysis was conducted using ISSR, microsatellite markers and 14 agro-morphological traits. The study revealed that the average polymorphic information content (PIC) value with ISSR markers was 0.85, which ranged from 0.79 (UBC 808) to 0.88 (UBC818). The SSR markers yielded mean PIC value of 0.49, ranging from 0.12 (OSR 13) to 0.74 (RM 1 and RM 20). The similarity coefficient of major clusters ranged from 0.48 to 0.88 (SSR and ISSR) and 0.46 to 0.99 (morphological). Among the 48 unique germplasm, the diversity analysis based on morphological characters showed that *Anterved Jal Ponga*, *Nariyal Phool* and *Ganga Baru* within cluster A were most similar with a similarity coefficient of 0.999. With SSR and ISSR diversity analysis, *Kapoor Sar* and *Chini Kapoor* were most similar with a similarity coefficient of 0.875. *Do Dana Bajrang Bali*, *Chepti Gurmatiya* and *Gathuwan*, *Badshah Bhog* and *Ganga Baru* were highly diverse indicating that these accessions can be used in future breeding program.

Key Words: Genetic diversity, ISSR, Morphological markers, Rice germplasm, SSR

Introduction

Rice is the important crop grown under different environmental conditions. Possibly the oldest domesticated grain (~10,000 years), rice is the staple food for 3 billion people (60% of the world's population) and is the largest single use of land for producing food, covering 9% of the earth's arable land (Nanda, 2000). Rice, a member of the family Poaceae, originated from South-East Asia, where more than 90% of world's rice is produced and consumed (Li and Xu, 2007), making it immensely important for food security of Asia. Out of 24 species of rice, only two species (*O. glabberima* and *O. sativa*) are cultivated. Variation within *O. sativa* is extensive, due to its adaption to a wide range of geographical and ecological niches and climatic regimes.

The understanding and knowledge of genetic variation and genetic similarities present within individuals or populations are useful for the efficient use of genetic resources in a breeding program. There are a number of markers available and used for diversity analysis like RFLP, AFLP, ISSR, SSR, RAPD and morphological *etc*. The majority of simple sequence repeats (SSR) that are present in high or intermediate frequencies in landraces ultimately survive into modern elite cultivars and hybrids (Singh *et al*., 2011). The high resolution power and efficient production of massive amount of SSR data is very useful for genetic diversity analysis and evolutionary studies of crop plants (Yang *et al*., 1994; Struss and Plieske, 1998; Tenzer and Gessler, 1999; Singh *et al*., 2011). The purpose of this study was to analyze the genetic diversity of selected germplasm to evaluate the potential usefulness of germplasm for development of better variety.

Materials and Methods

A total of 46 germplasm accessions from IGKV, Raipur and two check varieties (MTU 1010 and *Mahamaya*) of rice were taken for diversity analysis (Table 1). The germplasm lines represented a care sample of 23,250 accessions held at IGKV, Raipur. Fourteen morphological trait were recorded in 1 to 9 scale (Standard Evaluation System, IRRI) under normal transplanted field condition during *Kharif* 2011 at Research cum Instructional Farm, IGKV, Raipur ($21^0 16'$N and $81^0 36'$E at altitude of 289.6 masl). The morphological characters *viz*., coleoptyle color, early plant vigour, basal leaf sheath color, leaf blade color, leaf pubescence, flag leaf angle, ligule color, ligule shape, collar color, auricle color, stigma color, awning, hull color, seed coat color (kernel) were recorded.

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Table 1. Detail of germplasm used in diversity analysis

S.No.	Name of Germplasm	Accession No.	IC No.	Block	District	State
1	Kadam Phool	K:2382	IC390768	Bijapur	Bijapur	Chhattisgarh
2	Koudi Dhull	K:1849	IC390770	Dharamjaigarh	Raigarh	Chhattisgarh
3	Nariyal Phool	N:796	IC390772	Sarai pali	Mahasamund	Chhattisgarh
4	Do Dana	D:612	IC390777	Bilaspur	Bilaspur	Chhattisgarh
5	Pankhi	P:189	IC390778	Deobhog	Gariyaband	Chhattisgarh
6	Tulsi Manjari	BD:1290	IC390784	Sabour	Bihar	Bihar
7	Badshah Bhog	B:42	NA	Bakwand	Bastar	Chhattisgarh
8	Kari Gilas	K:760	NA	Charama	Kanker	Chhattisgarh
9	Parmal	P:445	NA	Paraswara	Balaghat	Madhya Pradesh
10	Roti	R:299	IC390790	Bastar	Bastar	Chhattisgarh
11	Layacha	L:114	NA	Dongargaon	Durg	Chhattisgarh
12	Hardi Gathi	H:17	NA	Darma	Bastar	Chhattisgarh
13	Bajrang Bali	B:640	IC390796	Bhatapara	Baloda bazar	Chhattisgarh
14	Bokra Mundi	B:2318	IC390797	Deobhog	Gariyaband	Chhattisgarh
15	Kapoor Sar	BD:1364	IC390798	Chhuriya	Rajnandgaon	Chhattisgarh
16	Chini Kapoor	C:459	IC390800	Sarona	Sukma	Chhattisgarh
17	Kali Kamod	BD:680	IC390802	Arang	Raipur	Chhattisgarh
18	Chhatri	BD:444	IC390803	Darba	Gwalior	Madhya Pradesh
19	Atma Shital	BD:293	IC390804	Chhindgarh	Sukma	Chhattisgarh
20	Jira Dhan	BD:575	IC390806	Tilda	Raipur	Chhattisgarh
21	Chinnor	BD:1295	IC390808	Tilda	Raipur	Chhattisgarh
22	Ganga Baru	BD:291	IC390811	Chhindgarh	Sukma	Chhattisgarh
23	Anterved	BD:956	IC390814	Jabera	Damoh	Madhya Pradesh
24	Kubri Mohar	BD:401	IC390816	Magarlod	Dhamtari	Chhattisgarh
25	Chepti Gurmatiya	C:843	IC390817	Chhui khadan	Rajnandgaon	Chhattisgarh
26	Farsa Phool	F:16	IC390821	Koili beda	Kanker	Chhattisgarh
27	Hanuman Langur	H:470	IC390822	Mahasamund	Mahasamund	Chhattisgarh
28	Jal Ponga	J:311	IC390826	Baihar	Balaghat	Madhya Pradesh
29	Suldhan	S:1470	IC390829	Deobhog	Gariyaband	Chhattisgarh
30	Loktimachhi	L:1250	NA	Darma	Bastar	Chhattisgarh
31	Jou Phool	J:333	IC390837	Lailunga	Raigarh	Chhattisgarh
32	Lahsun Bhog	L:985	IC390838	Kunkuri	Jashpur	Chhattisgarh
33	Jhilli	J:384	IC390840	Patthalgaon	Jashpur	Chhattisgarh
34	Shri Kamal	S:663	IC390842	Raipur naikin	Sidhi	Madhya Pradesh
35	Son Banko	S:167	IC390843	Baloda bazar	Baloda bazar	Chhattisgarh
36	Urai Butta	U:9	NA	Kundam	Jabalpur	Madhya Pradesh
37	Safri Deshi	S:99	NA	Masturi	Bilaspur	Chhattisgarh
38	Gathuwan	G:1039	IC390847	Abhanpur	Raipur	Chhattisgarh
39	Maharaji	M:504	IC390850	Ghughari	Mandla	Madhya Pradesh
40	Danwar	D:1363	IC390852	Sarona	Bastar	Chhattisgarh
41	Baisur	B:1611	IC390853	Dongargarh	Rajnandgaon	Chhattisgarh
42	Shital Bhog	S:1684	IC390856	Kunkuri	Jashpur	Chhattisgarh

Contd.....

Table 1. Contd.....

S.No.	Name of Germplasm	Accession No.	IC No.	Block	District	State
43	Vishnu Bhog	V:28	IC390859	Badraf nagar	Balrampur	Chhattisgarh
44	Jal Keshar	J:117	IC390869	Sihore	Jabalpur	Madhya Pradesh
45	Rani Kajar	R:123	IC390873	Tilda	Raipur	Chhattisgarh
46	Nariyal Chudi	N:174	IC390876	Koyalibeda	Kanker	Chhattisgarh
47	MTU 1010*	IET 15644	Krishnaveni × IR 64	Pedigree selection	Maruteru	Andhra Pradesh
48	Mahamaya*	R 320-298 IET 10749	Asha × Kranti	Pedigree selection	IGKV, Raipur	Chhattisgarh

NA= Not Available, * check variety

Molecular studies were carried out at Plant Molecular Biology Laboratory, Department of Genetics and Plant Breeding, IGKV, Raipur, during 2012. DNA was extracted from fresh leaf using MiniPrep method (Doyle and Doyle, 1987). The DNA samples were analyzed using 109 SSR and 14 ISSR primers. PCR amplification for SSR was performed in a total volume of 20 µl and the reaction mixture contained 10 X Assay buffer, 1 mM dNTP mix, 5 pM forward and reverse primers, 40 ηg of template DNA and 1 unit Taq polymerase. Reaction mixture was amplified using 96-well Veriti Applied Biosystems thermal cycler, USA. After an initial denaturation step of 95^0C for 5 min, the amplification was carried out for 34 cycles comprising 1 min each of 94^0C of denaturation, 55^0C of annealing and 72^0C of extension. The final elongation step was extended to 7 min at 72^0C followed by storage at 4^0C. After the PCR reaction was completed, 5 µl of 6 X loading dye was added to PCR reaction and 7 µl (PCR reaction with dye) was loaded on 5 % PAGE in a vertical gel electrophoresis system (CBS scientific, model MGV-202-33, USA) with 180V for 1.5 hours. Gel was then stained with ethidium bromide and DNA fragments were visualized with a UV transilluminator Bio-rad XR+ manufactured from USA (Fig. 1).

PCR amplification for ISSR was performed in a reaction volume of 25 µl containing 4 µl DNA (40 ng/µl), 2.5 µl 10X Buffer, 2 µl 1 mM dNTPs (dATP, dCTP, dTTP, dGTP), 1.75 µl 5 pM Primer, and 0.75 µl Taq polymerase (1 Unit). Amplification was carried out in a Veriti® thermal cycler (Applied Biosystems, USA) as follows: 1 cycle of 2 minutes at 95^0C, 35 cycles of 30 seconds at 95^0C, 35 cycles of 60 seconds at varying temperature, 35 cycles of 1.30 min at 72^0C, 1 cycle of 15 min at 72^0C and then stored at 4^0C. 4 µl BPB Dye/25 µl PCR reaction were mixed and loaded in 5 % PAGE gel and run at 120V for 2 h. After proper run gels were stained with ethidium bromide (EtBr) solution and gel images were recorded in Bio-Rad, Gel DOC unit manufactured from USA, under UV light (Fig. 2).

Specific amplification products were scored as present (1) or absent (0) depending on increasing order of their molecular weights of each DNA sample. Diversity analysis was done using NTSYSpc-2.02 software (Numerical Taxonomy System Biostatistics) and dendrogram was generated (Rohlf, 2000). The similarity matrix (SM) was generated with similarity coefficient for SSR, ISSR markers and morphological characters and cluster analysis was done using the SM similarity coefficient, with UPGMA (unweighted pair-group method with arithmetic averages) method. The polymorphism information content (PIC) value of SSR markers was calculated using the following formula (Anderson *et al*., 1993).

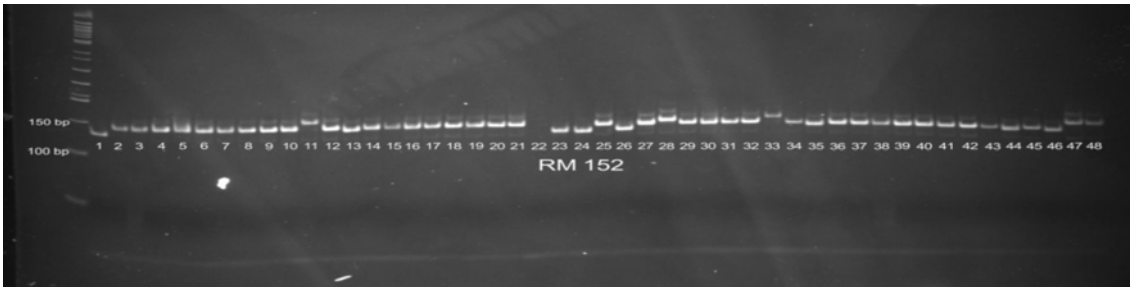

Fig. 1. SSR profile generated by microsatellite primer RM 152 of 48 germplasm (1-48 labels are as per the germplasm given in Table 1)

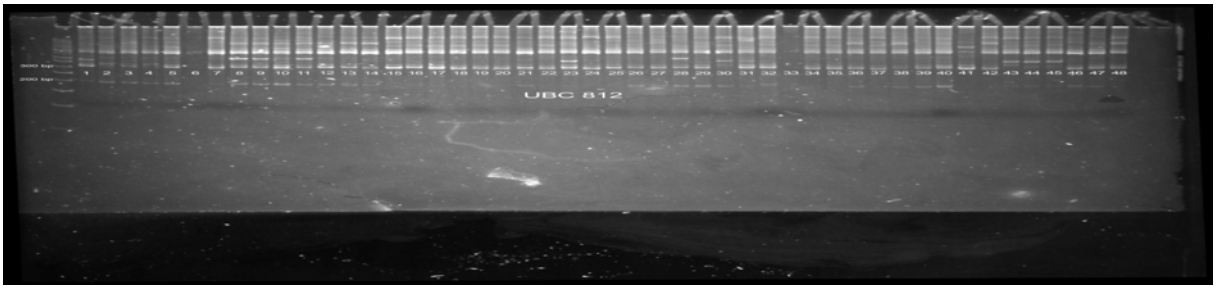

Fig. 2. ISSR profile of 48 germplasm generated by UBC 812 primer (1-48 labels are as per the germplasm given in Table 1)

$$PIC = 1 - \sum_{i=1}^{k} Pi^2$$

where, k is the total number of alleles (bands) detected for one SSR/ISSR locus and P_i is the frequency of the i^{th} allele (band) in all the samples analyzed.

Results and Discussion

Molecular diversity study using SSR and ISSR

Out of 109 SSR markers used in the study, 54 were polymorphic and produced a total of 160 alleles (Table 2). The number of alleles varied from 2 to 6 with an average of 2.96 polymorphic alleles per primer. Out of 54 primers 22, 19, 8, 3, and 2 primers showed 2, 3, 4, 5, and 6 alleles, respectively. RM 552 and RM 207 showed maximum 6 alleles, RM 341, RM 20 and RM showed 5 alleles. RM 224 and RM 208 showed similar allele and RM 1, RM 144, RM 25 and RM 242 showed dissimilar allele than earlier reported allele by Singh *et al.* (2011) for the same markers. The average PIC value was calculated 0.49 and which ranged from low of 0.12 (OSR 13) to a high of 0.74 (RM 1 and RM 20). Markers showing high PIC value are associated with higher level of polymorphism and therefore, more important.

Out of 14 ISSR primers used, 8 primers generated a total of 76 bands which were scored for determining the genetic relationship among genotypes (Table 3). UBC 812 showed maximum 12 bands and UBC 808 and UBC 810 showed minimum 7 bands. Average number of polymorphic bands per primer was 9.5. The average PIC value was calculated 0.85 and which ranged from low of 0.79 (UBC 808) to a high of 0.88 (UBC818).

Table 2. SSR markers used in diversity analysis

S.No.	Markers	Forward sequence (5' -------->3')	Reverse sequence (5' --------->3')	Ch #	No. of allele	PIC
1	RM 1	GCGAAAACACAATGCAAAAA	GCGTTGGTTGGACCTGAC	1	5	0.74
2	RM 5	TGCAACTTCTAGCTGCTCGA	GCATCCGATCTTGATGGG	1	3	0.64
3	RM 11	TCTCCTCTTCCCCCGATC	ATAGCGGGCGAGGCTTAG	7	3	0.55
4	RM 17	TGCCCTGTTATTTTCTTCTCTC	GGTGATCCTTTCCCATTTCA	12	3	0.48
5	RM 19	CAAAAACAGAGCAGATGAC	CTCAAGATGGACGCCAAGA	12	3	0.61
6	RM 20	ATCTTGTCCCTGCAGGTCAT	GAAACAGAGGCACATTTCATTG	12	5	0.74
7	RM 25	GGAAAGAATGATCTTTTCATGG	CTACCATCAAAACCAATGTTC	8	3	0.59
8	RM 44	ACGGGCAATCCGAACAACC	TCGGGAAAACCTACCCTACC	8	2	0.50
9	RM 55	CCGTCGCCGTAGTAGAGAAG	TCCCGGTTATTTTAAGGCG	3	2	0.50
10	RM 105	GTCGTCGACCCATCGGAGCCAC	TGGTCGAGGTGGGGATCGGGTC	9	2	0.47
11	RM 106	CGTCTTCATCATCGTCGCCCCG	GGCCCATCCCGTCGTGGATCTC	2	2	0.31
12	RM 116	TCACGCACAGCGTGCCGTTCTC	CAAGATCAAGCCATGAAAGGAGGG	11	2	0.49
13	RM 120	CACACAAGCCCTGTCTCACGACC	CGCTGCGTCATGAGTATGTA	11	2	0.49
14	RM 125	ATCAGCAGCCATGGCAGCGACC	AGGGGATCATGTGCCGAAGGCC	7	3	0.49

Contd.....

Table 2. Contd.....

S.No.	Markers	Forward sequence (5' -------->3')	Reverse sequence (5' --------->3')	Ch #	No. of allele	PIC
15	RM 144	TGCCCTGGCGCAAATTTGATCC	GCTAGAGGAGATCAGATGGTAGTGCATG	11	4	0.70
16	RM 152	CCGTAGACCTTCTTGAAGTAG	GAAACCACCACACCTCACCG	8	3	0.29
17	RM 161	TGCAGATGAGAAGCGGCGCCTC	TGTGTCATCAGACGGCGCTCCG	5	2	0.46
18	RM 178	TCGCGTGAAAGATAAGCGGCGC	GATCACCGTTCCCTCCGCCTGC	5	2	0.44
19	RM 207	CCATTCGTGAGAAGATCTGA	CACCTCATCCTCGTAACGCC	2	6	0.67
20	RM 208	TCTGCAAGCCTTGTCTGATG	TAAGTCGATCATTGTGTGGACC	2	2	0.38
21	RM 214	CTGATGATAGAAACCTCTTCTC	AAGAACAGCTGACTTCACAA	7	4	0.36
22	RM 221	ACATGTCAGCATGCCACATC	TGCAAGAATCTGACCCGG	2	3	0.45
23	RM 222	CTTAAATGGGCCACATGCG	CAAAGCTTCCGGCCAAAAG	10	3	0.53
24	RM 224	ATCGATCGATCTTCACGAGG	TGCTATAAAAGGCATTCGGG	11	2	0.46
25	RM 231	CCAGATTATTTCCTGAGGTC	CACTTGCATAGTTCTGCATTG	3	4	0.69
26	RM 234	ACAGTATCCAAGGCCCTGG	CACGTGAGACAAAGACGGAG	7	2	0.44
27	RM 242	GGCCAACGTGTGTATGTCTC	TATATGCCAAGACGGATGGG	9	2	0.33
28	RM 247	TAGTGCCGATCGATGTAACG	CATATGGTTTTGACAAAGCG	12	3	0.63
29	RM 248	TCCTTGTGAAATCTGGTCCC	GTAGCCTAGCATGGTGCATG	7	4	0.67
30	RM 268	GTGCTATGCACGATCCATAGCA	CGTTTCTTTGGAAGCGGAGGGA	2	3	0.44
31	RM 277	CGGTCAAATCATCACCTGAC	CAAGGCTTGCAAGGGAAG	12	2	0.47
32	RM 278	GTAGTGAGCCTAACAATAATC	TCAACTCAGCATCTCTGTCC	9	2	0.16
33	RM 281	ACCAAGCATCCAGTGACCAG	GTTCTTCATACAGTCCACATG	8	3	0.44
34	RM 298	CTGATCACTGGATCGATCATG	CATGCCAAGATGCAACAG	7	3	0.43
35	RM 341	CAAGAAACCTCAATCCGAGC	CTCCTCCCGATCCCAATC	2	5	0.70
36	RM 348	CCGCTACTAATAGCAGAGAG	GGAGCTTTGTTCTTGCGAAC	4	2	0.16
37	RM 403	GCTGTGCATGCAAGTTCATG	ATGGTCCTCATGTTCATGGC	1	4	0.64
38	RM 408	CAACGAGCTAACTTCCGTCC	ACTGCTACTTGGGTAGCTGACC	8	2	0.47
39	RM 411	ACACCAACTCTTGCCTGCAT	TGAAGCAAAAACATGGCTAGG	3	2	0.32
40	RM 433	TGCGCTGAACTAAACACAGC	AGACAAACCTGGCCATTCAC	8	2	0.48
41	RM 444	GCTCCACCTGCTTAAGCATC	TGAAGACCATGTTCTGCAGG	9	3	0.61
42	RM 447	CCCTTGTGCTGTCTCCTCTC	ACGGGCTTCTTCTCCTTCTC	8	4	0.52
43	RM 454	CTCAAGCTTAGCTGCTGCTG	GTGATCAGTGCACCATAGCG	6	2	0.30
44	RM 474	AAGATGTACGGGTGGCATTC	TATGAGCTGGTGAGCAATGG	10	4	0.66
45	RM 484	TCTCCCTCCTCACCATTGTC	TGCTGCCCTCTCTCTCTCTC	10	3	0.23
46	RM 495	AATCCAAGGTGCAGAGATGG	CAACGATGACGAACACAACC	1	3	0.47
47	RM 506	CGAGCTAACTTCCGTTCTGG	GCTACTTGGGTAGCTGACCG	8	2	0.49
48	RM 533	GCAACTGCTCTACGCCTCTC	CCTGAGGCTTCACCTACTCG	7	3	0.51
49	RM 536	TCTCTCCTCTTGTTTGGCTC	ACACACCAACACGACCACAC	11	2	0.35
50	RM 540	GCCTTCTGGCTCATTTATGC	CTAGGCCTGCCAGATTGAAC	6	3	0.45
51	RM 552	CGCAGTTGTGGATTTCAGTG	TGCTCAACGTTTGACTGTCC	11	6	0.72
52	RM 566	ACCCAACTACGATCAGCTCG	CTCCAGGAACACGCTCTTTC	9	3	0.63
53	RM 3825	AAAGCCCCCAAAAGCAGTAC	GTGAAACTCTGGGGTGTTCG	1	4	0.70
54	OSR 13	CATTTGTGCGTCACGGAGTA	AGCCACAGCGCCCATCTCTC	3	2	0.12

The dendogram generated by UPGMA method indicated that all the 48 genotypes were grouped into two sub-clusters A and B. The major cluster A consisting of 42 genotypes and sub-clustering near the 0.490 similarity level. The other major cluster B consisted of 6 genotypes having 0.485 similarities coefficient with cluster A and sub clustering near the 0.505 similarity level (Fig. 3). The similarity coefficient ranged from 0.48 to 0.88. Germplasm *Kapoor Sar* and *Chini Kapoor* within cluster A were most similar with a similarity coefficient of 0.875 and germplasm *Badshah Bhog* and Ganga *Baru* were the least similar with similarity

Table 3. ISSR markers used in diversity analysis

S.No.	Markers	Primer sequence	No. of amplicons generated	TM (^{o}C)	Fragment size (bp)	No. of bands	PIC
1	UBC 807	AGAGAGAGAGAGAGAGT	17	53	300-1000	10	0.87
2	UBC 808	AGAGAGAGAGAGAGAGC	17	49	300-750	7	0.79
3	UBC 809	AGAGAGAGAGAGAGAGG	17	52	250-800	10	0.86
4	UBC 810	GAGAGAGAGAGAGAGAT	17	52-53	200-900	7	0.84
5	UBC 812	GAGAGAGAGAGAGAGAA	17	50	200-900	12	0.84
6	UBC 818	CACACACACACACACAG	17	52	250-1000	10	0.88
7	UBC 834	AGAGAGAGAGAGAGAGAT	18	50	380-850	11	0.85
8	UBC 836	AGAGAGAGAGAGAGAGGA	18	50	330-900	9	0.85

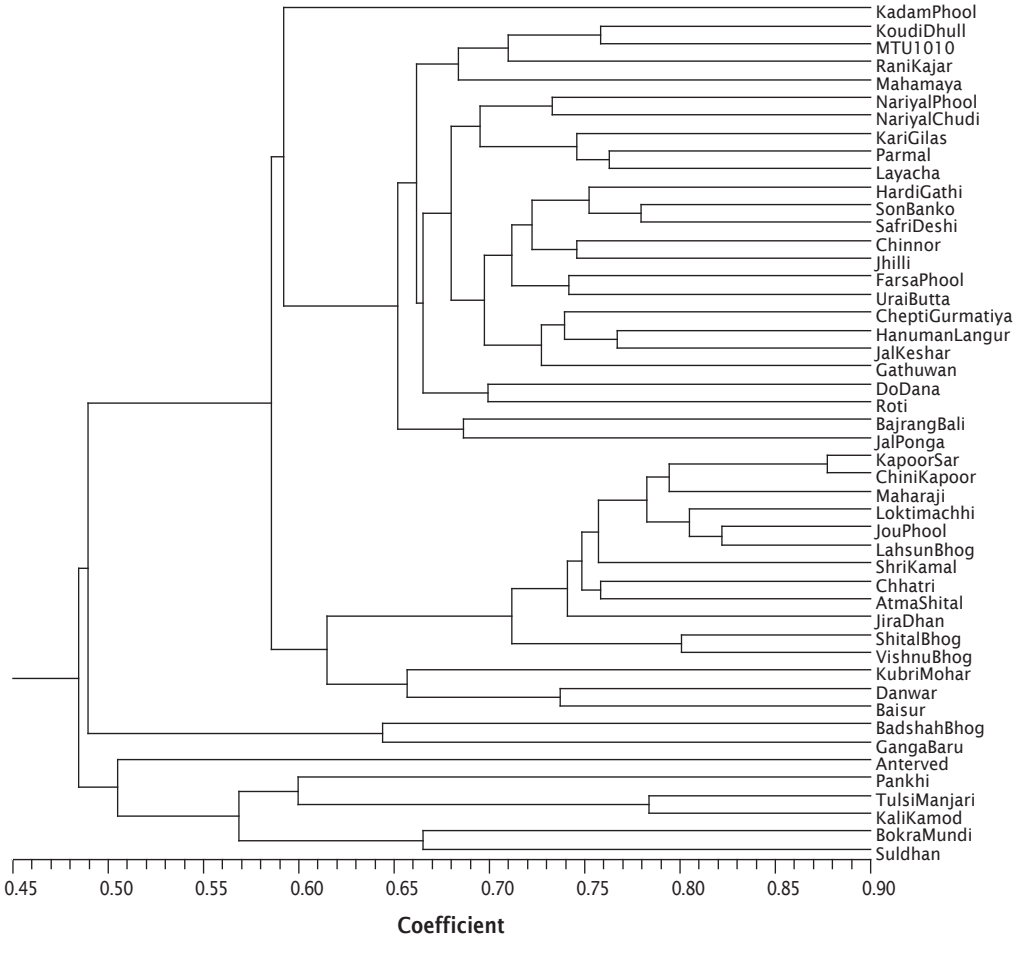

Fig. 3. Dendrogram constructed using UPGMA based on SM coefficient of 48 germplasm (SSR and ISSR markers) (A= Cluster A, B= Cluster B)

coefficient of 0.643. This study reveals the similarity and dis-similarity pattern between the germplasm accessions. The entries having high similarity shows that they have common genes in their ancestry whereas, the dissimilar ones clearly distinguish that these entries are of diverse nature (Thomson *et al*., 2007).

Morphological diversity

Fourteen morphological traits were recorded in 0-9 scale for diversity analysis. Similarity coefficient ranged from 0.460 to 0.999 for morphological based diversity. The dendogram indicates that there was a major cluster A consisting of 40 genotypes, showing sub clustering near the 0.518 similarity level. The other major cluster B consisted of 8 genotypes having 0.485 similarities coefficient with cluster A and clustering near 0.512 similarity level (Fig. 4). Germplasm *Anterved* and *Jal Ponga*, *Nariyal Phool* and *Ganga Baru* within cluster A were most similar with a similarity coefficient of 0.999 and germplasm *Do Dana* and *Bajrang Bali*, *Chepti Gurmatiya* and *Gathuwan* within cluster B were the least similar with similarity coefficient of 0.692.

The comparative analysis of SSR, ISSR and agro-morphological markers indicates that *Kadam Phool*, *Jal Ponga*, *Koudi Dhull*, *Hardi Gathi*, *Nariyal Phool*, *Ganga Baru*, *Kapoor Sar*, *Jouphool*, *Lahsun Bhog*, *Layacha*, *Hanuman Langur*, *Tulsi Prasad*, *Safri Desi*, *Chini Kapoor*, *Kubri Mohar*, *Jira Dhan*, *Sonbanko*, *Chinnor*, *Jhilli*, *Loktimachhi*, *Nariyal Chudi*, *Atmashital*, *Maharaji*, MTU1010, *Vishu Bhog*, *Rani Kajar*, *Badsah Bhog*, *Shital Bhog*, *Baisur*, *Chhatri*, *Mahamaya*, *Shri Kamal*, *Parmal*, *Farsa Phool* and *Roti* were common in cluster A using all the markers mentioned above.

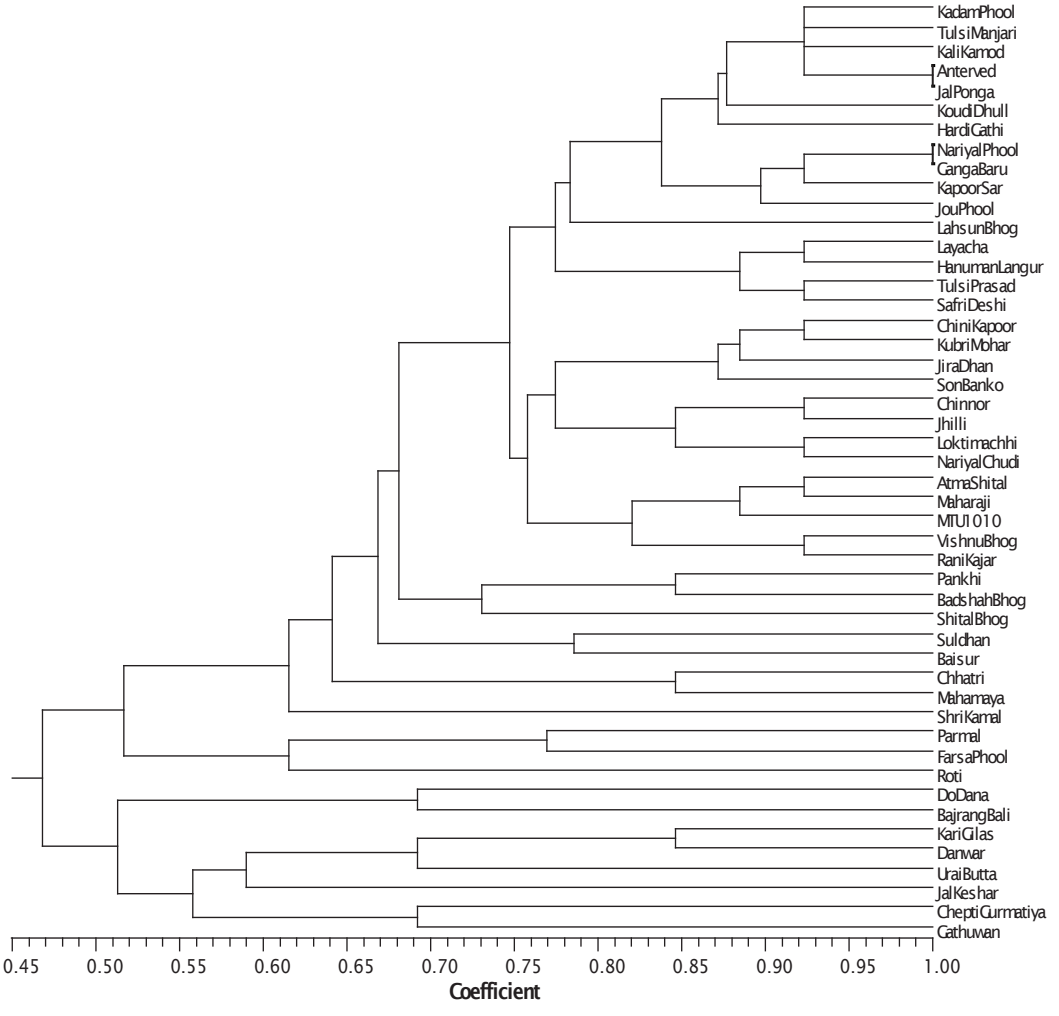

Fig. 4. Dendrogram constructed using UPGMA based on SM coefficient of 48 germplasm (Morphological markers) (A= Cluster A, B= Cluster B)

Conclusions

The local germplasm of rice used in the present study showed a lot of potential for various traits and hence, could be used for further improvement for incorporating certain important and valuable traits. Based on diversity analysis germplasm, *Do Dana* and *Bajrang Bali*, *Chepti Gurmatiya* and *Gathuwan*, *Badshah Bhog* and *Ganga Baru* were least similar so that these combination can be further utilized for developing better varieties.

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Evaluation of Indigenous and Exotic Germplasm of Indian Mustard [*Brassica juncea* (L.) Czernj & Cosson] for Morpho-Physiological and Quality Characters

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Sixty germplasm accessions from India (27), Australia (25) and China (8) along with 5 check varieties (Bio-902, Bio-772, PCR-7, Rohini and Varuna) of Indian mustard [*Brassica juncea (*L.) Czernj. & Cosson] were grown in an augmented block design with four blocks during *rabi* season of 2007-08 to assess magnitude and nature of variability for morpho-physiological and quality characters. Significant mean sum of squares due to genotypes indicated presence of substantial variability for all the morpho-physiological characters investigated except protein content. Seed yield/plant, secondary branches/plant, biological yield, 1000-seed weight, specific leaf weight at 50% and full flowering, leaf area index at full flowering and total dry matter at 50% flowering had high genetic variability and could be exploited through selection. The Chinese accessions were very late in maturity due to fact that they were selected under long day conditions and no seed could be harvested. Indian varieties such as GM-2, RGN-13, JM-3, VSL-5 and Australian accession JM-018 showed very low saturated fatty acids (<2 %). Oleic acid content in the indigenous germplasm was low varying from 6.0-18.1 % and all had high erucic acid in the range of 31.5% (Basanti)-52.5% (GM-2). The Australian accessions exhibited low erucic acid (< 2 %) and high oleic acid (29.7-58.4%). Glucosinolate content in the indigenous germplasm ranged from 75-136.6 µ moles/g defatted seed meal. In the Australian accessions it was up to 30 µ moles/g defatted seed meal. Several potentials accessions were identified from exotic as well as indigenous germplasm for utilization in the breeding programme.

Key Words: *Brassicca juncea*, Genetic resources, Indian mustard, Physiological characters, Promising accessions, Quality characters, Variability

Introduction

Genetic resources of any crop species constitute the reservoirs of new and valuable genes, which could be of immense help in the varietal improvement programme. The precise evaluation of genetic resources of rapeseed-mustard would play a pivotal role in breeding programme by continuously providing new genes for the target character(s). Valuable donors for various biotic, abiotic stresses, agro-morphological characters have been identified among the indigenous Indian mustard germplasm (Chauhan *et al.*, 2005, 2006; Misra *et al.*, 2007). However, limited variability existed for oil and seed meal quality characters. Exotic Indian mustard germplasm from Canada, China and Australia were reported to possess low erucic, high oleic and low glucosinolate content (Chauhan and Kumar, 2007). Furthermore, use of exotic germplasm along with indigenous ones often results in the increased genetic variability for desired selection. Khalf *et al.* (1984) reported that there was greater variability for yield in populations where exotic genotypes contributed to the crosses. The present investigation attempts to assess the magnitude and nature of variability, heritability and genetic advance in indigenous and exotic germplasm of Indian mustard for morpho-physiological, oil and seed meal quality characters.

Materials and Methods

The materials for the present investigation comprised 60 germplasm accessions from India (27), Australia (25), China (8) and 5 check varieties of Indian mustard [*Brassica juncea* (L.) Czernj & Cosson]. There were grown in an augmented block design (Federer, 1956) with 4 blocks during *rabi* season of 2007-2008. In each block, 15 accessions and 5 checks were grown. There were 3 rows of 5 m length for each accession in a block. The row spacing was 30 cm and plant spacing within a row was maintained at 10 cm by thinning. A fertilizer dose of 40: 40: 20 kg/ha (N: P_2O_5: K_2O) was applied at the time of sowing and 40 kg N/ha was applied after first irrigation (36 days after sowing). Second irrigation was

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applied at 72 days after sowing. Standard plant protection measures were adopted as and when required.

To study different growth parameters, plant samples from 30 cm running length were harvested above ground level at 50% flowering and full flowering stages. The shoot and leaves were separated and leaf area was recorded by leaf area meter (LICOR: LI 3000 A). Shoot and leaves were dried in an oven ($65^o \pm 2^o$ C) for at least 72 h till constant weight was achieved. The samples were weighed and total dry matter (TDM) of leaves, shoot as well as shoot + leaves was expressed in g/m^2. Fourth fully expanded leaf from the top was chosen from three randomly selected plants in each block for recording photosynthesis and transpiration by photosynthesis system (CIRAS-2). On the same leaves chlorophyll meter readings (SCMR) were recorded by SPAD chlorophyll meter (Konica Minolta: SPAD-502). Leaf area index (LAI) and specific leaf weight (SLW) were computed using leaf area and dry weight of leaves (Radford, 1967). Transpiration quotient (TQ) was measured as ratio of transpiration to photosynthesis.

Days to maturity (DM) were recorded on plot basis. At the time of harvest, 10 randomly competitive plants were taken from the middle row to record plant height (PH, cm), primary branches/plant (PB, no.), secondary branches/plant(SB, no.), main shoot length (MSL, cm), siliquae on main shoot (SMS, no.), siliqua length (SL, cm),seeds/siliqua (SS, no.), 1000-seed weight (SW, g), seed yield/plant (SY, g), biological yield/plant (BY, g) and harvest index (HI, %). Oil (OC) and protein content (PC) were recorded on a composite sample of 10 plants taken for recording observations on seed yield and related characters using NIRS (Kumar *et al*., 2003). Two plants were selfed in each accession and seeds were harvested separately. The fatty acid profile was analysed using selfed seeds (Paquot and Hautfenne, 1987) and open-pollinated seeds of the same plant was used for glucosinolate analysis (Kumar *et al*., 2004).

The mean data for agro-morphological and physiological characters were subjected for analysis of variance of an augmented block design as suggested by Federer (1956). The data were analyzed using software *SPAD* (IASRI, New Delhi). Genotypic and phenotypic coefficients of variation, heritability (in broad-sense) and genetic advance expressed as percentage of mean were computed following Johnson *et al.* (1955), Hanson *(*1963) and Lush (1949), respectively.

Results and Discussion

The ANOVA indicated significant differences among the checks for DM and BY and highly significant differences for PH, SB, MSL, SMS, SL, SW, SY and OC. The analysis of variance also revealed highly significant differences among the test genotypes for DM, PH, SB, MSL, SMS, SL, SW, SY, HI and OC. The mean sum of squares due to genotypes for BY was significant. The mean sum of squares due to checks *vs* test genotypes were highly significant for PH, SB, MSL, SL, SW, OC and PC. The differences among the checks *vs* test genotypes were significant for BY and SY (Table 1).

Table 1. Analysis of variance for seed yield and morphological characters in Indian mustard (recorded on 35 entries and 5 checks)

Source of variation	DF	Mean sum of squares						
		DM	PH	SB	MSL	SMS	SL	SW
Block	3	1.517	126.102*	4.305	24.994	13.012	0.011	0.157*
Entries	59	3.798**	278.764**	20.792**	84.637**	49.041**	0.243**	0.557**
Checks	4	3.700*	842.47**	15.733**	156.534**	125.213**	0.120**	5.709**
Test genotypes	54	3.863**	238.067**	21.140**	65.945**	43.962**	0.203**	1.000**
Checks vs test genotypes	1	0.875	99.458**	23.25**	750.320**	3.413	0.740**	13.348**
Error	12	0.933	29.283	2.256	20.357	10.656	0.025	0.039
Critical difference (CD)		–	13.95	3.87	11.63	–	0.41	0.51
Genotypes vs checks		–	**19.56**	**5.43**	**16.31**	–	**0.57**	**0.72**
Checks vs checks		1.49	8.34	2.31	6.95	5.03	0.25	0.31
		2.08	**11.69**	**3.24**	**9.75**	**7.05**	**0.34**	**0.43**
Genotypes within same block		2.98	16.68	4.63	13.90	10.06	0.49	0.61
		4.17	**23.38**	**6.49**	**19.49**	**14.10**	**0.69**	**0.86**
Genotypes in different blocks		3.26	18.27	5.07	15.23	11.02	0.54	0.67
		4.57	**25.61**	**7.10**	21.35	**15.45**	**0.75**	**0.94**

Cont ....

Table 1. Cont ....

Source of variation	DF	Mean sum of squares				
		BY	SY	HI	OC	PC
Block	3	573.366*	30.855**	20.787	0.181	0.703*
Entries	56	349.157*	25.665**	32.735**	1.104**	0.448*
Checks	4	489.699*	20.048**	14.538	1.305**	0.327
Test genotypes	51	327.964*	25.966**	34.680**	1.052**	0.365
Checks vs test genotypes	1	867.827*	32.745*	6.306	2.916**	5.152**
Error	12	128.437	5.47	6.735	0.293	0.163
Critical difference (CD)		29.22	6.03	-	1.40	1.04
Genotypes vs checks		**40.97**	**8.46**	-	**1.96**	**1.46**
Checks vs checks		17.46	3.60	-	0.84	0.62
		24.48	**5.05**	-	**1. 17**	**0.87**
Genotypes with in same block		34.92	7.21	8.00	1.67	1.25
		48.96	**10.11**	**11.21**	**2.34**	**1.75**
Genotypes in different blocks		38.26	7.90	8.76	1.83	1.37
		53.64	**11.07**	**12.28**	**2.57**	**1.91**

*, ** Significant at 5% and 1% probability level, respectively, Values in light and bold face indicate CD at 5% and 1% probability level, respectively.

The checks also showed highly significant differences for SLW and SCMR and significant differences for TQ at 50% flowering. The genotypic differences were highly significant for SLW at 50% and full flowering, total dry matter (TDM) at full flowering. There were significant differences for LAI at full flowering and TQ at 50% and full flowering and SCMR at 50% flowering. The genotypes had significant differences for TQ at full flowering (Table 2). The test genotypes had significant to highly significant differences from the checks for all the physiological characters except TQ at full flowering, TDM and SCMR at 50% flowering. The significant mean sum of squares indicated presence of substantial variability in the experimental materials for all the morpho-physiological characters investigated except protein content.

The experimental materials showed high genotypic and phenotypic variability for seed yield/plant, secondary branches/plant, biological yield/plant, 1000-seed weight, specific leaf weight at 50% and full flowering, LAI at full flowering and TDM/plant at 50% flowering. The harvest index, main-shoot length, siliquae on main shoot, siliqua length and transpiration quotient at full flowering also exhibited moderate genetic variability (Table 3). The findings of the present investigation confirmed the earlier reports of high variability for 1000-seed weight, siliquae on main shoot, seed yield/plant (Meena *et al.*, 2006; Patel *et al.*, 2006), total biomass and harvest index (Singh *et al.*, 2006); secondary branches/plant (Meena *et al.*, 2006). Low variability as observed in the present investigation for days to maturity, plant height and oil content were also recorded by Misra *et al*. (2007). But Sikarwar *et al.* (2000) observed low variability for primary and secondary branches/plant and Meena *et al.* (2000) reported high variability for days to maturity. Variable trend of genetic variability in the present study and the earlier reports could be due to differential genetic background of the experimental materials and/or genotype x environmental (g x e) interactions. No published report dealing with genotypic variation for physiological characters in Indian mustard was available to support or contradict the findings of the present investigation. Presence of moderate to high genetic variability in morpho-physiological characters recorded in the present investigation could be exploited through selection.

The Chinese accessions were very late in maturity, flowering was initiated in mid-February and seeds could not be harvested. This could be due to fact that they were selected under long day conditions in China. As a matter of fact some of the accessions like Berry (EC597329), Loiret (EC597326) and Ekla (EC597327) appeared to be introduced from Canada to China. In earlier studies, similar trend of maturity and segregation

Table 2. Analysis of variance for some physiological characters in Indian mustard (recorded on 35 entries including 5 checks)

Source of variation	Mean sum of squares							
	DF	LAI	SLW		TDM	TQ		SCMR
		Full flowering	50% flowering	Full flowering	50% flowering	50% flowering	Full flowering	50% flowering
Block	3	0.113	0.834	7.827**	3. 673	0.006**	0.0029	4.266
Entries	34	0.983*	4.453**	2.963**	52.848**	0.006	0.0027*	6.447**
Checks	4	0.744	4.314**	0.874	21.107	0.006*	0.0009	26.008**
Test genotypes	29	0.993*	4.594**	3.026**	58.803**	0.005*	0.0030*	3.870*
Checks vs test genotypes	1	3.236**	1.676*	8.143**	16.079	0.003**	0.0049	2.889
Error	12	0.373	0.304	0.850	11.177	0.001	0.0011	1.484
Critical difference (CD)		1.57	1.42	2.37	8.61	0.033	–	–
Genotypes *vs* checks		**2.20**	**1.99**	**3.33**	**12.08**	**0.047**	–	–
		–	0.85	–	–	0.020	–	1.87
Check vs check		–	**1.19**	–	–	**0.028**	–	**2.63**
		1.88	1.70	2.84	10.30	0.040	0.010	3.75
Genotypes within same block		**2.64**	**2.38**	**3.98**	**14.44**	**0.056**	**0.14**	**5.26**
		2.06	1.86	3.11	11.28	0.044	0.11	4.11
Genotypes in different blocks		**2.89**	**2.61**	**4.36**	**15.82**	**0.062**	**0.16**	**5.76**

*, ** Significant at 5 % and 1 % probability level, respectively, Values in light and bold face indicate CD at 5 % and 1 % probability level, respectively.

Table 3. Range, mean, phenotypic (PCV) and genotypic (GCV) coefficient of variability for morpho-physiological characters in Indian mustard

Character	Range	Mean ± SEM	PCV (%)	GCV (%)
Days to maturity	133.6 - 143.6	141.0 ± 1.0	1.4	1.2
Plant height (cm)	126.0 - 200.4	165.0 ± 5.4	9.4	8.8
Secondary branches/plant (no.)	3.0 - 28.8	11.9 ± 1.5	38.8	35.5
Main shoot length (cm)	37.2 - 75.8	62.2 ± 4.5	13.0	11.2
Siliquae on main shoot (no.)	33.3 - 64.1	45.9 ± 3.3	14.4	12.6
Siliqua length (cm)	2.2 - 4.4	3.6 ± 0.2	12.7	12.3
1000- seed weight (g)	1.8 - 6.4	3.8 ± 0.2	26.2	25.7
Biological yield / plant (g)	11.3 - 101.0	56.4 ± 11.3	32.0	26.1
Seed yield/plant (g)	2.7 - 24.9	15.0 ± 2.3	33.9	31.0
Harvest index (%)	15.2 - 39.1	27.0 ± 2.6	21.8	19.4
Oil content (%)	36.1 - 41.2	38.8 ± 0.5	2.6	2.2
LAI - Full flowering	0.70 – 4.8	2.33 ± 0.61	41.4	29.3
SLW (mg/cm^2) - 50% flowering	1.5 – 12.8	3.73 ± 0.55	57.4	53.2
Full flowering	3.2 – 10.4	6.40 ± 0.92	27.2	24.4
TDM/plant (g) 50% flowering	4.8- 35.8	13.51 ± 3.34	56.8	49.4
TQ (m moles/µ mole) -50% flowering	0.23-0.38	0.34 ± 0.01	6.5	5.4
Full flowering	0.27- 0.56	0.37 ± 0.03	14.7	11.7
SCMR - 50% flowering	44.24 – 52.10	47.23 ± 1.21	4.2	3.3

Table 4. Promising Accessions identified for seed yield and physiological characters

Character	Best Check	Accessions				
Days to maturity (< 139 days)	PCR-7 (139)	Kranti	JM-06011 (EC-597316)	JM-06004 (EC-597312)	JM- 06010 (EC-597315)	JM- 06002 (EC-597310)
Plant height (< 165 cm)	Varuna (164.5)	JM-06014 (EC-597319)	JM- 06013 (EC-597318)	JM- 06012 (EC-597317)	JM- 06018 (EC-597321)	JM- 06011 (EC-597316)
Secondary branches/plant (>12.8)	Varuna (12.8)	JM- 06002 (EC-597310)	JM- 06003 (EC-597311)	JM- 06019 (EC-597322)	Ashirwad	RGN- 13
Main shoot length (>71.5 cm)	Varuna (71.5)	JM- 1	VSL - 5	Ashirwad	JR- 049 (EC-552584)	Geeta
Siliquae on main shoot (>52.0)	Bio-772 (52.0)	Geeta	JM- 06002 (EC-597310)	JM- 06010 (EC-597315)	VSL- 5	JM- 1
Siliqua length (>4.0 cm)	Varuna and Bio-772 (4.0)	Laxmi	JM- 1	CS –54	Basanti	JM- 009 (EC-552582)
1000-seed weight (> 6.6 g)	Bio-902 (6.6)	Urvashi				
Biological yield/plant (>72.6 g)	Varuna (72.6)	JM- 06010 (EC-597315)	JM- 06003 (EC-597311)	JM- 1	JM- 06002 (EC-597310)	GM- 2
Seed yield/plant (>18.7 g)	Varuna (18.7)	JM- 06003 (EC-597311)	JM- 06010 (EC-597315)	JR- 042 (EC-552583)	GM- 2	Ashirwad
Harvest index (>29.3%)	Bio 902 (29.3)	Pusa mahak	JM- 06014 (EC-597319)	JN- 004 (EC-552573)	JM- 016 (EC-552579)	JM- 3
Oil content (>39.3%)	Rohini (39.3)	Kranti	CS- 52	JN- 004 (EC-552573)	JM- 033 (EC-552578)	JM- 032 (EC-552577)
LAI full flowering (>2.3)	Rohini (2.3)	VSL- 5	Swaran Jyoti	CS-62	JM- 2	JM- 06006 (EC-597313)
SLW (mg/cm^2) 50% flowering (>5. 3)	Bio-902 (5.3)	Datonghuangy oucai (EC-597337)	Ekla (EC-597327)	Berry (EC-597329)	RH-13 (EC-597330)	Qianxianjiecai (EC-597338)
Full flowering (>7.3)	Varuna (7.3)	Berry (EC-597329))	Qianxianjiecai (EC-597338)	Loiret (EC-597326)	RH-13 (EC-597330)	Ekla (EC-597327)
TDM/plant (g) 50 % flowering (>15.9 g)	Varuna (15.9)	Qianxianjiecai (EC 597338)	Berry (EC-597329)	Datonghuangy-oucai (EC-597337)	Loiret (EC-597326)	Ekela (EC-597327)
TQ (mmoles / µmole) 50 % flowering (< 0.34)	Bio-902 (0. 34)	JM-3	NDYR-8	JM-1	VSL-5	Pusa mahak
Full flowering (< 0.36)	PCR-7 (0.36)	VSL-5	JM-1	RH-13 (EC-597330)	Vasundhra	CS-52
SCMR 50% flowering (>50.8)	Bio-902 (50.8)	VSL-5				

* Within parenthesis is the actual mean value (adjusted).

for various morphological traits in 30 exotic rapeseed-mustard strains from Sweden was observed because of breeding and selection under long day conditions. The Chinese accessions were extremely tall, had excellent vigour, produced few secondary branches and showed compact plant type. They could be evaluated for certain physiological characters only. The Australian accessions were also slightly late in maturity but comparable to indigenous accessions. Based on the mean performance, the top five promising accessions from indigenous as well as exotic germplasm each for different morpho-physiological characters were identified (Table 4).

The indigenous accessions predominnantly had long main shoot, long siliqua, high seed weight, oil content

and leaf area index at full flowering. The Australian accessions appeared to be good sources of short plant stature, secondary branches/plant, siliquae on main shoot, biological yield/plant as well as seed yield/plant. Pusa Mahak and three Australian accessions exhibited high harvest index. The Chinese accessions seemed promising for specific leaf weight and total dry matter/ plant. The accessions- Qianxianjiecai (EC597338), Berry (EC597329), Loiret (EC597326), RH-13 (EC597330), Datonghuangyoucai (EC597337) and Ekla (EC597327) showed thicker leaves as indicated by high SLW. Since SLW has been reported to be associated with water use efficiency in groundnut (Nageswara Rao *et al.*, 1993) it would be quite interesting to study these accessions in detail for drought tolerance in terms of osmotic adjustment, water use efficiency and root characters. Further, Indian varieties, VSL-5, JM-1, Vasundhra, CS-52 and RH-13 (EC597330) from China showed low transpiration quotient, *i.e.*, high water use efficiency.

In the present investigations the saturated fatty acids in the genotypes were in the desirable range (< 7%) and some Indian varieties such as GM-2, RGN-13, JM-3, VSL-5 and Australian accession JM-018 showed very low saturated fatty acids (< 2 %). An Australian accession, JM-06011 had slightly higher amount (10.1%) of saturated fatty acids. Oleic acid is very important for increased shelf life as it reduces photo-oxidation as well as for reducing the blood cholesterol (Grundy, 1986). Oleic acid content in the indigenous germplasm was low varying from 6.0-18.1% and all had high erucic acid in the range of 31.5% (Basanti)-52.5% (GM-2). All the Australian accessions exhibited low erucic acid (<2%) and high oleic acid (29.7-58.4%). The investigated genotypes showed wide variation for linoleic acid. This fatty acid was lower in indigenous accessions (12.5-28.8%) than that of exotics (7.8-49.7%). Preferred ratio of oleic: linoleic acid in edible oil should be at least 2.0, Australian accessions JM-06001 and JM-06002 had very high ratio (5.0-6.0) but in Indian accessions such ratio was only 0.75. Similarly, linolenic acid also showed considerable variability in the germplasm investigated and exotics had higher amount (11.9-29.3%) as compared to indigenous ones (9.0-23.0%). Similar pattern of fatty acids had been reported earlier in Indian mustard varieties and exotic germplasm from Canada (Chauhan *et al.*, 2006, 2007). Since oleic acid is the precursor for the synthesis of eicosenoic and erucic acid through chain elongation and also of linoleic and linolenic acid through desaturation pathway (Jonsson, 1977) and any reduction in erucic acid in oil would simultaneously increase oleic, linoleic and linolenic acid. Therefore, high amount of erucic acid in Indian varieties obviously caused reduction in oleic acid while, low erucic acid in Australian accessions resulted in concomitant high level of oleic acid. Glucosinolate content in the indigenous germplasm ranged from 75-136.6 µ moles/g defatted seed meal. In the Australian accessions, it was up to 30 µ moles/g defatted seed meal. These accessions could serve as valuable sources of low glucosinloate in the Indian breeding programme. Indigenous germplasm and varieties of Indian mustard have also been reported to have high glucosinolate content (Chauhan *et al*., 2007). Potential donors for different morpho-physiological characters, desirable fatty acid profile and low glucosinolate content were identified (Tables 4 and 5).

The present gene pool of Indian mustard investigated proved to be quite valuable and several potentials accessions were identified from exotic as well as indigenous germplasm for possible utilization in the breeding programme. The Chinese accessions appeared

Table 5. Promising accessions identified for desirable fatty acid and glucosinolate content

Character	Accessions				
Palmitic + stearic acid (< 2.0 %)	GM-2	RGN-13	JM-3	JM-018 (EC552580)	VSL-5
Oleic acid (> 37%)	JM-06002 (EC597310)	JM-06001 (EC597309)	JN-033 (EC552578)	JM-06020 (EC597323)	JR-042 (EC552583)
Linoleic acid (15-20%)	JM-1	Arawali	CS-52	CS-54	NDYR-8
Linolenic acid (5-10 %)	VSL-5	Ashirwad	GM-2	Laxmi	JM-3
Eurcic acid (< 2 %)	JM-06002 (EC597310)	JM-06004 (EC597312)	JM-016 (EC552579)	JN-010 (EC552574)	JM-06020 (EC597323)
Glucosinolate content (< 25µmoles/g defatted seed meal)	JM-06001 (EC597309)	JM-018 (EC552580)	JM-016 (EC 552579)	JR- 042 (EC 552583)	JM-0009 (EC552582)

quite different but very late and needs to be grown for at least one/two seasons more for identifying better adapted segregating plants under Indian conditions. All the Australian accessions would serve as an important reservoir of gene(s) for low erucic acid, high oleic acid, high oleic:linoleic acid ratio and low glucosinolate content. It is also expected that utilization of this gene pool would lead to broadening of the genetic base of Indian cultivars because of its divergent nature.

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Assessment of Genetic Variability for Iron Content in Grain of Rice (*Oryza sativa* L.) Germplasm Accessions and Identification of Transgressant Lines

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Iron and zinc deficiencies are serious global health problems among the people dependent on staple crops like rice and maize. Enrichment of nutrients in these crops can be achieved by adopting biofortification methods. The objective of this experiment was to identify high iron containing lines in rice by developing new mapping populations. Three mapping populations were developed based on grain iron content and yield viz., IRRI38 X Jeerigesanna, BI33 X Jeerigesanna and Azucena X Moromutant after the two seasons screening of 960 germplasm accessions under aerobic and wetland condition. Iron and zinc concentrations were estimated from RILs and the values ranged from 4.45 to 76 mg/kg and 7.73 to 146 mg/kg, respectively. Thirty two high iron and zinc containing genotypes were identified for all India trial in *Kharif* 2011; these genotypes were evaluated for iron and zinc content. AM127 and Karidaddi were found to have high iron content while AM65 and AM143 were found to be have high zinc content.

Key Words: Iron, Perls' Prussian blue, 2, 2-dipyridyl, RILs aerobic

Introduction

Rice (*Oryza sativa* L.) is India's pre-eminent crop, and is the staple food for people in the eastern and southern parts of the country. India is the second largest producer of rice, after China, accounting for 20% of world rice production. It is estimated that more than 3.5 billion people in the world are deficient in vitamin A, iodine, iron and zinc (Virk *et al.*, 2007). According to WHO (2011) approximately 1.62 billion people suffer from iron deficiency (anemia) and more than half of world population suffers from zinc deficiency.

Iron is a vital mineral required for all living organisms for their well being. But, iron deficiency is found to be the most prevalent nutritional deficiency worldwide. It is a major public health problem with adverse consequences (anemia) particularly among the women of reproductive age and for young children.

Mineral malnutrition is now considered to be one of the most serious global challenges to humankind and is unavoidable. This can be addressed by mineral supplementation, dietary diversification and food fortification. The first two approaches are not easy to adopt in developing countries where majority of people depend on a staple food like rice to suppress hunger. Hence crop biofortification is advocated. This method is cost effective, sustainable and will balance the micronutrient daily requirement in people of rural and urban areas where micronutrient malnutrition is prevalent.

Prussian blue staining is a rapid and cost effective screening method employed for localization of iron in large number of genotypes by scoring colour intensity in the embryo of cut and treated seeds with 2% Prussian blue through a stereomicroscope (Pearse, 1972). Use of 2, 2-dipyridyl for grain iron estimation is a simple, time saving and high throughput method (Snell and Snell, 1959). It involves the serial addition of a set of reagents to finely ground grains sample and finally measuring the intensity of coloured complex developed using UV-visible spectrophotometer.

These semi-quantitative methods have the potential to provide an easy screening technique for identification of genotypes with high Fe content in the grains, which can be further used for subsequent breeding programme. The genotypes selected for higher Fe and Zn in the grains can

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serve as targets for immediate utility as donors for the trait. The trait of high Fe and Zn containing genotypes needs to be combined with high yield potential, tolerance to biotic and abiotic stresses, and good grain quality (Martinez *et al*., 2007).

It is reported that aromatic rice varieties are associated with higher Fe content in the grains. This might be due to pleiotrophic effects or linkages of the traits (Graham *et al*., 2001). A gene controlling aroma in rice on chromosome 8 was identified (Ahn *et al*., 1992), which is located 4.5 cM away from RFLP marker RG28 in near isogenic lines (NILs). Similarly, three groups of genes associated with high Fe-trait were found to be located on chromosomes 7, 8 and 9 and three groups of genes associated with aroma were located on chromosomes 5, 7 and 8. Thus, the two chromosomes, common for the two traits show linkage between aroma and high Fe concentration (Gregorio, 2002).

Around 75% of Asia's rice is produced in irrigated lowland fields where irrigation requirements can often be high, while irrigation water is becoming an increasingly limited resource (Bouman *et al*. 2007). Therefore, water-saving production systems such as aerobic rice may provide viable adaptation strategies for farmers who want to continue growing rice under water-deficit conditions. Generally, rice is grown under flooded condition, where availability of Fe^{2+} is more as compared with aerobic and well drained soils (Ponnamperuma, 1972; Shashidhar, 2007). But in some cases availability of grain iron content is more in well drained condition (Beyrouty, 1994). Thus, in this study an effort is made to identify genotypes with higher Fe concentration in the grains of rice grown under aerobic condition.

Materials and Methods

Genetic Material and Evaluation Methods

Experiment was conducted in *Kharif* 2005 using 751 local germplasm and 209 advance stage breeding lines collected from IRRI, in farmer's field at Shettigere, outskirts of Bangalore, Karnataka, India (130 10'47"N, 770 39'56"E) in augmented experimental design with two checks (Rasi and BI 48) under aerobic condition.

At crop harvesting stage plant height, number of tillers, grain yield and straw yield were recorded per plant. The iron content was analyzed by using Perls' Prussian Blue Method (Perls *et al*,.1867, Doucet and Viel, 2002) from the dehusked grains.

Out of 960 genotypes used for this experiment, initially 68 genotypes were selected during *Kharif* 2005, based on high iron content in grains and high grain yield. In *Rabi* 2006, the related 68 genotypes were grown both in irrigated and aerobic conditions. Iron content of dehusked grains was estimated using 2, 2-dipyridyl method in both conditions.

Population Development

Five superior genotypes were selected from 68 genotypes to serve as potential parents and three mapping population (IRRI 38 X Jeerigesasnna, B I33 X Jeerigesanna and Azucena X Moro mutant) were developed during *Kharif* 2006 (Table 1).

In *Kharif* 2007, these three mapping population were evaluated for aroma in F_1 and F_2 generation using the method suggested by Sood and Siddiq (1978) and these population were advanced till F_7 generation to develop recombinant inbred lines by continuous selfing.

Table 1. Salient features of the parents used for the development of mapping populations

Accession	Origin / pedigree	Plant height	Maturity (days)	Grain type	Yield (t ha^{-1})	Fe content (mg kg^{-1})	Salient features
IRRI 38	Line from IRRI, Philippines	Semi-dwarf	100-105	Medium slender	3.5	8.71	Drought tolerant
Jeerigesanna	Traditional	Tall	130-140	Short bold	2.5	28.02	Non basmati aromatic
B I33	Budda X IR64	Semi-dwarf	116-122	Long slender	4.5	14.7	Drought tolerant
Azucena	Japonica	Tall	131-145	Medium bold	3.2	19.8	Non basmati aromatic
Moro mutant	Mutant from Moroberekan	Semi-dwarf	115-124	Medium bold	4.2	13.25	Drought tolerant

In *Kharif* 2010, these populations were evaluated for iron and zinc using ICP-OES.

Results and Discussion

Breeding for high micronutrient content depends on exploitation of new genotypes from existing germplasm accessions. Once donor genotypes for Fe content in grains are identified, this trait can be combined with high yield and tolerance to biotic and abiotic stresses (Welch, 1999; Pfeiffer and McClatterty, 2007).

Genetic Differences for Iron Content and Morphological Characters

In this study 960 genotypes were categorized based on grain iron content using Perls' Prussian blue method and also grain iron content was compared against phenotypic characters. Among 960 genotypes, it was found that iron content in the grain was high in 18 genotypes, medium in 72 genotypes and low in 870 genotypes (Table 2). The genotypes with high iron content in grains exhibited less number of tillers, low grain yield and high straw yield when compared to medium and low iron containing genotypes. The genotypes showing medium iron content in grains showed high number of tillers, highest yield and low straw yield when compared to high and low iron containing genotypes. The genotypes showing low iron content in grains showed less number of tillers, medium grain yield and straw yield when compared to high and medium iron containing genotypes. This indicates that high iron content was negatively correlated with grain yield. Similar results were reported by Velu *et al.* (2006) in pearl millet using Perls' Prussian blue method. In transgenic rice grains, Perls' Prussian blue staining showed distribution of iron in aleurone and sub layers of aleurone and also in the central layers of endosperm, whereas in non-transgenic grains it was shown only in aleurone layer (Sivaprakash *et al.,* 2006). Thus, Prussian blue staining was effective in differentiating genotypes with high and low Fe content.

Table 2. Genotypes selected for high iron content in the grains

Sl.no	Genotype	Sl.no	Genotype
1	CTH3	10	RSK2-4
2	HP44	11	IR80312-6-B-3-2-B
3	IET13693	12	IR80021-B-86-3-4
4	IET13796	13	IR79913-B-102-B-3
5	IET16346	14	IET5784
6	IET16666	15	IET7191
7	IET18757	16	IET8794
8	IET18814	17	IET8957
9	Karidaddi	18	IET13142

Analysis of variance revealed significant differences among the genotypes for all the traits. Rice genotypes in this study showed high GCV (21.62, 19.85) and PCV (36.65, 36.08) for straw yield and grain yield, respectively. Similar results were reported for biological yield (Pandey *et al*,. 2012) and grain yield (Bisne *et al.*, 2009; Akinwale *et al.,* 2011) indicating these characters to be genetically controlled. Moderate GCV (16.05) and high PCV (23.47) was observed for number of tillers per plant. This coefficient values indicated considerable amount of variability for this characters. High GCV and PCV for number of tillers were reported (Kole *et al.,* 2008 and Bisne *et al.,* 2009). Moderate PCV and GCV were observed for plant height (Bisne *et al.,* 2009). High heritability (75.00) coupled with high genetic advance as per cent mean (28.69) was observed for plant height; moderate heritability with high genetic advance as percent mean were observed for number of tillers per plant, straw yield and grain yield (Kumar *et al.,* 2001, Suman *et al.,* 2005, Bisne *et al.,* 2009 and Akinwale *et al.,* 2011). This indicated that these traits were not much influenced by environmental factors. Hence, these traits can be improved by direct selection.

Correlation Studies

Highly significant and positive correlation was observed for grain Fe content with grain yield and number of tillers per plant at genotypic level whereas, it had significant negative correlation with plant height and straw yield (Table 3). Similarly, significant positive correlation for iron content with grain yield is reported in soybean (Achakzai, 2004). However, non-significant correlation between iron content with grain yield was also reported (Govindaraj *et al.*, 2009, Nagesh *et al.,* 2012).

Grain yield per plant showed significant positive correlation with straw yield per plant at genotypic and phenotypic level. Grain yield also showed significant positive correlation with number of tillers at genotypic level but showed negative correlation at phenotypic level. Significant correlation between grain yield and number of tillers per plant (Shashidhar *et al*. 2005, Nagesh *et al.,* 2012) and also between biomass and grain yield was reported (Chandrababu *et al.,* 2003).

Table 3. Genotypic and phenotypic correlation coefficient matrix

S.No	Character	Plant height	No of tillers	Grain yield	Straw yield	Fe content
1	Plant height	1	-0.20**	-0.14**	0.15**	-0.11**
2	No of tillers	-0.09**	1	0.26**	0.22**	0.29**
3	Grain yield	0.01	0.31**	1	0.27**	0.42**
4	Straw yield	0.17**	0.30**	0.24**	1	-0.69**
5	Fe content	-0.05	0.05	0.04	0	1

*Significant at 0.05 % level, ** Significant at 0.01 % level

Comparison of rice genotypes for grain Fe content grown under wetland and aerobic condition

In the present study, Fe content in the grains of rice was compared among genotypes grown under wetland and aerobic conditions. It has been observed that Fe content was higher in genotypes grown under aerobic condition than those grown under wetland conditions. Similar results were reported for genotypes grown under dry land and wetland conditions Ponnamperuma, 1972. Biomass and grain yield was higher for those genotypes grown under wetland condition compared to aerobic condition (Table 4). The probable reason for higher Fe content in aerobic condition compared to wetland condition can be ascribed to the iron absorbed from the soil is distributed to all the grains and biomass of the individual plant. Similarly, in the wetland condition absorbed iron is distributed to more grains and biomass. Grain Fe content has inverse relationship with grain yield and biomass under aerobic condition.

Genetic difference for aroma in F_2 mapping population

The aroma evaluation in leaves of three mapping population at F_1 generation showed that all are non-aromatic. Similar results were reported in grains and leaves of F_1 population (Tsuzuki and Shimokwa, 1990). In F_2 generation out of 347 plants of IRRI38 X Jeerigesanna cross, 256 were found to be non-aromatic and 91 were aromatic, in BI33 X Jeerigesanna cross out of 280 population, 213 plants were found to be non-aromatic and 67 plants were aromatic and in Azucena X Moromutant cross out of 378 populations, 283 were non- aromatic and 95 were found to be aromatic. In all the three crosses, segregation of aroma was not significantly deviating from the monogenic ratio of 3:1, as revealed by the chi-square test. However, F_2 generation followed standard mendelian ratio of 3:1. This indicated that the inheritance of aroma in rice is possibly due to a single recessive gene (Sun *et al*., 2008).

The results of ICP-OES showed that the iron and zinc content in brown rice ranged from 4.45 to76.0 mg/kg and 7.73 to 146.0 mg/kg respectively. From these results 26 lines of mapping population and six local genotypes with high iron and zinc content were nominated for all India trial in *Kharif* 2011 (Table 5).

From this study three mapping populations were developed from parental lines selected for high iron content and yield parameters. These mapping populations were advanced to develop RILs under aerobic condition for further evaluation of iron and zinc content in brown rice and selection of transgressant lines using marker assisted selection.

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Table 4. Comparison of genotypes for iron content grown under wetland and aerobic condition (n= 68)

	Fe content (mg kg^{-1})		Grain yield (t ha^{-1})		Straw yield (t ha^{-1})	
	Wetland	Aerobic	Wetland	Aerobic	Wetland	Aerobic
Mean ± S.E	10.48 ± 0.52	17 ± 0.81	4.38 ± 0.29	3.08 ± 0.38	8.37 ± 0.46	5.34 ± 0.57
Variance	18.71	44.29	7.14	3.42	22.73	13.71
t α = 0.05	6.67		4.07		3.24	

Table 5. Iron and zinc content of genotype nominated for all India trial in *Kharif* 2011

S.No.	Genotype	Iron (mg/Kg)	Zinc (mg/Kg)	Sl.no.	Genotype	Iron (mg/Kg)	Zinc (mg/Kg)
1	AM-158	23.6	38.2	17	AM-79	33.9	37.7
2	Karna	23.2	30.0	18	AM-36	32.0	34.4
3	Pushpaka	20.3	23.8	19	AM-132B	32.5	39.3
4	BJ-22	24.5	41.1	20	BJ-18	25.7	25.7
5	AM-81C	24.1	33.5	21	AM-94B	27.2	42.4
6	BJ-6	30.9	38.0	22	AM-127B	29.5	38.3
7	AM-72	29.3	42.4	23	AM-144	27.8	36.2
8	AM-127	34.7	40.7	24	KHP-2	29.7	31.7
9	BJ-23	33.4	41.2	25	BJ-17	24.2	34.2
10	AM-27	29.8	41.0	26	BJ-16	31.2	33.5
11	AM-143	24.3	43.8	27	AZUCENA	32.0	40.2
12	AM-1	31.7	42.3	28	Karidaddi	34.3	32.5
13	BJ-2	30.9	36.2	29	BJ-5	32.3	36.1
14	AM-132	28.1	33.0	30	IVT(SHW) /91/10608	31.1	33.4
15	AM-81	33.2	41.4	31	Jeerigesanna	28.3	33.9
16	AM-65	33.8	43.9	32	BJ-66	25.8	33.0

Note: **AM** (Azucena X Moromutant), BJ (BI33 X Jeerigesanna)

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Characterization of Wheat (*Triticum aestivum* L.) Germplasm for Yield and Yield Attributing Traits

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There is a huge germplasm available in the genus *Triticum* which comprises vast number of wild relatives with different ploidy levels as well as domesticated wheat with different breeding lines from different locations all over the world. The objective of present study was to analyze the available germplasm collected from different locations within India (922 accessions) and characterize them for yield and yield attributing traits. The results yielded a wide range of variability for all the traits. On the basis of their comparison with standard checks, few accessions have been identified which can be used in breeding program for yield improvement.

Key Words: Characterization, Germplasm, Wheat, Yield

Introduction

Wheat (*Triticum aestivum* L.), being a crop of global significance, is grown in diversified environments. It is a staple food throughout the world. Growing population and industrialization has caused a gradual shrinkage in the acreage of agricultural land; this presents the enormous challenge of feeding the people using the restricted amount of land and water that is available today. Developing high yielding varieties is the top most priority of a breeder. In wheat, high yield coupled with better quality is the most desirable type for wheat growers across the country. Increasing yield is a generalized term as it accounts for improving various yield attributing characters as well as imparting resistance/tolerance against a wide range of biotic and abiotic stresses. Crop domestication practiced years ago has led to artificial selection accounting for decreased genetic variability. The challenging environment we are in, the use of genetic variability present naturally is a key to success of any breeding program, thus extensive use of genetic resources can do wonders in plant breeding research.

Yield is the foremost factor to be considered for acceptance by wheat growers. With the popularity of few high yielding varieties, the variability in farmer's field has been reduced to extreme extent. Moreover, these varieties have been developed form only six broad groups (Rao, 1988). Thus, its genetic base is already narrow which is further narrowing down. There is a need to break this trend of using less diverse wheat lines so that the genetic load can be shifted and better breeding lines can be developed by using more diverse parents. This requires collecting diverse lines from various locations, their conservation, evaluation and successful utilization in breeding programs. In this study, wheat germplasm was collected from different locations of India and its characterization is done for yield attributing traits so that useful genotypes are identified and will be used for the development of high yielding varieties.

Materials and Methods

Nine hundred twenty two wheat germplasm lines were obtained from National Bureau of Plant Genetic Resources (NBPGR), New Delhi, which belonged to different geographic locations within India, including Delhi, Haryana, Uttarakhand, Himachal Pradesh, Andhra Pradesh, Madhya Pradesh, Karnataka, Punjab and Sikkim (Fig. 1). The experiment was planned in an augmented design with four local checks *viz.,* PBW 343, Lok 1, GW 322 and Sonalika at G.B. Pant University of Agriculture and Technology (GBPUAT), Pantnagar, Uttarakhand during *rabi*, 2008-09 and 2009-10. Nine quantitative characters contributing for yield *viz.,* spikelet emergence, days to maturity, grain filling duration, plant height, spike length, spikelets/spike, grains/spike, 1000 grain weight and grain yield *per se* were recorded. All the quantitative observations on most of the characters were recorded on single plant basis except for spikelet emergence and days to maturity. Five representative plants from each plot were randomly selected and tagged for recording

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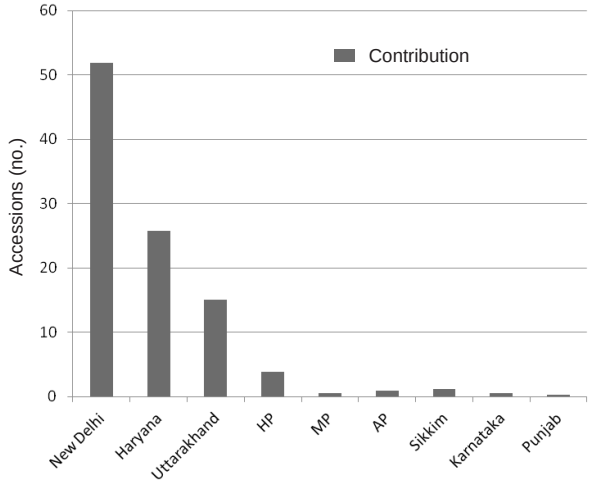

Fig. 1. Representation of accessions from different states

the observations on single plant basis. Average data from selected plants in respect of different characters were used for the statistical analyses.

Results and Discussion

The data was recorded for 922 accessions for nine quantitative traits. The analysis of variance revealed considerable inherent genetic differences among the material for all the traits under study (Table 1). The frequency distribution was found to be variable for the characters *viz.,* spikelet emergence (very early, early, medium, late, very late), days to maturity (early, medium, late), grain filling duration (long, medium, short), plant height (very tall, tall, medium, short, very short), spike length (long, medium, short), spikelets/spike (more, medium, less), grains/spike (more, medium, less), 1000-grain weight (bold, medium, small) and grain yield (very high, high, medium, low, very low) (Table 2).

The accessions were classified state-wise on the basis of the passport data available. Thus, there were nine geographic groups representing nine different states of India. Out of these groups the maximum contribution was from New Delhi (479) followed by Haryana (238) and Uttarakhand (139), whereas lowest contribution was from Punjab (3). Overall, the geographical distribution of the entire collection showed a disparity in the collection from different locations (states) (Fig. 1). However, this represented a wide distribution of wheat growing areas over the country. Same results in earlier studies were also obtained in chickpea germplasm collection that some parts of the geographic distributions were under represented (Upadhyaya *et al.,* 2001). The unequal representation of the accessions from different states may be the result of using well established improved varieties instead of landraces according to farmer's need. The poor representation of some states could also be attributed to the difficulties in collection from the fields, the political situations in the prospected areas or the socio-economic conditions of the farmers (Bhattarcharjee *et al.,* 2007)

Characterization of all the accessions was done on the basis of the frequency distribution of all the nine

Table 1. Analysis of variance for different characters

Source of variation	Degree of Freedom	Mean squares									
		Spikelet emergence	Days to maturity	Grain filling duration	Plant height	Spike length	Spikelets/ spike	Grains/ /spike	100-grain weight	Total grain weight	Grain yield
Block (b)	5	3.366**	1.175**	1.141**	10.072**	0.112**	0.075**	7.219**	0.018**	6.136**	27.068**
Check (c)	3	62.832	0.819**	53.819	61.509	1.863	28.880	230.210	0.009	64.270**	508.059
Error (e)	15	3.233	1.086	4.253	10.425	0.075	0.532	4.284	0.021	4.007	30.288

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

Table 2. Frequency distribution of different characters

Characters	Frequency distribution
Spikelet emergence (days)	Very early <70 (40), Early 70-80 (322), medium 81-90 (462), late 91-100 (49), Very late >100 (49)
Days to maturity (days)	Early <110(165), medium 110-130 (737), late >130 (20)
Grain filling duration (days)	Short <30(140), medium 30-40(586), long >40(196)
Plant height (cm)	Very tall >110cm(44), tall 89-110cm (309), intermediate 80-89cm (89), short 70-79cm (367), Very short <70cm (22)
Spike length (cm)	Short <10cm(46), medium 30-40cm(827), long >20cm (53)
Spikelets/spike (no.)	More >25 (7), medium 15-25(592), less <15 (323)
Grains/spike (no.)	Less <50 (684), medium 50-80 (231), more >80 (7)
1000 grains weight (g)	Small <20g(63), medium 20-40g (672), bold >40g(187)
Grain yield (g)	V high >700g (13), high 500-700g (166), medium 300-499g (200), low 100-299g (312), v low <100g (231)

characters (Table 2). For all the characters most of the accessions were found to fall under medium category except plant height, grains/spike and grain yield. The frequency distribution was studied and was found to be maximum for spikelet emergence (68-115 d), plant height (68-122 cm) and grain yield (20-800 g). Rest of the six characters were divided into three categories each for days to maturity (early, medium and late), grain filling duration (short, medium, long), spikelet length (short, medium, long), spikelets/spike (more, medium, less), grains/spike (more, medium, less) and 1000-grain weight, with values ranging from 108 to 142 for days to maturity, 10-66 for grain filling duration, 5.5 to 28.5 for spikelet length, 8.8 to 43.2 for spikelets/spike, 6 to 155 for grains/spike and 10.56 to 70 for 1000 grain weight (Tables 2 and 3). Pal *et al.* (2007) evaluated 150 wheat germplasm and selected few potential accessions and suggested their utilization in wheat improvement program. Range of frequency distribution was an indicator of coefficient of variation which was highest for grain yield (30.78) followed by grains/spike (27.57), spikelets/spike (25.00) and 1000-grain weight (23.11) (Table 3). This indicates that the data points for these characters are spread out over a large range of values. Spike length possessed lowest coefficient of variation (4.37) followed by spikelet emergence (9.56) indicating that they are very close to the mean. Coefficient of variation was used as an estimate to select superior genotypes from chickpea minicore collection by Parameshwarappa *et al.* (2012). The mean for grain yield (260.65) was found to be significantly superior over checks (105.93) which points towards the assumption that the accessions studied possesses good combinations of genes for better yield. As the diversity for yield was high it is obvious that there are few genotypes which have the high yield potential. Thus, these superior accessions were found out by calculating the differences in the means of checks and genotypes. This was further validated by subtracting the checks mean LSD so that the differences found were significant. Thus, 580 out of 922 accessions were significantly superior over check for grain yield, although most of these accessions are late maturing. Amulaka *et al.* (2013) characterized wheat germplasm for Russian wheat aphid and stem rust. Bux *et al.* (2012) also characterized 200 wheat germplasm for stripe rust. Upon correlating all the characters with grain yield, it was also found that maturity was positively correlated with grain yield with a correlation coefficient of 0.384 (Table 4). However, farmers are interested in varieties which have early maturity but there is compensation of yield too. Other characters were also classified on the basis of their performance over standard checks. This way the best performing accessions were selected for different trait. The superior accessions are presented in Table 5. Thus, based on preference, the accessions can be used in breeding program whether to breed for enhanced yield or for shortening of maturity without sacrificing yield.

Table 3. Mean, range and coefficient of variation for different characters in 922 wheat accessions

Characters	Mean	Range	Coefficient of variation
Spikelet emergence (days)	82.67	68-115	9.56
Days to maturity (days)	117.58	108-142	17.09
Grain filling duration (days)	34.91	10-66	16.38
Plant height (cm)	86.13	68-122	15.31
Spike length (cm)	16.09	5.5-28.5	4.37
Spikelets per spike (no.)	15.81	8.8-43.2	25.00
Grains per spike (no.)	40.59	6-155	27.57
1000-grain weight (g)	32.57	10.56-70	23.11
Grain yield (g)	260.65	20-800	30.78

Table 4. Correlation of grain yield with other traits

Characters	Correlation coefficient with grain yield
Days to heading	0.126
Days to maturity	0.384
Grain filling duration	0.118
Plant height	0.063
Spike length	0.030
Spikelets per spike	0.245
Grains per spike	0.142
1000-grain weight	0.040
Grain yield	1.000

Table 5. Promising accessions of wheat germplasm for different characters

Characters	Promising accessions
Spikelet emergence	IC535220, IC535223, IC535239, IC535541, IC535260, IC262042, IC535199, IC535226, IC535450, IC535228, IC535232, IC535452, IC535386, IC535505, IC535453, IC535488, IC26740, IC290074, IC535460, IC290023, IC290035, IC535236, IC535234, IC535377, IC25614, IC290073
Days to maturity	IC279439, IC535218, IC535445, IC535529, IC26734, IC535447, IC535532, IC290069, IC290080, IC290317, IC535523, IC47014, IC535527, IC535525, IC535528, IC535537, IC313148, IC260967, IC260970

Characters	Promising accessions
Grain filling duration	IC31774, IC290231, IC290023, IC290035, IC535220, IC535260, IC535199, IC535543, IC535239, IC535541, IC535228, IC535452, IC535386, IC535505, IC535453, IC535488, IC535460, IC255632, IC535236, IC535223, IC535226, IC535293, IC535234, IC25614, IC26728
Plant height	IC290271, IC535382, IC535400, IC535561, IC290304, IC535383, IC535358, IC290272, IC535381, IC535357, IC535217, IC31774, IC290046, IC535368, IC290247, IC535468, IC535414, IC535242, IC266884, IC535576, IC290324, IC535365, IC535331, IC535555, IC535360
Spike length	IC535374, IC535376, IC535525, IC535520, IC535198, IC47016, IC47011, IC290245, IC279336, IC535371, IC535383, IC535288, IC535305, IC, 35372, IC535202, IC290093, IC535438, IC535449, IC535516, IC313157, IC290265, IC290250, IC290227
Spikelets per spike	IC535415, IC260871, IC535543, IC535374, IC535368, IC535376, IC260941, IC41877, IC315871, IC535372, IC535576, IC36900, IC535303, IC316093, IC535297, IC535425, IC535492, IC535515, IC535575, IC28566, IC535554, IC535484, IC290305, IC316085, IC31529, IC310127, IC60939, IC290057
Grains per spike	IC535374, IC535372I, C260871I, C260870, IC535317, IC535376, IC535479, IC31614, IC266977, IC535338, IC535326, IC535268, IC535368, IC535474, IC41877, IC535521, IC535554, IC535266, IC535509, IC290026, IC535311, IC31615, IC535407, IC535269, IC535402, IC535365, IC535472
1000 grain weight	IC535438, IC535425, IC313152, IC535349, IC535396, IC535348, IC290260, IC290211, IC535404, IC535411, IC535397, IC290240, IC535344, IC535395, IC535299, IC535307, IC535483, IC535401, IC535449, IC535413, IC535507, IC535506, IC535476, IC535549
Grain yield	IC535552, IC535197, IC535239, IC535303, IC535309, IC535538, IC535546, IC535547, IC535569, IC535338, IC535220, IC535263, IC535274, IC535201, IC535259, IC53528, IC535296, IC535299, IC53532, IC535323, IC535324, IC535330, IC535335, IC535337, IC535436, IC535438, IC535496, IC535501, IC535549, IC535211, IC535286, IC535317, IC535401

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Variability, Heritability and Genetic Divergence in Yellow Sarson *(Brassica campestris.* var. Yellow Sarson) Genotypes under the Mid-hills of Sikkim

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Forty two genotypes of yellow sarson (*Brassica campestris* L. var. yellow sarson) were evaluated under organic conditions in the mid-hills of Sikkim in RBD during the *rabi* season of 2007 and 2008 for eight quantitative traits namely, plant height, number of primary branches, days to 50% flowering, days to maturity, number of siliqua/plant, length of siliqua, number of seeds/siliqua and seed yield/plant. High heritability with high genetic advance was observed for number of siliqua/plant, number of seeds/siliqua and seed yield/plant. The 42 genotypes were grouped into 9 clusters. The number of siliqua/plant contributed maximum towards genetic divergence. The performance and seed yield of seven genotypes *viz.*, Pusa Gold, NDYS 2018, SSY-1, *Ragini, Jhumka*, NDYS 9504 and GS-1 were found better.

Key Words: *Brassica campestris,* Genetic divergence, Variability, Yellow sarson

Introduction

Indian rapeseed (*Brassica rapa* L. Syn. *Brassica campestris* L.) is the second largest oilseed brassica grown mostly in the North-eastern parts of India, occupying an important position in rainfed agriculture. India stands first both in acreage and production of rapeseed and mustard in Asia. In India it covers an area of 5.92 mha, with production of 6.78 mt and yield of 1,145 kg/ha in 2011-12 (DRMR, 2013). Among the three ecotypes in this group, yellow sarson is the most important oilseed crop and is most favored in mountainous state of Sikkim. This crop is cultivated solely for obtaining edible oil, as almost all state population utilizes this oil as main edible oil, indicating its importance in the state. In Sikkim it is being cultivated during *rabi* season in low and mid-hills in about 5,80,000 ha area with an annual production and productivity of 4,55,000 tonnes and 784.48 kg/ha, respectively, in 2010-11 (FS&ADD, 2011).

For an organic state like Sikkim, it is imperative to identify rapeseed varieties which perform well under rainfed and low input conditions. Information on the nature and magnitude of variability present in the existing material and association among the various morphological characters is a pre-requisite for any breeding programme to be initiated by the local breeders for high yields. Knowledge on the extent of allelic variations which is expressed in terms of genetic divergence is helpful to identify lines having contrasting alleles and using them as parental lines to tailor the existing genotypes for improving the limiting traits to perform better under target environment. The quantitative characters are polygenic in nature, whose expression is influenced by the environment in which it is grown. The degree of influence of environment on the character decides the methodology to be improvised for improvement of character. This study was carried out with the objective to identify the yellow sarson genotypes suitable for cultivation under Sikkim organic conditions and also selection of the lines with desired characters for further utilization in breeding programmes for improvement of yield and its component traits in yellow sarson.

Materials and Methods

The experimental material for the present study consisted of 42 genotypes of yellow sarson, namely, Binoy, GS 1, IC374356, IC385666, IC385670, IC385678, IC385704, IC385705, IC385767, IC395576, IC398652, IC398654, Jhumka, NDYS 2, NDYS 2018, NDYS 9504, PROYS 2105, PROYS 9805, PS 66, Pusa Gold, PYS 2005, PYS 9804, Ragini, RS 1, Sikkim Sarson yellow 1 (SSY -1), SKYS 13, SKYS 17, YSB 2003, YSC 20, YSC 36, YSC 37, YSC 38, YSC 60, YSC 66, YSC 68, YSC 84, YSC 86, YSK 8501, YSP 842, YST 151, YSWB 952 and YSWB 955. These entries were evaluated in randomized block design with two replications during *rabi* 2007 and *rabi* 2008 at the experimental farm of ICAR Research Complex for NEH Region, Sikkim

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Centre, Tadong, Gangtok which represent the mid hills of Sikkim (1,350 m amsl). Each genotype was sown in 3 rows of 2 m length with spacing of 30 cm x 15 cm.

Observations were recorded on five randomly selected plants in each replication and in each genotype for eight characters namely, plant height (cm), number of primary branches, days to 50% flowering, days to maturity, number of siliqua/plant, length of siliqua (cm), number of seeds/siliqua and yield/plant (g). The combined analysis of variance was performed as per the statistical procedures (Gomez and Gomez, 1984). The variance (GCV and PCV) were estimated following Burton and Devane (1953), heritability in broad sense by Hanson (1963) and genetic advance following Johnson (1955). Mahalanobis (1936) D^2 - statistic analysis was used for assessing genetic divergence among the test entries. The clustering of D^2 values was formed by using Tocher's method as described by Rao (1952) while the intra- and inter-cluster distance was calculated using formula given by Singh and Choudhary (1985). Statistical software INDOSTAT was used for analysis.

Results and Discussion

The yellow sarson genotypes expressed significant variation for all the eight quantitative traits studied as shown by combined analysis of variance (Table 1). Environment plays a major role in expression of quantitative characters and is highly influenced by G x E interaction. Our studies found non-significant variation in all the eight characters when combined variance was computed for two years which signifies that the lines performed consistent in both the years of testing with nil year x variety effect on the characters studied. The extent of genetic variation in characters studied suggests that selection can be exercised in the material either by identifying the suitable donors for traits or selecting the most diverse genotypes for obtaining heterotic progenies.

Ten genotypes *viz.*, *Jhumka* (147 cm), YSC 38 (148 cm), YSC 20 (150 cm), PROYS 2105 (150 cm), YSC 84 (154 cm), PROYS 9805 (156 cm), YST 151 (163 cm), YSK 8501 (165 cm), PS 66 (165 cm) and NDYS 2 (166 cm) were significantly taller than the general mean (135.02 cm). Genotype YSC 38 recorded maximum number of primary branches (9.50). Days to 50% flowering in the mid-hills of Sikkim was seen at 34^{th} day after sowing in IC374356, SKYS 17, RS 1, SSY 1 and YSWB 955 whereas, the flowering was delayed till 48^{th} day in genotypes like PROYS 9805 and PS 66. Days to maturity ranged from 143 days in IC374356 to 156 days in PS 66. The average days to maturity of 42 yellow sarson genotype tested in the mid-hills of Sikkim was 145.83 days. Wide variation in number of siliqua/plant was noticed among the entries with range between 77 in IC396852 to 352 in PYS 9804.

High siliqua number/plant was recorded in genotypes Pusa Gold (207), PROYS 9805 (207), IC374356 (210), YSC 68 (210), NDYS 9504 (223), YSC 60 (224), YSK 8501 (240), SSY (245), YSC 20 (247), PS 66 (249), YSC 66 (261), NDYS 2018 (262), YSC 36 (277), YSC 37 (280), SKYS 37 (280), YSWB 952 (312), GS 1 (316), YSC 38 (345) and PYS 9804 (352). Genotype RS 1 exhibited longest siliqua length (8.70 cm) higher than the general mean of 5.12 cm. The number of seeds/siliqua varied from 14 in genotype PYS 2005 to 40 in IC398652. Seven genotypes namely, YSC 20 (28 seeds/siliqua), IC385670 (31 seeds/siliqua), IC385678 (32 seeds/siliqua), IC385666 (35 seeds/siliqua), PS 66 (36 seeds/siliqua), IC385704 (38.50 seeds/siliqua) and IC398652 (40 seeds/siliqua) showed superiority in seeds/siliqua among test entries. Seed yield, an important

Table 1. Combined ANOVA over two years for eight quantitative traits in yellow sarson

Source of variation	df	Plant height (cm)	No. of primary branches	Days to 50% flowering	Days to maturity	No. of siliqua/ plant	Length of siliqua (cm)	No. of seeds/ siliqua	Yield/ plant (gm)
Year	1	45.79*	9.27*	0.03	2.62	21.39*	38.41*	27.85*	17.16*
Replications within year	2	0.37	0.81	2.43	0.39	0.54	0.17	6.59*	0.12
Variety	41	181.06*	1.81*	4.63*	5.00*	1452.05*	4.20*	35.18*	15.54*
Year x Variety	41	0.13	0.03	0.03	0.01	0.06	0.10	0.09	0.05
Pooled error	82								

* refers to significant at 1% probability level

economic trait, ranged from 2.83g/plant to 9.67 g/plant with an overall mean of 5.80g/plant. Seven genotypes GS-1 (7.67g/plant), Jhumka (7.83g/plant), NDYS 9504 (7.83g/plant), Ragini (8.67g/plant), NDYS 2018 (9.33g/plant), SSY 1 (9.27g/plant) and Pusa Gold (9.67g/plant) performed consistently well during course of study (Table 2).

The estimates of environmental coefficient of variation (ECV%), genotypic coefficient of variation (GCV%), phenotypic coefficient of variation (PCV%) and expected genetic advance (GA) for eight yield related characters of 42 yellow sarson genotypes grown at the mid hills of Sikkim is presented in Table 3. The PCV value of all the characters (plant height, days to 50% flowering, days to maturity, number of siliqua/plant, length of siliqua, number of seeds/siliqua and yield/plant) except number of primary branches were greater in magnitude than the value of GCV or ECV for the corresponding characters which imply that the apparent variation seen for these characters in the above genotypes is not only due to genotypes but also due to the influence of environment. The extent of influence of these two determinants (environment and genotype) on the phenotype can be assessed from the magnitude of GCV and ECV. In the case of number of primary branches, the value of ECV was relatively higher (22.63%) than the GCV (8.46%) and PCV (18.10%) which indicates that the environment has played greater role in the expression of the trait and therefore, for the improvement of number of primary branches selection will not be effective at all.

For characters such as days to 50% flowering and siliqua length the magnitude of ECV was lesser than the value of PCV but greater than the value of GCV which is the sign of predominance role of environment on the expression of these trait than the influence of genotype. For traits such as plant height, days to maturity, number of siliqua/plant, number of seeds/siliqua and seed yield/plant, the difference between GCV and PCV was narrow. The narrow difference is suggestive of the fact that phenotypic variation was determined by and large by genotype with negligible influence of extraneous factors and therefore,

Table 2. The performance of selected high yielding genotype in the mid-hills of Sikkim

High yielding genotypes	Plant height (cm)	No. of primary branches	Days to 50% flowering	Days to maturity	No. of siliqua/plant	Length of siliqua (cm)	No. of seeds/siliqua	Yield/plant (g)
GS 1	130.00	8.00	39.00	153.00	316.00	3.80	18.00	7.67
Jhumka	147.00	8.50	43.00	146.00	168.00	4.90	16.00	7.83
NDYS 9504	137.00	7.00	44.00	148.00	223.00	4.70	18.00	7.83
Ragini	127.00	9.00	36.00	144.00	133.00	5.10	18.00	8.67
NDYS 2018	110.00	8.00	36.00	143.00	262.00	4.50	15.50	9.33
SSY-1	137.00	7.50	34.00	145.00	245.00	5.80	20.00	9.27
Pusa Gold	130.00	6.00	40.00	146.00	207.00	6.00	23.00	9.67
Minimum	95.00	4.00	34.00	141.00	77.00	3.20	14.00	2.83
Maximum	166.00	9.50	48.00	156.00	352.00	8.70	40.00	9.67
Mean	135.02	6.95	39.40	145.93	196.81	5.12	22.31	1.70
CD (5%)	10.99	NS	6.81	8.10	7.50	1.89	4.25	1.70
CV %.	1.83	22.62	8.54	2.92	1.97	18.43	9.89	14.69

Table 3. Estimates of variability and genetic parameters among 42 genotypes of yellow sarson evaluated at mid-hills of Sikkim

Parameters	Plant height (cm)	No. of primary branches	Days to 50% flowering	Days to maturity	No. of siliqua/plant	Length of siliqua (cm)	No. of seeds/siliqua	Seed yield/plant (g)
ECV %	1.83	22.63	8.55	2.92	1.97	18.43	9.90	14.70
GCV %	12.72	8.46	6.90	3.91	36.62	14.33	27.60	28.16
PCV %	12.79	18.10	9.17	4.42	36.64	19.37	28.48	30.02
h^2 (BS)	0.99	0.22	0.57	0.78	1.00	0.55	0.94	0.88
GA as % of Mean 5%	26.08	8.15	10.70	7.11	75.38	21.84	55.12	54.42

selection for such traits will be rewarding as also reported by Khan *et al.* (2006). Among the eight traits under study, greater magnitude of phenotypic variation was recorded for number of siliqua/plant (36.64%) followed by number of seeds/siliqua (28.48%). For improvement of these traits under mid-hill conditions the genotype donors PYS 98014 (352 siliqua/plant), IC398652 (40 seeds/siliqua) and Pusa Gold (9.67g/plant) could very well be utilized for improving number of siliqua/plant, seeds/siliqua and seeds yield/plant, respectively.

Heritability in broad sense was the highest for number of siliqua/plant followed by plant height, number of seeds/siliqua and yield/plant. Barring plant height, in the other traits mentioned above, the high heritability value was coupled with high genetic advance (50%). This situation most likely occurs if preponderance of additive gene action prevails as reported by Misra *et al.* (2007). Therefore, direct selection based on phenotypic observations may be effective for improvement of number of siliqua/plant, number of seeds/siliqua and seed yield/plant.

The 42 yellow sarson genotypes were grouped in to 9 clusters in which three clusters (VI, VIII and IX) were solitary in nature (contain only one genotype in each cluster) while the other six were multi-genotype clusters. The distribution pattern of genotypes in various clusters reflected the considerable genetic variability present in the genotypes under study. Cluster I had maximum number of 10 genotypes followed by cluster II with seven genotypes. Cluster IV and V encompass six genotypes each while cluster III and VII consisted of five genotypes each. The constituent genotypes of each cluster are shown in Figure 1. Genotype YSC 37, NDYS 2108 and Binoy were divergent from other genotypes as each one of them represents a separate cluster.

The mean of each character in each cluster are presented in Table 4. Murty and Arunachalam (1966) have opined that hybridization programmes should be formulated in such a way that the parents belonging to different clusters with maximum divergence should be utilized to get desirable transgressive segregants. The genotypes from cluster VIII with highest yield/plant, moderate plant height, earliness for 50% flowering and maturity and cluster IX with shorter plant height, early maturity and genotypes in cluster III with highest number of siliqua/plant could be utilized in hybridization programme for getting desirable segregants and high heterotic response. The inter- and intra-cluster distances are shown in Table 5. The maximum inter-cluster distance (4166.6) was observed between cluster III and V, followed by cluster II and III (3174.53), cluster III and IX (2810.19), cluster V and VI (2656.48), cluster V and VIII (2291.88), and cluster V and VII (2149.79). The intra-cluster distance was the highest (159.44) in cluster VII and lowest (0.00) in cluster VI, VIII and IX. The genotypes grouped in a same cluster would display the lowest degree of divergence from one another, and therefore, crosses made between genotypes belonging to same cluster may not give heterotic progenies or transgressive segregants, as also reported by Singh *et al.* (2009). On the other hand, crosses between genotypes

Table 4. Cluster mean of different characters in yellow sarson genotypes

Cluster	Plant height (cm)	No. of primary branches	Days to 50% flowering	Days to maturity	No. of siliqua/ plant	Length of siliqua (cm)	No. of seeds/ siliqua	Seed yield/ plant (g)
Cluster I	130.70	6.60	38.10	119.70	203.30	5.28	21.55	5.77
Cluster II	139.86	6.50	38.71	121.14	128.00	5.53	21.14	4.95
Cluster III	139.21	8.50	38.60	120.80	324.80	4.80	19.20	6.69
Cluster IV	156.40	7.20	42.60	124.40	179.60	4.78	19.30	5.87
Cluster V	112.50	5.92	41.66	121.17	101.17	4.70	31.75	5.56
Cluster VI	128.00	6.00	37.00	118.00	280.00	5.60	19.00	6.50
Cluster VII	149.83	7.67	39.67	125.67	253.17	5.08	22.67	5.66
Cluster VIII	110.00	8.50	36.00	118.00	262.00	4.50	15.50	9.33
Cluster IX	95.00	6.00	36.00	114.39	147.00	5.20	22.00	5.00
CV%	15.50	14.81	5.97	2.84	36.37	7.57	20.88	21.59

Table 5. Mahalanobis Euclidean² cluster distances between and within cluster

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	101.38	562.03	1262.30	287.75	991.65	524.18	367.62	469.94	513.60
II		70.53	3174.53	326.04	296.46	1948.43	1347.77	1780.12	471.82
III			104.34	1897.60	4166.60	219.55	563.15	474.27	2810.19
IV				115.01	925.57	1087.40	576.00	1116.97	841.01
V					121.11	2656.48	2149.79	2291.88	333.04
VI						0.00	240.88	95.47	1552.54
VII							159.44	419.69	1456.90
VIII								0.00	1160.38
IX									0.00

Diagonal values refers to intra-cluster distance and upper diagonal values refers to inter-cluster distance

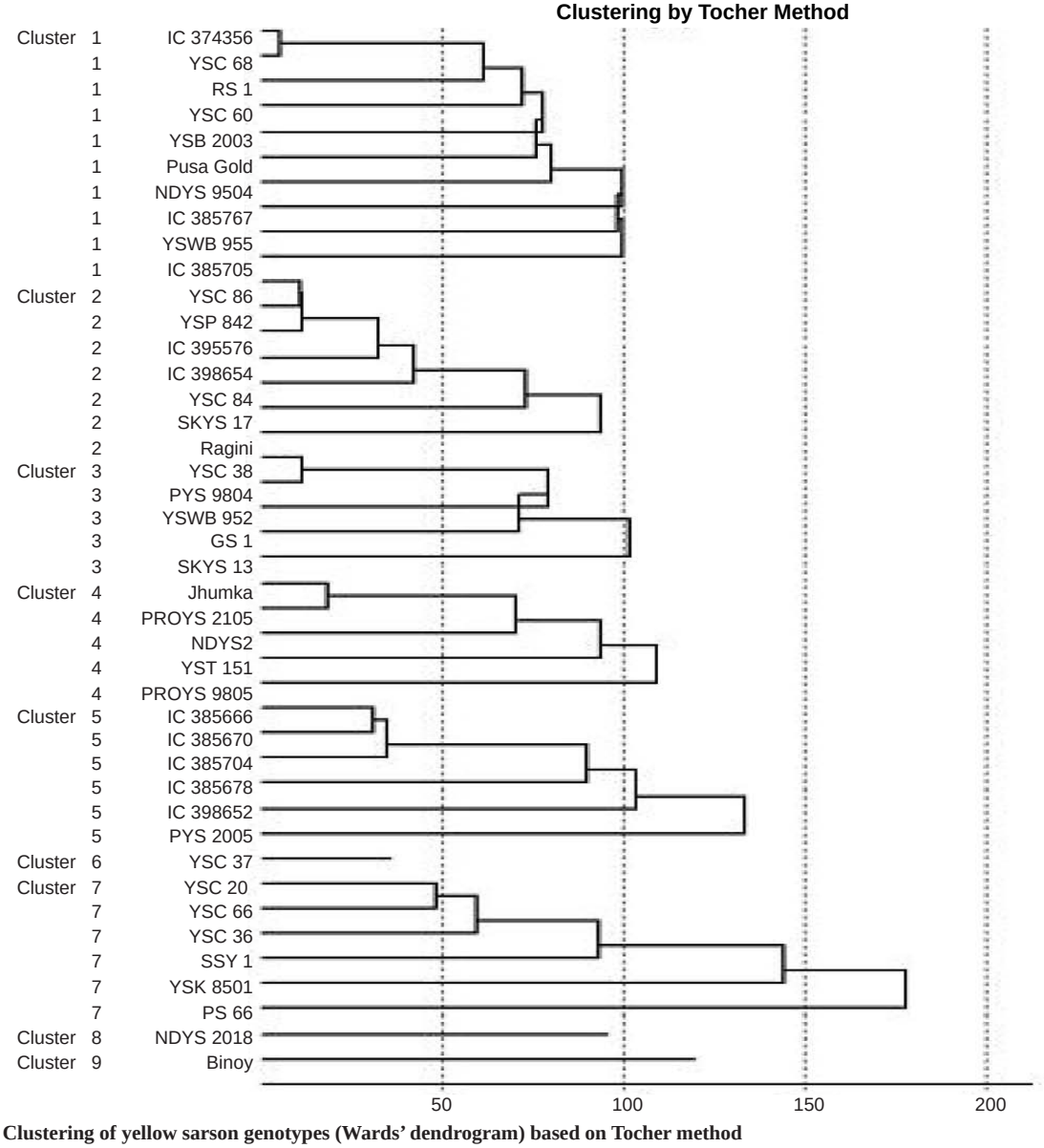

Fig. 1. Clustering of yellow sarson genotypes (Wards' dendrogram) based on Tocher method

belonging to distant clusters like cluster III (SKYS 13, GS 1, YSC 38, YSWB 952 and PYS 9804) and V (IC385666, IC385670, IC385678, IC385704, IC398652 and PYS 2005), cluster III and cluster II (IC395576, IC398654, SKYS 17, YSC 86, RAGINI, YSC 84 and YSP 842) and cluster V with cluster VI (YSC 37), VI (YSC 20, YSC 66, YSC 36, YSK 8501 and PS 66), VIII (NDYS 2108) would result in heterotic progenies and sometime transgressive segregants as reported by Aunwinithul *et al*. (2004).

The contribution of individual characters towards divergence was assessed by ranking d_1 ($=Y_i^j - Y_i^k$) values. In the present study, the number of siliqua/plant has contributed maximum towards divergence followed by plant height (Table 6). At inter-cluster level the number of siliqua/plant followed by seed yield/plant was the contributor towards divergence. Irrespective of the procedure applied, the number of siliqua/plant is the potential contributor of genetic divergence in yellow sarson. Earlier reports by Singh *et al.* (2009), Somu (2001) and Shalini (1998) also emphasized the contribution of number of siliqua/plant towards genetic divergence.

Our study reports siliqua/plant as the character which contributed maximum to the divergence of the yellow sarson genotypes under mid-hill conditions. This character is directly associated with yield, so scientific acumen can be exercised in selection of these economic characters in yellow sarson. Based on our studies genotypes Pusa Gold, NDYS 2018, SSY-1, Ragini, Jhumka, NDYS 9504 and GS-1 showed superiority in terms of yield and other component traits and can be promoted for cultivation in organic and mid-hill conditions.

Table 6. Contribution of characters towards divergence in 42 yellow sarson genotypes

Characters	Number of times ranked first	Percent contribution
Plant height	162	16.84
Number of primary branches	0	0.00
Days to 50% flowering	0	0.00
Days to maturity	2	0.00
Number of siliqua/plant	661	78.86
Length of siliqua	4	0.46
Number of seeds/siliqua	17	2.32
Seed yield/plant	12	1.51

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Correlation Studies for Quantitative Traits in Greengram [*Vigna radiata* (L.) Wilczek] Genotypes

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Greengram, an important grain legume of the arid and semi-arid regions has enough genetic diversity both for quantitative and qualitative characters. Genotypic correlation studies enable breeders to assess the inherent pattern relationship between various traits since it is based on heritable traits. The genotypic correlation for 40 greengram germplasm for 10 quantitative traits *viz.,* days to 50 per cent flowering, number of branches/plant, plant height (cm), number of clusters/plant, number of pods/plant, number of pods/cluster, number of seed/pod, pod length (cm), single plant yield (g) and hundred seed weight (g) were evaluated at two different centers *viz.,* Agricultural College and Research Institute, TNAU, Madurai (*kharif* 2012 and *rabi* 2012), and Agricultural Research Station, TNAU, Vaigai Dam (*kharif* 2012*)*. The correlation of yield and yield contributing characters indicated that seed yield/plant was positive and significantly associated with days to maturity, plant height, number of pods/plant, number of seeds/pod and hundred seed weight. Hence, characters such as plant height, numbers of pods/plant, number of branches/plant, number of clusters/plant and number of seeds/pod has to be given importance during the selection programme to improve the yield potential of the crop.

Key Words: Correlation, Germplasm, Mungbean, Quantitative characters

Introduction

Pulses are major source of dietary protein in the vegetarian diet in our country. Among the cultivated Asian *Vigna*, mungbean [*V. radiata* (L.)Wilczek] is the most important one (Rahman *et al.,* 2003). Besides being a rich source of protein, it maintains soil fertility through biological nitrogen fixation in soil and thus, plays a vital role in furthering sustainable agriculture. Mungbean is a short duration grain legume crops with wide adaptability and deep root system, low input requirements, and suitable for crop rotations, intercropping, relay cropping and as catch crop (Payasi *et al*., 2010). Genetic diversity in mungbean is an important factor and also a pre-requisite in any hybridization programme. Inclusion of diverse parents in hybridization programme serves the purpose of combining desirable recombinations (Gokulakrishnan *et al.,* 2012). Genotypic correlation enables the breeder to assess the inherent pattern relationship between various traits, since it is based on the heritable part. Hence, the present investigation was carried out with the aim to study the genotypic correlation for the yield contributing characters over different environments in mungbean germplasm.

Materials and Methods

The present investigation was carried out in 40 mungbean genotypes during *kharif* 2012 and *rabi* 2012. The trials were laid out in randomized block design with three replications at three different environments *viz.*, Agricultural College and Research Institute (ACRI), TNAU, Madurai (E1) *kharif* 2012, Agricultural Research Station, TNAU, Vaigai Dam (E2) *kharif* 2012 and ACRI, TNAU, Madurai (E3) *rabi* 2012. In this study, genotypic correlation for 10 quantitative traits *viz.*, days to 50 per cent flowering, number of branches/plant, plant height, number of clusters/plant, number of pods/plant, number of pods/cluster, number of seed/pod, pod length, single plant yield and hundred seed weight were analyzed. Phenotypic and genotypic correlation coefficients were calculated as outlined by Kwon and Torrie (1964). Genotypic correlation was tested for its statistical significance using the method of Reeve (1955). The genotypic correlation between yield and its component traits and among themselves was worked out as per the method suggested by Johnson *et al.* (1955) for three different locations.

Results and Discussion

Genetic diversity analyses can be performed on both qualitative and quantitative data or on a combination of both. To formulate any breeding programme with an objective of improving the yield and quality through selection, the inter-relationship among different characters is of paramount importance. It has been generally accepted

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that correlation between different characters represents a coordination of physiological processes, which is often achieved through well regulated gene expression (Mather and Jinks, 1971). Correlation coefficients at genotypic level were generally of higher magnitude than the corresponding phenotypic level indicating the strong association between the characters. The genotypic correlation for the 10 quantitative traits are presented location wise in Table 1 (E1 location), Table 2 (E2 location) and Table 3 (E3 location).

Seed yield was significant and positively correlated to number of pods/plant, hundred seed weight at genotypic level in E1 and E2 locations. Seed yield was significant and positively correlated to number of pods/cluster, at genotypic level in E2 and E3 locations. The correlation of yield and yield contributing characters indicated that seed yield/plant was positive and significantly associated with days to maturity, plant height, number of pods/plant, number of seeds/pod and hundred seed weight. Parameswarappa and Salimath (2007) reported similar findings in greengram.

It is obvious that improvement of one trait results in the simultaneous improvement of all positively associated component characters (Kalloo, 1998). Number of branches/plant exhibited positive and significant association with days to 50 percent flowering at E1 and E3 locations. Similar results were reported by Suresh *et al.* (2010) in greengram. Plant height had significant positive correlation with days to 50 percent flowering, number of branches/plant at all the locations. Number of pods/plant exhibited positive and significant association with number of clusters/plant at all the three locations. This was in confirmation with the findings of Muhammad Zubair *et al*. (2007) for number of pods/plant, number of clusters/plant and 100-seed weight, Rahim *et al.* (2010) for number of pods/plant and pod length in mungbean.

Table 1. Genotypic correlation coefficient of yield and yield attributing characters in AC & RI, Madurai, Kharif 2012 (E1)

Trait	Days to 50% flowering	Number of branches/ plant	Plant height	Number of clusters/ plant	Number of pods/ plant	Number of pods/ cluster	Number of seeds/ pod	Pod length	Hundred seed weight	Seed yield/ plant
Days to 50% flowering	1.000	0.747*	0.657*	-0.158	0.036	0.169	0.180	-0.179	-0.121	-0.193
Branches/ plant		1.000	0.813*	0.139	0.110	0.034	0.383*	-0.217	0.192	0.061
Plant height			1.000	0.069	0.204	0.053	0.395*	-0.228	0.228	0.122
Clusters/plant				1.000	0.445*	0.247*	0.596*	0.661*	0.283*	1.031*
Pods/plant					1.000	0.147	-0.012	-0.072	0.496*	0.522*
Pods/cluster						1.000	0.282*	0.223	0.026	0.153
Seeds/pod							1.000	0.923*	0.280*	0.539*
Pod length								1.000	0.194	0.574*
100-seed weight									1.000	0.456*
Seed yield/plant										1.000

*Significance at 5% level

Table 2. Genotypic correlation coefficient of yield and yield attributing characters in ARS, Vaigai Dam, Kharif 2012 (E2)

Trait	Days to 50% flowering	Branches/ plant	Plant height	Clusters/ plant	Pods/ plant	Pods/ cluster	Seeds/ pod	Pod length	100-seed weight	Seed yield/ plant
Days to 50% flowering	1.000	0.235	0.389*	0.084	0.307*	0.014	0.083	-0.325*	0.266*	0.198
Branches/plant		1.000	0.712*	-0.087	0.160	0.029	0.159	-0.353*	0.010	-0.005
Plant height			1.000	-0.070	0.014	-0.093	0.217	-0.274*	-0.118	-0.072
Clusters/plant				1.000	0.438*	0.063	0.406*	0.205	0.435*	0.300*
Pods/plant					1.000	0.604*	0.299*	-0.137	0.676*	0.765*
Pods/cluster						1.000	0.273*	-0.251*	0.186	0.445*
Seeds/pod							1.000	0.340*	0.015	-0.088
Pod length								1.000	0.040	-0.113
100-seed weight									1.000	0.487*
Seed yield/plant										1.000

*Significance at 5% level

Table 3. Genotypic correlation coefficient of yield and yield attributing characters in AC &RI, Madurai, Rabi 2012 (E3)

Trait	Days to 50% flowering	Branches/ plant	Plant height	Clusters/ plant	Pods/ plant	Pods/ cluster	Seeds/ pod	Pod length	100-seed weight	Seed yield/ plant
Days to 50% flowering	1.000	0.409*	0.624*	0.023	-0.218	0.019	0.120	0.016	-0.026	-0.052
Branches/ plant		1.000	0.654*	-0.174	-0.134	0.068	0.355*	0.104	0.040	0.096
Plant height			1.000	0.118	-0.022	0.031	0.249*	-0.004	0.008	0.256*
Clusters/plant				1.000	0.297*	0.161	0.668*	-0.073	-0.178	0.420*
Pods/plant					1.000	0.243	0.270*	-0.226*	0.360*	0.217
Pods/cluster						1.000	0.299*	-0.056	0.190	0.311*
Seeds/pod							1.000	0.009	0.302*	0.131
Pod length								1.000	-0.224	-0.124
100-seed weight									1.000	0.243
Seed yield/plant										1.000

*Significance at 5% level

The positive association between number of pods/ plant and plant height was observed by Suresh *et al.* (2010) in greengram. The positive association between number of pods/plant with number seeds/plant was observed by Konda *et al*. (2008). Number of seeds/pod had positive significant correlation with number of clusters/plant, number of pods/plant, number of pods/cluster at E1 and E3 locations. Mallikarjuna Rao *et al*. (2006) found significant positive correlation for number of branches/ plant in greengram. Hundred seed weight exhibited positive and significant association with number of pods/ plant, number of seeds/pod at E1 and E2 locations. In this study, the estimated correlation coefficients showed that not all the characters were interrelated with seed yield or among themselves.

Conclusions

It is concluded from the present study that seed yield/ plant was positive and significantly associated with days to maturity, plant height, number of pods/plant, number of seeds/pod and hundred seed weight. All the yield component traits *viz.*, days to 50 % flowering, plant height, number of branches/plant, number of clusters/ plant, number of pods/plant, pod length, number of seeds/pod and hundred seed weight were inter correlated among themselves. Therefore, these traits are to be given priority during selection programme to increase the single plant yield in greengram.

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Association and Multivariate Analysis of Yield and Yield Component Traits in Mungbean [*Vigna radiata* (L.) Wilczek]

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Magnitude of the genetic variability present in a population and divergence among the accessions are of paramount importance to a plant breeder for development of improved variety. In the present study correlation and path coefficient analysis, principal component analysis (PCA) and some selection parameters were computed for yield and its contributing characters in 51 mungbean genotypes. Significant variations among the genotypes were observed for all the characters. High heritability (broad-sense) along with high genetic advance was observed for all the characters except days to maturity. Pods/plant showed very high positive direct effect and significant positive genotypic correlation with seed yield/plant. The PCA segregated the 51 accessions into eight clusters in the scatter diagram. Eigen value more than one of the first four principal components contributed 79.18% of the total variability among 51 genotypes evaluated for 10 quantitative traits. Cluster VII had high mean value for plant height, primary branches/plant, secondary branches/plant, pods/plant, seeds/pod and seed yield/plant. Therefore, genotypes of cluster VII (ML-515, PUSA-105, T-44, and RMG-991) could be directly selected and utilized for improvement of these traits.

Key Words: Correlation, Mungbean, Path coefficient, Principal component analysis

Introduction

Green gram or mungbean [*Vigna radiata* (L.) Wilczek] is one of the important food legumes of many tropical and sub-tropical parts of the world. Among the pulse crops in India, mungbean is a highly valuable short duration crop with many desirable characters like high protein content, wide adaptability, low-input requirement and ability to improve soil fertility. The area under this crop is 3.55 million ha with an annual production of 1.82 million tonnes and productivity 512 kg/ha during 2010-11 (AICRP-MULLaRP, 2014). This low yield cannot meet the demand of our rising population. Development of high yielding varieties is one approach to overcome this problem and it is largely depend on the presence of heritable genetic variation in the base population. The estimation of genetic parameters like genotypic and phenotypic variability, genotypic and phenotypic coefficient of variation, heritability and genetic advance are useful for the effective selection and improvement of the base population. The study of correlation and path analysis for yield and its attributing traits will be helpful in improving the grain yield. Breaking the yield plateau which generally is due to narrow genetic base is achieved through diversification of parents. The present study was undertaken to assess the genetic variability, heritability, genetic advance, correlation, path coefficient and multivariate analysis of various desirable characters in 51 genotypes of mungbean, to identify promising lines for hybridization programmes and to explore yield potential and quality of mungbean.

Materials and Methods

The study was undertaken at Agricultural Research Farm, Banaras Hindu University, Varanasi during *kharif* and summer season of 2010-11. The experiment was laid out in a randomized complete block design with three replications in 51 mungbean genotypes. All the genotypes were collected from All India Coordinated Research Project of Pulses, Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, BHU, Varanasi. Each plot consisted of 3 m length with row-to-row and plant-to-plant distances being 45 and 10 cm, respectively. All cultural operations were carried out as per the package and practices recommended for raising a good crop. 15 plants were randomly selected from each genotype per replication for recording the data of 10 characters *viz* days to 50% flowering, days to maturity, plant height, number of primary branches/plant, number of secondary branches/plant, clusters/plant, pods/plant, seeds/pod, 100-seed weight and seed yield/plant. The pooled mean values over replications were

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subjected to computation for various genetic parameters. The genotypic and phenotypic variance, genotypic and phenotypic coefficient of variation and heritability were estimated (Singh and Choudhary, 1985). Genetic advance was computed by the procedure of Johnson *et al.* (1955). The data were also analyzed for estimating the correlation coefficient (Al-Jibouri *et al.,* 1958) and path analysis (Dewey and Lu, 1959) for grain yield and its component characters. Cluster and PCA was computed by Windostat Version 9.1.

Results and Discussion

Genetic Variability, Heritability and Genetic Advance

Analysis of variance revealed that there was significant variability for all the characters among the genotypes studied (Table 1). Range of variation was highest for plant height followed by pods/plant and clusters/plant, indicating maximum scope for the selection to improve these characters. Similar findings are reported by Gupta *et al.* (2004) and Kumar *et al.* (2010). The magnitude of phenotypic coefficient of variance (PCV) was higher than the genotypic coefficient of variance (GCV) for all the traits, indicating that significant role of environmental interaction for the expression of all the traits studied. Secondary branches/plant showed high difference between PCV and GCV in comparison to other characters indicating more environmental influence on this character.

The estimated values of broad sense heritability were high (>50%) for all the traits. Estimation of heritability along with genetic advance is more useful to understand the type of gene action involved in the expression of various polygenic characters. High heritability associated with high genetic advance as percent of mean (>20%) was obtained for all the characters except days to maturity. It indicates that probably heritability is due to additive gene effect and selection may be effective. Rahim *et al.* (2008) also reported high heritability coupled with high genetic advance for number of pods/plant, seed yield/plant and plant height in mungbean. Days to maturity had high heritability along with low genetic advance indicating non-additive type of gene action where genotype x environment interaction plays a significant role in the expression of this trait. Rao *et al.* (2006) also reported similar findings in mungbean.

Correlation and Path Coefficient Analysis

Genotypic and phenotypic correlations were estimated among 10 characters in 51 genotypes and these indicated inherent relations between any two traits were due to linkage or pleiotropic action of genes or both. The genotypic correlation coefficients were slightly higher in magnitude than the phenotypic correlation coefficients indicating the genetic variance is predominant in expression of characters (Table 2). Seed yield/plant showed significant positive genotypic and phenotypic correlation with pods/plant, 100-seed weight, primary branches/plant, seeds/pod, plant height and clusters/plant indicating these characters were strongly associated and positive correlation occurs due to coupling phase of linkage of genes controlling the characters. Rohman *et al*. (2003) also reported that seed yield showed strong

Table 1. Analysis of variance and estimates of genetic parameters for ten characters in 51 mungbean genotypes

Traits	Mean sum of squares (genotype)	Mean±S.E.	Range of variation	Coefficient of variation		Heritability (in broad sense %)	Genetic advance (% of mean)
				GCV	PCV		
Days to 50% flowering	64.52**	34.97±0.370	27.00-43.66	13.22	13.35	98.0	34.56
Days to maturity	80.46**	69.27±0.405	62.00-82.00	7.45	7.52	98.1	19.49
Plant height (cm)	418.56**	63.05±.963	42.66-91.00	18.67	18.86	97.9	48.79
Primary branches/plant	10.66**	5.92±.350	1.66-11.00	31.27	32.94	90.1	78.36
Secondary branches/plant	13.39**	4.57±.351	1.66-10.66	45.59	47.53	92.1	115.44
Pods/plant	116.03**	23.25±.696	9.66-41.66	26.57	27.08	96.2	68.82
Seeds/pod	4.01**	10.79±.352	8.00-15.00	10.20	11.69	76.1	23.50
Clusters/plant	73.78**	12.14±.667	3.66-26.66	40.48	41.61	94.6	103.98
100-seed weight (g)	1.67**	4.42±.056	3.30-6.16	16.83	16.98	98.2	44.05
Seed yield/plant (g)	18.11**	10.69±.276	3.83-6.16	22.84	23.29	96.2	59.15

*, **Significant at 5% and 1% level of significance, respectively

Table 2. Genotypic (G) and Phenotypic (P) correlation coefficients among seed yield and component traits in 51 mungbean genotypes

Traits		Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Pods/ plant	Seeds/ pods	Clusters/ plant	100-Seed weight (g)	Seed yield/ plant (g)
Days to 50% flowering	**G**	**1.000**	0.810**	0.201*	0.099	0.072	0.082	-0.023	-0.010	-0.056	0.033
	P	**1.000**	0.804**	0.200*	0.093	0.064	0.079	-0.030	-0.0048	-0.055	0.029
Days to maturity	G		**1.000**	0.013	-0.035	-0.057	0.078	-0.079	-0.072	0.123	0.090
	P		**1.000**	0.014	-0.033	-0.052	0.074	-0.073	-0.067	0.119	0.083
Plant height (cm)	G			**1.000**	0.562**	0.387**	0.333**	-0.087	0.462	-0.114	0.257**
	P			**1.000**	0.544**	0.366**	0.320**	-0.081	0.452**	-0.109	0.246**
Primary branches/ plant	G				**1.000**	0.569**	0.363**	-0.059	0.637	-0.044	0.338**
	P				**1.000**	0.540**	0.338**	-0.076	0.605**	-0.035	0.310**
Secondary branches /plant	G					**1.000**	0.374**	-0.199*	0.540	-0.369	0.059
	P					**1.000**	0.342**	-0.159*	0.490**	-0.347**	0.055
Pods/plant	G						**1.000**	-0.334**	0.453	-0.440**	0.574**
	P						**1.000**	-0.329**	0.432**	-0.431**	0.555**
Seeds/pods	G							**1.000**	-0.203*	0.256**	0.305**
	P							**1.000**	-0.177*	0.212**	0.320**
Clusters/plant	G								1.000	-0.160*	0.255**
	P								1.000	-0.158*	0.242**
100-seed weight (g)	G									**1.000**	0.339**
	P									**1.000**	0.336**

*, **Significant at 5% and 1% level of significance, respectively

positive genotypic and phenotypic correlation with pods/ plant, 100-seed weight and seeds/pod. Days to 50% flowering, days to maturity and secondary branches/plant showed non-significant correlation with seed yield/plant indicating these characters were independent and genes controlling these traits are located distantly on the same chromosome or located on different chromosomes.

Path analysis measures the direct and indirect contribution of various independent characters on a dependent character. The genotypic correlation coefficients were partitioned into direct and indirect effects by various yield contributing characters. Path coefficient analysis showed that pods/plant showed very high (>1) while 100-seed weight and seeds/ pod showed high (0.3-1) positive direct effect with seed yield/plant, as also reported by Gupta *et al*. (1982) and Rao *et al*. (2006). In contrast, days to 50% flowering, plant height, secondary branches/plant and primary branches/plant showed very low (0.0-0.09) positive direct effect with seed yield/plant while, days to maturity and clusters/ plant showed very low negative direct effects with seed yield/plant indicating that these characters are less important for yield improvement. Highly positive and indirect effect on seed yield/plant *via* clusters/plant, secondary branches/plant, primary branches/plant and plant height were exhibited by pods/plant which also showed high order negative indirect effect via 100-seed weight and seeds/pod. Seeds/pod exhibited high positive effect on 100-seed weight and negative indirect effect on seed yield *via* pods/plant, respectively. 100-seed weight showed low to high negative indirect effect on seed yield/plant through pods/plant, secondary branches/ plant and clusters/plant while, low positive indirect effect through seeds/pod. Thus, path coefficient analysis indicates that pods/plant, 100-seed weight and seeds/pod are important direct yield contributing traits and selection for these traits would be useful for yield improvement. Pods/plant, seeds/pod and 100-seed weight exhibited positive indirect effect *via* some characters on seed yield along with considerable negative indirect effect of some other characters, indicating that one character inhibits the effect of other character and is required to attain a proper balance of yield related traits for determining the ideotype for high seed yield in mungbean.

Principal Component Analysis

The PCA is a measure of the divergence between genotypes in terms of spatial distance. Fig. 1 gives the two-dimensional scatter diagram using principal component score II as X-axis and principal component score I as Y-axis wherein the 51 genotypes were distributed into eight clusters. Maximum number of genotypes grouped in cluster III and minimum in cluster IV. The maximum inter-cluster distance was observed between cluster VII and VIII (893.67), demonstrating maximum genetic diversity between these groups (Table 4). Hybridization between genotypes selected from these clusters are likely to produce most variable progeny and produce high heterotic response. The cluster mean values are presented in Table 5. Cluster VII had high mean value for plant height, primary branches/plant, secondary branches/plant, pods/plant, seeds/pod and seed yield/plant. This indicates that genotypes of cluster VII (ML-515, PUSA-105, T-44, and RMG-991) could be directly selected and utilized for improvement of these traits (Table 4).

Eigen value more than one of the first four principal components, contributed 79.18% of the total variability present among the 51 genotypes evaluated for 10 quantitative traits (Table 6). Rahim *et al.* (2008) have also observed that principal components which have eigen value more than one mostly contribute towards variability among the genotype. Eigen vector value of days to 50% flowering was positive for the all four principal components indicating this trait contributes maximum towards divergence. In the present study each principal

Table 3. Genotypic path coefficient matrix of seed yield vs. yield components of 51 mungbean genotypes

Traits	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Pods/plant	Seeds/ pods	Clusters/ plant	100-Seed weight (g)	Correlation with seed yield /plant (g)
Days to 50% flowering	**0.0686**	0.0556	0.0138	0.0068	0.0049	0.0056	-0.0016	-0.0007	-0.0039	0.0331
Days to maturity	-0.0791	**-0.0976**	-0.0013	0.0034	0.0057	-0.0076	0.0078	0.0070	-0.0120	0.0901
Plant height (cm)	0.0051	0.0003	**0.0253**	0.0142	0.0098	0.0084	-0.0022	0.0117	-0.0029	0.2575
Primary branches/plant	0.0013	-0.0005	0.0076	**0.0135**	0.0077	0.0049	-0.0008	0.0086	-0.0006	0.3386**
Secondary branches/plant	0.0011	-0.0008	0.0057	0.0083	**0.0146**	0.0055	-0.0029	0.0079	-0.0054	0.0590
Pods/plant	0.0857	0.0813	0.3469	0.3785	0.3898	**1.0403**	-0.3479	0.4713	-0.4587	0.5745**
Seeds/pods	-0.0107	-0.0370	-0.0408	-0.0277	-0.0929	-0.1558	**0.4659**	-0.0947	0.1195	0.3058**
Clusters/plant	0.0005	0.0031	-0.0200	-0.0275	-0.0234	-0.0196	0.0088	**-0.0432**	0.0070	0.2559**
100-seed weight (g)	-0.0393	0.0857	-0.0797	-0.0310	-0.2573	-0.3073	0.1788	-0.1121	**0.6969**	0.3399**

*, **Significant at 5% and 1% level of significance, respectively

Table 4. Cluster distances and distribution of 51 mungbean genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	No. of genotypes	Genotypes
I	**58.90**	140.47	192.56	204.31	169.20	251.33	400.52	226.10	10	ML-1465,HUM-12, ML-1451, MH-521,MH-318, DBG-1030,ML-713,ML-717,PDM-11, K-851
II		**134.76**	288.83	211.77	267.38	277.62	306.59	363.51	6	HUM-8, HUM-9, HUM-7, PUSA-0672, PUSA-9531, P-16
III			**210.84**	366.05	382.64	584.72	361.47	509.57	11	HUM-1, HUM-2, HUM-16, HUM-26, PUSA-0871, PUSA VISHAL, ML-1294, TM-96-2, HUM-15, SML-668, IPM- 02-17-3
IV				**0.00**	202.07	381.38	517.88	313.08	2	TARM-18, UPM-98-1
V					**0.00**	377.16	648.16	292.60	8	ML-1296, IPM-02-17,BDYR-1, DBG-1045, UPM-98-1, IPM- 02-17-19, T-9, DPM-90-1
VI						**0.00**	677.35	153.42	3	ML-5, PUSA RATNA, VRMGG-1/ V. Silvestris
VII							**0.00**	893.67	4	ML-515, PUSA-105, T-44, RMG-991
VIII								**0.00**	7	HUM-6, PDM-54,COGG-912,AKM-9904, TARM-1, VRMGG-1/V. trilogata,TM-2000-1

Table 5. Cluster means for different characters in 51 mungbean genotypes

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Pods/plant	Seeds/pods	Clusters/ plant	100-seed weight (g)	Seed yield/ plant (g)
I	38.58	70.58	46.42	4.83	4.67	20.25	10.33	9.00	3.85	7.80
II	35.58	67.58	68.50	5.92	4.25	13.83	10.50	12.08	4.40	6.51
III	30.71	65.24	57.83	5.19	4.50	23.90	10.69	10.57	4.10	10.27
IV	40.40	76.00	61.37	5.43	3.77	25.57	10.67	10.97	4.52	11.73
V	32.38	68.52	60.62	5.95	3.52	20.38	11.43	10.43	5.64	12.93
VI	35.17	74.83	50.17	4.33	2.17	13.17	11.33	11.17	5.62	8.37
VII	40.00	71.53	87.13	8.40	7.53	28.60	12.93	16.07	4.89	14.88
VIII	31.13	64.00	74.47	7.93	6.00	29.47	10.67	20.27	3.91	12.00

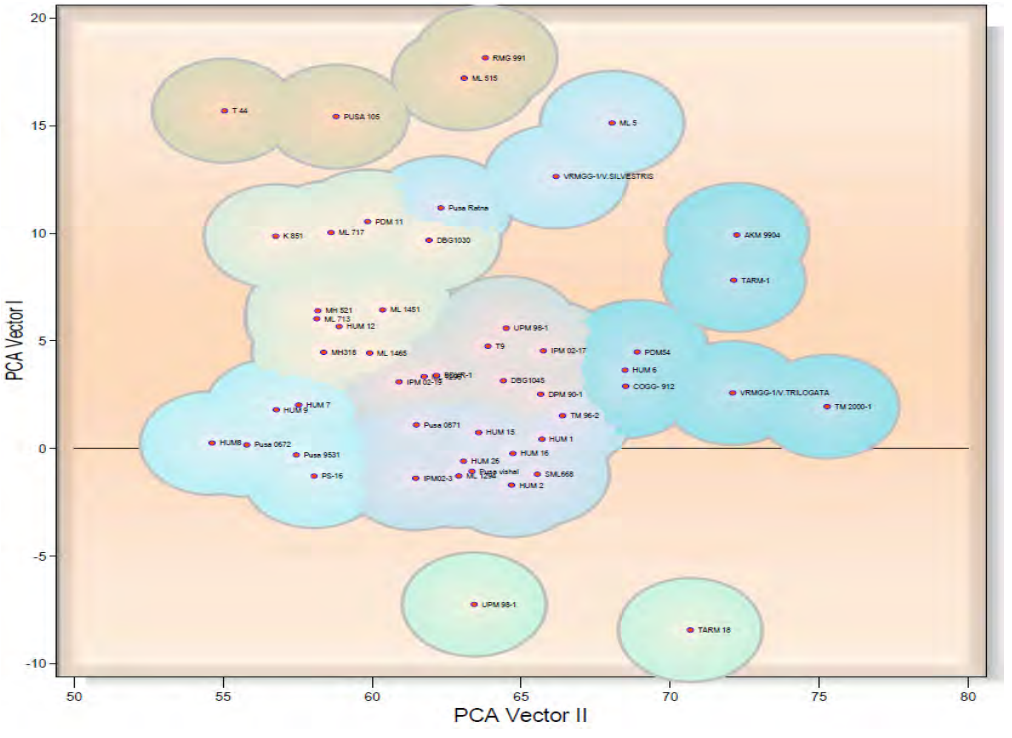

Fig. 1. Scatter diagram of 51 mungbean genotypes

component with traits having coefficient value greater than 0.3 are considered to be important on the overall variation. The first principal component contributes 36.40% of total variance and is determined by traits of pods/plant, seed yield/plant, seeds/pod, secondary branches/plant and plant height. Second principal component, accounting for 19.89% of the total variation, was determined by days to maturity, days to 50% flowering and seeds/ pod. Third and fourth principal components contributed 12.53% and 10.34%, respectively, of the variability present among the genotypes for the characters used in the present study. The variation present in third principal component was positively associated with plant height and negatively associated with primary branches/plant and clusters/plant whereas, fourth principal component was positively associated with days to 50% flowering and secondary branches/plant while negatively correlated with 100-seed weight and yield/plant. These results suggest that traits such as pods/plant, seed yield/plant, seeds/ pod, secondary branches/plant, plant height, days to 50% flowering and maturity were the principal discriminatory characteristics.

On the basis of finding of present study, it can be concluded that pods/plant, 100-seed weight, primary branches/plant, seeds/pod, plant height and clusters/ plant were identified as major components of seed yield

Table 6. Weighting coefficient (eigen vector), eigen values, variance (%) and cumulative variance (%) of first four principal components

Traits	Principal component			
	I	II	III	IV
Days to 50% flowering	0.073	0.559	0.169	0.468
Days to maturity	-0.082	0.583	0.015	-0.045
Plant height (cm)	0.362	-0.115	0.344	-0.110
Primary branches/plant	0.011	0.196	-0.788	0.137
Secondary branches/plant	0.374	-0.142	-0.057	0.464
Pods/plant	0.477	0.116	-0.025	-0.148
Seeds /pods	0.400	0.362	-0.003	-0.100
Clusters/plant	0.294	-0.252	-0.460	-0.066
100-seed weight (g)	-0.244	0.247	-0.127	-0.564
Seed yield /plant (g)	0.428	0.077	0.028	-0.422
Eigen value (root)	3.64	1.99	1.254	1.034
Variance (%)	36.402	19.899	12.539	10.341
Cumulative variance (%)	36.402	56.301	68.84	79.181

and should be given top priority for determining the ideotype for high seed yield in mungbean.

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Evaluation of Chinese Potato [*Plectranthus rotundifolius* (Poir.) Spreng.] for Yield Contributing Traits

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A replicated field evaluation trial was conducted involving 26 accessions of Chinese potato [*Plectranthus rotundifolius* (Poir.) Spreng.], an under-utilised tuber crop. In the present study, there were significant differences for the yield contributing characters between the accessions. Maximum yield was observed in IC468968 which showed highest value for both single plant yield (216.25g) and average weight of single marketable tuber (56.63g) and can be directly utilised in the crop improvement programme. IC412975 performed very poorly and had least value for all characters except for length of unmarketable tuber. A positive significant correlation between all the yield and yield contributing characters except tuber length and width of both marketable and unmarketable tuber was observed. Accessions grouped in the first cluster were high yielders with more than 150 g tubers/ plant, which can be further enhanced by adopting improved agronomic practices.

Key Words: Clustering, Evaluation, Tuber yield, Variability

Introduction

Chinese potato [*Plectranthus rotundifolius* (Poir.) Spreng.; syn. *Coleus parviflorus* Benth., *Solenostemon rotundifolius* (Poir.) J.K. Morton] is an important under-utilized tuber crop mainly grown in the tropical regions of India, Indonesia, Malaysia, Sri Lanka and Africa. It belongs to family Lamiaceae and is believed to have originated in Central or East Africa (Shoeninger *et al.*, 2000; Edison *et al.*, 2006) and spread throughout the tropics. The crop is cultivated for its edible underground tubers which are used as vegetables. Tubers are small with dark brown peel and creamish flesh, produced in clusters at the base of the stem. The aromatic flavour of the tuber makes it a sought vegetable and is reported to have medicinal properties due to the presence of flavanoids that help to lower the cholesterol level of blood (Horvath *et al*., 2004; Abraham and Radhakrishnan, 2005; Sandhya and Vijayalakshmi, 2005) and enzyme inhibitors (Prathiba *et al*., 1995). Tuber contains nutritional and large amount of secondary metabolites which helps in improving body immune system and defense against diseases (Anbuselvi and Hemapriya, 2013). Commercially, tuber size, shape and appearance are important physical quality features that determine both market value and consumer preference in Chinese potato. The most unfavourable feature of Chinese potato is the small and non-uniform size and often odd shape of the tuber due to which cleaning and de-skinning for culinary preparations becomes time consuming.

Chinese potato is normally propagated vegetatively by suckers or soft wood cuttings. Hence, gene flow among the individuals in a population is limited and heterogeneity in population is largely due to environmental variations. Lack of seed setting in the species is also responsible for low genetic variability. Highly irregular meiosis is reported to be a reason for sterility of the species (Ramachandran, 1976; Rajmohan, 2007). Hence, genetic component of the population variation from different regions can be identified and exploited through selection of superior populations.

Studies on characterisation and evaluation of Chinese potato in India are very limited (Muraleedharan *et al.* 1985; Sreekumari and Abraham, 1985; Amalraj *et al.* 1989). Mutation studies have been done in the past to introduce variability (Vasudevan and Jos, 1988, 1992; Abraham and Radhakrishnan, 2005). Though most of the morphological characters among the accessions studied showed less variation, tuber yield was found to vary significantly among them. An extensive study on morpho-agronomic characterization of 155 accessions of Chinese potato in Ghana was done by Nanema *et al.* (2009). They also observed variability in quantitative morphological traits within the germplasm collection. The research on improvement of Chinese potato is very scanty. Only few varieties have been released in this crop which includes Nidhi, Sreedhara and CO-1 from Kerala Agricultural University, Thrissur, Kerala; Central Tuber Crops Research Institute, Thiruvananthapuram, Kerala

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and Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, respectively.

The study of agro-morphological variability is the traditional method of assessing genetic diversity. Agro-morphological characterization, however, is often hindered by the limited number of polymorphic features and the need for multiple test environments (Kresovich *et al*., 1997). The present investigation was done to study the extent of genetic diversity in local collections of Chinese potato, using cluster analysis based on yield parameters with the aim to identify some promising genotypes.

Materials and Methods

The plant materials for the present study consisted of 26 accessions of Chinese potato collected from different parts of Goa (1), Karnataka (1) and Kerala (24) along with the check variety, Nidhi. The experiment was laid out in a completely randomised block design with two replications. One month old terminal shoot cuttings were used for planting. The cuttings were planted on raised beds at a distance of 1 m × 1 m between beds and 50 cm between plants in each bed during August 2013. Ten cuttings were planted on single bed size of 4.5 m × 0.50 m × 0.50 m dimension. Package of practices recommendations of Kerala Agricultural University, Kerala, India were followed (http://www.kau.edu/pop/contents.htm). The tubers were harvested separately for individual plants in each replication. Five randomly selected plants per replication per accession were used for recording yield data. The tubers were classified manually as marketable (having tuber circumference > 7 cm) and unmarketable (tuber circumference 0-7 cm) tubers, based on visual scrutiny for recording observation. The total rainfall obtained during the crop season was 110 cm with 54 rainy days. The minimum and maximum temperature observed were 22.2^{o}C and 32.6^{o}C, respectively. Flowering of all the accessions were observed during October-November. It started from 60 days of planting and continued for 2 months.

A total of nine yield contributing characters, namely, single plant yield and weight, length, diameter and circumference of tubers were recorded for five marketable and unmarketable tubers, respectively, and averaged for each replication and accession at the time of harvest. The length and diameter of the tuber was measured using Zoom Digimatic Calliper (Model no. Mitutoyo 500-322). The single plant yield in grams was measured using Docbel Braum Balance of maximum capacity of 1kg and minimum grading 5g. The weight of 5 marketable and unmarketable tubers was recorded separately using Afcoset Electronic Balance with a precision of 0.01g. Freely downloadable OPSTAT Package developed by CCS Haryana Agricultural University, Hisar, India was used for statistical analysis (http://www.hau.ernet.in/opstat.html). Cluster analysis was done using NTSYS (Rohlf, 2000).

Results and Discussion

Morphological Characterization

The crop was harvested after five months of planting. Significant differences between accessions were observed for all the characters except for average weight and width of single unmarketable tuber (Fig.1). Hence, there exists wide variability for yield contributing characters in the Chinese potato accessions under study (Table 1).

Table 1. ANOVA for yield characters in 26 Chinese potato accessions

Source of variation	Replication	Treatment	Error
DF	1	26	26
Single plant yield	5,007.41	4388.311**	577.13
Marketable tuber weight	400.493	199.891**	89.88
Marketable tuber length	1.376	0.818**	0.329
Marketable tuber width	0.252	0.423**	0.12
Marketable tuber circumference	1.457	3.792**	0.967
Unmarketable tuber weight	18.177	4.001	3.131
Unmarketable tuber length	2.311	0.179**	0.104
Unmarketable tuber width	0.955	0.033	0.026
Unmarketable tuber circumference	7.752	0.377**	0.206

DF= Degrees of freedom; ** Significant at 1% level

The tuber yield varied among the accessions from 58.50 g to 216.25 g on a per plant basis. Tarpaga (2001) and Nanema *et al*. (2009) observed mean single plant yield of 369.31 g and 62.07 g, respectively. After inducing mutation on 45 days old single node cuttings, Abraham and Radhakrishnan (2005) obtained single plant yield ranging from 54-126 g according to the cultivar.

Mean weight of marketable tubers was 36.51 g with a range of 8.74-56.63 g. The weight of unmarketable tubers ranged from 2.22-9.71 g with a mean value of 3.90 g. The mean length, breadth and circumference of marketable and unmarketable tubers observed were

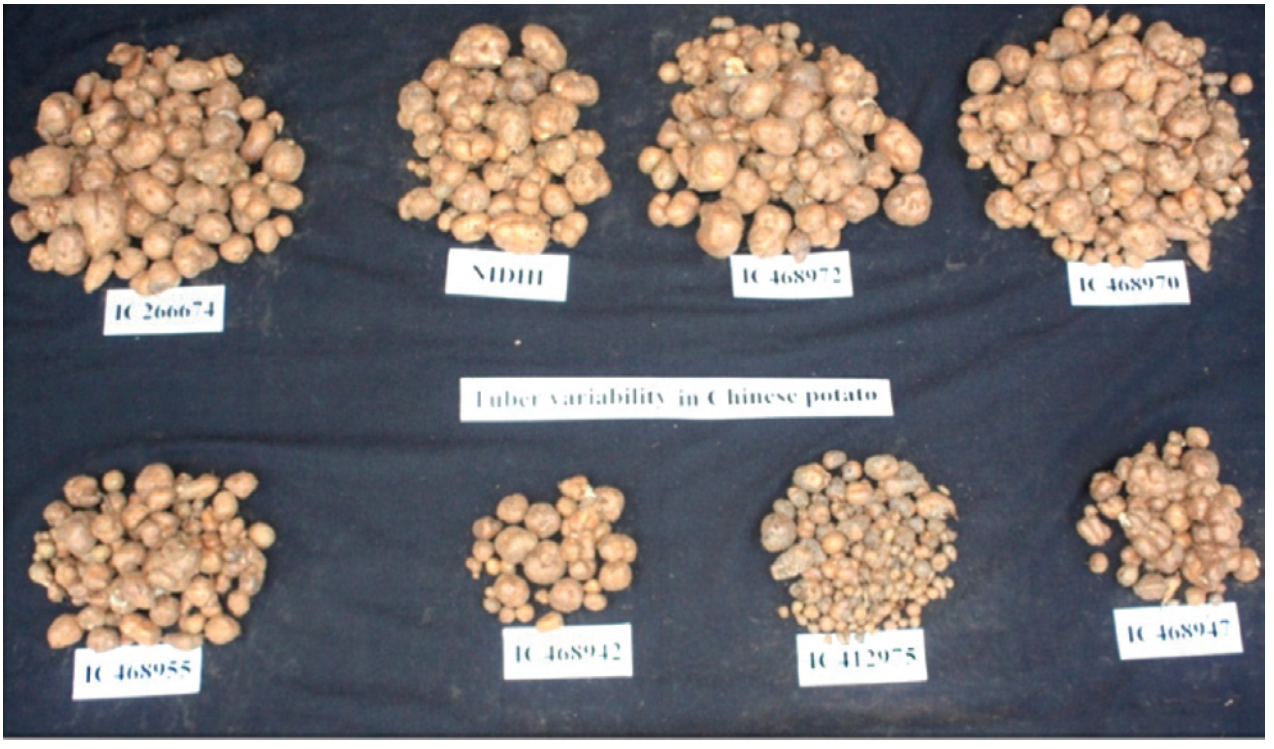

Fig. 1. Tuber variability in Chinese potato accessions

Table 2. Statistical and genetic parameters for yield contributing characters of 26 Chinese potato accessions

Traits	Range			PCV	GCV	H^2	Genetic advance	Genetic gain
	Minimum (g)	Maximum (g)	Mean (g)	(%)	(%)	(%)		(%)
Single plant yield (g)	58.50	216.25	145.89	34.15	29.92	76.75	157.57	54.00
Weight of marketable tuber (g)	8.74	56.63	36.51	32.97	20.32	37.97	9.41	25.79
Length of marketable tuber (cm)	2.66	5.86	4.12	18.40	12.01	42.57	0.66	16.14
Width of marketable tuber (cm)	2.29	4.37	3.83	13.61	10.17	55.90	0.60	15.67
Circumference of marketable tuber (cm)	7.07	13.74	12.12	12.72	9.80	59.37	1.89	15.56
Weight of unmarketable tuber (g)	2.22	9.71	3.90	48.38	16.90	12.20	0.48	12.16
length of unmarketable tuber (cm)	1.49	2.79	2.07	18.15	9.34	26.47	0.21	9.90
Width of unmarketable tuber (cm)	1.41	1.95	1.70	10.11	3.41	11.37	0.04	2.37
Circumference of unmarketable tuber (cm)	4.63	6.47	5.50	9.82	5.33	29.42	0.33	5.95

4.12 cm, 3.83 cm, 12.12 cm for marketable tubers and 2.07 cm, 1.70 cm and 5.50 cm for unmarketable tubers respectively. Nanema *et al*. (2009) recorded comparatively low values for average weight, length and diameter of big and small tubers in their study on morpho-agronomic characterisation of Chinese potato germplasm from Ghana. According to them, the average weight, length and diameter of big and small tubers were 0.34 g, 6.15 cm, 2.85 cm for big tubers and 46.06 g, 3.55 cm and 1.30 cm for small tubers, respectively.

In general, phenotypic coefficient of variation (PCV) was higher than its genotypic counterpart (GCV) for all the characters studied. PCV which measure total relative variance was high for single plant yield, average weight of single marketable and unmarketable tubers. It is likely that continuous vegetative propagation and selection has contributed to the phenotypic diversity observed. Relatively low to moderate GCV was recorded in all the characters except for single plant yield and average weight of single marketable tuber. Broad sense heritability

(H^2) ranged from11.37% (unmarketable tuber width) to 76.75% (single plant yield). High estimates of all the genetic parameters viz. PCV, GCV, H^2 and genetic gain as percentage of mean were observed for single plant yield character, was in consistent with the earlier study by Abraham and Radhakrishnan (2005), which indicate the presence of additive gene action. Hence, direct selection can easily be done for improvement of this character. Unmarketable tuber characters showed low values of PCV, GCV, heritability and genetic gain, depicting very low genetic variability for this character. Low variability in this species is attributed mainly to pollen sterility and problems of seed set (Rajmohan, 2007).

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Table 3 depicts the estimates of mean for yield contributing characters in 26 Chinese potato accessions. IC266674 (179.25 g), IC468961 (197.75 g), IC468963 (185.75 g), IC468964 (198.00 g), IC468966 (170.25 g), IC468967 (171.50 g), IC468968 (216.25 g), IC468969 (206.00 g), IC468970 (209.25 g), IC468972 (199.00 g) and IC469741 (187.00 g) out-yielded the check variety Nidhi (157.75 g) for single plant yield. Maximum yield was observed in IC468968 (216.25 g), which also showed highest values for marketable tuber weight (56.63 g) and was collected from Vettithodi area of Palakkad district (Kerala). IC412975 performed very poor and has recorded least values for all characters except unmarketable tuber

Table 3. Estimates of mean for yield contributing characters of 26 Chinese potato accessions and check variety Nidhi

Accn. No.	Single plant yield (g)	Marketable tuber weight (g)	Marketable tuber length (cm)	Marketable tuber width (cm)	Marketable tuber circum-ference (cm)	Unmarketa-ble tuber weight (g)	Unmarket-able tuber length (cm)	Unmarket-able tuber width (cm)	Unmarketable tuber circum-ference (cm)
IC266674	179.25	49.17	4.56	4.35	13.34	3.13	1.91	1.69	5.49
IC412974	122.25	32.63	3.51	4.13	12.96	3.65	2.27	1.71	5.61
IC468942	70.75	35.31	3.63	4.11	12.88	3.25	1.62	1.75	5.39
IC468945	96.25	35.76	3.43	3.98	13.31	3.16	1.49	1.81	5.25
IC468946	108.25	40.34	4.07	4.04	12.53	3.86	2.15	1.78	5.67
IC468947	81.75	27.52	3.57	3.62	11.65	2.76	1.81	1.59	5.33
IC468948	97.25	24.01	4.44	3.28	10.14	2.80	1.88	1.55	4.98
IC468950	91.00	27.93	3.79	3.79	11.62	3.22	1.92	1.74	5.58
IC468952	137.00	49.71	4.37	4.23	13.74	3.75	2.09	1.64	5.41
IC468955	105.00	26.77	3.75	3.49	10.72	3.38	2.03	1.60	4.92
IC468956	129.25	34.11	3.82	3.71	12.33	3.62	1.99	1.61	5.16
IC468957	115.00	29.76	3.40	3.98	12.78	2.95	1.90	1.54	4.94
IC468960	137.50	45.66	4.37	4.37	12.96	2.93	1.76	1.74	5.51
IC468961	197.75	43.83	4.68	3.85	12.20	9.71	2.15	1.66	5.37
IC468963	185.75	28.53	3.77	3.63	11.32	3.61	2.02	1.70	5.66
IC468964	198.00	33.44	4.13	2.91	11.08	3.51	2.10	1.52	5.33
IC468965	156.00	44.55	4.34	4.36	13.64	4.44	2.10	1.89	6.29
IC468966	170.25	35.02	4.21	3.93	12.58	3.62	2.10	1.74	5.69
IC468967	171.50	39.21	4.87	3.74	11.73	4.22	2.52	1.66	5.39
IC468968	216.25	56.63	5.08	4.36	13.56	3.52	1.94	1.67	5.36
IC468969	206.00	40.73	5.86	3.69	10.98	4.31	2.59	1.64	5.39
IC468970	209.25	39.82	4.57	3.77	11.87	3.21	2.05	1.63	5.21
IC468972	199.00	45.28	4.53	4.20	12.98	5.82	2.79	1.95	6.13
IC469690	155.50	29.14	3.49	3.76	12.13	5.24	2.47	1.89	6.15
IC469741	187.00	33.57	4.01	3.92	12.32	4.67	2.43	1.87	6.07
NIDHI	157.75	48.61	4.27	4.01	12.94	4.91	2.18	1.87	6.47

length (2.27 cm). No accession surpassed the control variety Nidhi (6.47 cm) for small tuber circumference.

Correlation studies were done in order to analyze the relationship between the yield characters in Chinese potato accessions. A positive significant correlation was observed between most of the yield characters studied except between single plant yield and marketable tuber width and between marketable tuber length and width. Unmarketable tuber length also did not correlate positively with unmarketable tuber width (Table 4). The lack of significant correlation between tuber yield with tuber length and girth was also observed by Sreekumari and Abraham (1985) and was stated to be due to the high heterogeneity of tubers observed among the accessions.

Cluster Analyses

The accessions were clustered into 3 groups based on the yield characters at a Euclidean distance of 27.88 (Fig. 2). Fourteen accessions were grouped in cluster I including the check variety Nidhi, 10 accessions in Cluster II and 3 in cluster III. The mean value for all other characters except marketable tuber width was maximum for cluster 1 as compared to cluster II and III. All the accessions grouped in the first cluster were high yielders having average single plant yield of 166.75 g (Table 5) which were collected from varied locations ie, one each from Mysore (Karnataka), South Goa (Goa), Kasaragod (Kerala) and 10 accessions from Palakkad (Kerala) districts.

All the yield characters recorded for accessions in cluster III were the lowest. However, accessions in the second cluster yielded between 91.00g to 137.50 g whereas accessions in the third cluster were low yielders with yield less than 82.00 g/plant. The accessions grouped in cluster II and III were from Palakkad and Malappuram districts of Kerala. Hence, on comparing the geographic locations of collections, homogeneity among accessions for yield characters were present even though there are collections from Goa and Mysore in first cluster.

This pattern of grouping of genotypes belonging to same location in different clusters and genotypes inhabiting from different localities in same cluster was earlier reported by Abraham and Radhakrishnan (2005) and indicated that factors other than geographical diversity may be responsible for such clustering. Absence of parallelism between geographical distribution and the

Table 4. Correlation matrix between different tuber characters in 26 Chinese potato accessions and check variety Nidhi

	Single plant yield (g)	Marketable tuber weight (g)	Marketable tuber length (cm)	Marketable tuber width (cm)	Marketable tuber circum-ference (cm)	Unmarket-able tuber weight (g)	Unmarket-able tuber length (cm)	Unmarket-able tuber width (cm)	Unmarketable tuber circum-ference (cm)
Single plant yield (g)	1								
Marketable tuber weight (g)	0.705**	1							
Marketable tuber length (cm)	0.846**	0.654**	1						
Marketable tuber width (cm)	0.260NS	0.880**	0.236NS	1					
Marketable tuber circumference (cm)	0.303*	0.836**	0.235NS	1.001**	1				
Unmarketable tuber weight (g)	1.351**	1.365**	1.443**	0.904**	0.662**	1			
Unmarketable tuber length (cm)	1.055**	0.750**	1.060**	0.491**	0.441**	1.080**	1		
Unmarketable tuber width (cm)	0.796**	1.842**	0.764**	2.013**	1.852**	0.330*	0.232NS	1	
Unmarketable tuber circum-ference (cm)	0.694**	1.000**	0.464**	1.157**	1.033**	0.453**	0.584**	1.200**	1

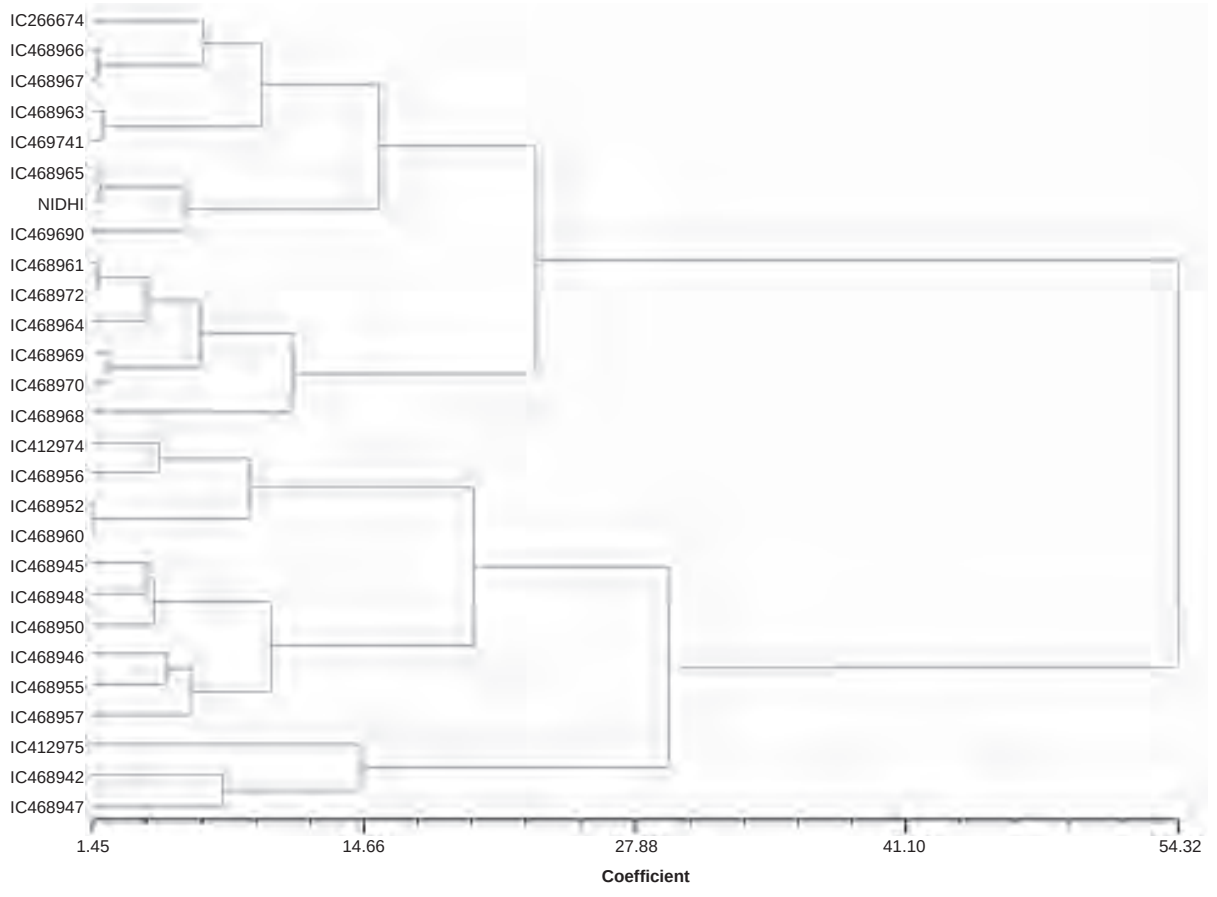

Fig. 2. Cluster analysis based on yield contributing characters in Chinese potato

Table 5. Cluster means for the characters under study in 26 Chinese potato accessions and check variety Nidhi

Trait	Cluster I 14 IC266674, IC468966, IC468967, IC468963, IC469741, IC468965, IC469690, IC468961, IC469972, IC468969, IC468964, IC468970, IC468968 and Nidhi	Cluster II 10 IC412974,IC468956, IC468952, IC468960, IC468945, IC468948, IC468950, IC468946, IC468955 and IC468957	Cluster III 3 IC412975, IC468942 and IC465947
Single plant yield (g)	166.75	113.89	70.33
Marketable tuber weight (g)	40.54	34.66	23.86
Marketable tuber length (cm)	4.45	3.89	3.28
Marketable tuber width (cm)	3.89	3.90	3.34
Marketable tuber circumference (cm)	12.33	12.31	10.53
Unmarketable tuber weight (g)	4.56	3.33	2.74
Unmarketable tuber length (cm)	2.24	1.95	1.71
Unmarketable tuber width (cm)	1.74	1.67	1.58
Unmarketable tuber circumference (cm)	5.71	5.30	5.12

genetic diversity was observed by Mannan *et al*. (1993) in *Colocasia*.

The single plant yield was found to be very significant among the accessions studied. High estimates of all the genetic parameters *viz.*, PCV, GCV, H^2 and genetic gain as percentage of mean observed for single plant yield character indicate the presence of additive gene action. Hence simple direct selection can be easily done for improvement of this character. IC468968 is a promising accession which can be further utilized in the crop improvement programme. The present study envisaged that the variability in Chinese potato can only be enriched by widening the germplasm collections. This underexploited tuber can be popularized among farmers by integrating in the sole cropping as well as to different farming systems such as rotation and intercropping.

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Identification of Transgressive Segregants for Yield and Its Components in Basil (*Ocimum basilicum* L.)

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The objective of this study was to estimate gene effects and identification of transgressive segregants for five quantitative traits of seven crosses of *Ocimum basilicum* L. *viz*. EC388788 × IC333322, EC387893 × IC326711, EC388896 × IC369247, EC388887 × IC386833, EC387837 × EC338785, IC369247 × IC370846 and IC344681 × IC326735 by generation mean analysis. In cases both type of epistasis (complementary and duplicate) model was sufficient to explain variation in generation means. Generation mean analysis with three parameter model with $\chi 2$ test indicated that additive-dominance model was inadequate for all the traits like number of inflorescence, length of inflorescence, fresh herb yield, dry herb yield and oil content in all the crosses used of six parameter models to estimate the gene effects. The observed frequencies of transgressive segregants for trait oil content (4.942), fresh herb yield (11.824), dry herb yield (13.97) and length of inflorescence (5.820). A comparison of generation mean analysis for observed and predicted frequencies of transgressive segregants indicated that the potential crosses for transgressive segregants were those that had additive and dominance gene effects. The adequacies of certain models of inheritance as well as the importance and significance of gene effects and identifications of transgressive segregants for analyzed traits were dependent upon the particular crossing combination and experimental site. The present study indicated that early generation selection is effective and should be practiced for future breeding programme.

Key Words: Gene effects, Generation mean analysis, Joint scaling test, *Ocimum basilicum*, Quantitative traits, Transgressive segregation

Introduction

The genus *Ocimum* of the family *Lamiaceae* is characterized by a great variability of morpho- and chemotypes (Balyan and Pushpangadan, 1988; Lawrence, 1988). The ease of cross-pollination leads to a large number of subspecies, varieties and forms (Guenther, 1949). The aromatic leaves of many *Ocimum* species are used fresh or dried as a flavouring agent for foods and as a remedy for many diseases, confectionery products and beverages. Traditionally, the basil plant has been used as medicine for its carminative, stimulant and antispasmodic properties. Based on chemical composition, several chemotypes of basil, like methyl cinematic, methyl chavicol, eugenol and linalool rich have been identified (Pareek *et al.,* 1982). Basil essential oil finds diverse uses in perfumery, pharmaceutical, cosmetics, food and flavour industries (Duglas, 1969). *Ocimum tenuiflorum* L. (the *tulsi)* leaf, when eaten, can control thirst, and so was invaluable to weary travellers (Lal *et al*., 2008; Lal, 2014). Generation mean analysis is a simple but useful technique for estimating gene effects for polygenic traits, its greatest merit lying in the ability to estimate epistatic gene effects such as additive x additive (aa), dominance x dominance (dd) and additive x dominance (ad) effects (Singh and Singh, 1997). Besides gene effects, breeders need information on the variation in a crop genepool and to what extent this variation is heritable, because efficiency of selection mainly depends on additive genetics variance, influence of the environment and genotype and environmental interaction (Lal *et al.,* 2013). The estimates of genetic parameters can be used to predict the frequencies of transgressive segregants that would appear in a F_2 generation. In the present study, attempts were made to predict the frequencies of transgressive segregants for yield and its components using generation mean analysis (GMA) and to test the validity of predictions by isolating the transgressive segregants for traits in F_2 population and carried out to provide information about gene effects for the most important quantitative traits of basil.

Materials and Methods

The present study was conducted at the Research Farm, Department of Genetics and Plant Breeding (formerly,

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Agricultural Botany), Ch. Charan Singh University, Meerut during 2007-08 and 2008-09. Experimental material of this study comprised 13 accessions of basil (*Ocimum basilicum* L.) obtained from National Bureau Plant Genetic Resources (NBPGR), New Delhi. The selection of parents was made on the basis of contrasting traits like number of inflorescence, length of inflorescence, fresh herb yield, dry herb yield and oil content. Thirteen accessions used in the study were, EC388788, EC387893, EC388896, EC388887, EC338785, EC387837, IC369247, IC344881, EC333322, IC326711, IC386833, IC370846 and IC326735. The six basic generation of P_1, P_2, F_1, F_2, B_1 (F_1 x P_1) and B_2 (F_1x P_2) of seven crosses *viz*. (i) EC388788 × IC333322, (ii) EC387893 × IC326711, (iii) EC388896 × IC369247, (iv) EC388887 × IC386833, (v) EC387837 × EC338785, (vi) IC369247 × IC370846 and (vii) IC344681 × IC326735 selected on the basis of GMA were used to determine gene effects and to predict the frequencies of transgressive segregants.

Six basic generations were grown in a randomized block design with three replications. The data on quantitative traits of number of inflorescence, length of inflorescence, fresh herb yield, dry herb yield and oil content were recorded on five randomly selected plants in each of P_1, P_2 and F_1 generations, 15 randomly selected plants each of B_1 and B_2 and 30 randomly selected plants of F_2 generation. The essential oil was extracted from the air dried herb by hydro-distillation using Clevenger's apparatus for 2.5 h. The estimates of GMA following a three parameter model of Jinks and Jones (1958) with joint scaling test of Cavalli (1952) were carried out to estimate the presence or absence of nonallelic interaction. A six parameter model suggested by Hayman (1958) to estimate variance components to fit models of increasing complexity until an adequate description of the means were found as shown by non-significance in the $\chi 2$ test. The type of epistasis was determined only when dominance (d) and dominance x dominance (dd) effects were significant; when these effects had the same sign the effects were complementary while different sign indicated duplicate epistasis (Kearsey and Pooni, 1996). The significance of genetic parameters was tested by t-test. In order to identify transgressive segregants in F_2 population, a total of 30 plants in each F_2 population from each replication were taken randomly. The predicted and observed frequencies of transgressive segregants for different traits in F_2 population of seven crosses were compared and the validity of prediction was tested using χ^2 test (Jinks and Pooni, 1976 and 1980). The frequencies of transgressive segregants were predicted as described by Yadav *et al*. (1998), on the basis of GMA and F_2 families. The estimates of d and D, D and H and d, h, i, j, and l calculated from generation mean analysis and were used to determine the frequency of transgressive segregation in above populations (F_2 population). The significance of transgressive segregation was tested using $\chi 2$ test.

Results and Discussion

Analysis of Variance (ANOVA)

The ANOVA for five quantitative traits recorded for 13 parents (P_1, P_2, F_1's, $F_{2's}$, $B_{1's}$ and $B_{2's}$) in the study are presented in Table 1. The mean squares due to treatment of all the five traits were highly significant, thereby, suggesting the presence of sufficient genetic variability in the materials under study.

Gene Effects

The GMA was performed for the additive – dominance model on six generation for all the traits (Table 2). The χ^2 (3d.f.) values were found to be significant in the six crosses except one cross (EC388788 × IC333322) for all the traits except for oil content in the three crosses EC388788 × IC333322, IC369247 × IC370846 and IC344681 × IC326735. In presence or absence of non-allelic interaction, rest of the traits were used in six parameters model to estimates of gene effects (Table 2). The additive component [d] was significant and pronounced for all

Table 1. Analysis of variance for five quantitative traits of 13 parents, F_1s F_2s, B_1s, and B_2s of seven crosses in basil

Source of variation	d.f.	Number of inflorescence	Length of inflorescence (cm)	Fresh herb yield (g)	Dry herb yield (g)	Oil content (%)
Replication	2	0.75	0.50	18848.00	3966.00	.020
Treatment	40	391.30**	48.82*	390958.40**	103503.00**	2.63**
Error	80	0.94	0.36	9650.60	9887.36	0.04

*, ** significant at 5% and 1% level of significance, respectively

Table 2. Estimates of genes obtained from three and six parameter model and observed and predicted frequencies of transgressive segregants in F_2 population for five traits of seven crosses in basil (*Ocimum basilicum* L.)

Model	Parameter	Traits				
		Number of inflorescence/ plant	Length of inflorescence (cm)	Fresh herb yield/plant (g)	Dry herb yield/plant (g)	Oil yield (%)
(1)	(2)	(3)	(4)	(5)	(6)	(7)
		EC388788 x IC333322				
3-Parameter	m	91.37**±0.64	18.55**±0.64	2269.09**±0.64	1158.73**±0.60	3.45**±0.64
	[d]	19.83**±0.63	1.87**±0.63	68.09±0.63	-84.50**±1.18	0.10±0.63
	[h]	1.38±1.18	0.19±1.18	286.89**±1.18	-100.43**±1.18	0.07±1.18
χ2 (3 d.f.)	Epistasis	25.71**	12.10**	38522**	26556.91**	1.20
Observed frequencies	TS	0.115	0.260	11.824**	1.176	0.029
χ2 (5 d.f.) Expected frequencies	3.841					
6-parameter	m	82.34**±0.56	14.25**±0.17	1580.00**±18.55	790.00**±5.77	–
	[d]	24.53**±1.21	4.98**±0.47	21.66**±119.28	-277.00**±28.14	–
	[h]	66.74**±3.20	19.22**±1.22	2435.83**±902.62	1531.45**±66.60	–
	[i]	29.57**±3.10	7.48**±1.17	2070.00**±901.62	1059.33**±62.00	–
	[j]	31.30**±1.20	4.31**±0.51	-1591**±443.94	-265.71**±31.40	–
	[1]	38.40**±5.38	18.51**±0.21	18.51**±0.21	-2831±1800.00	1062.90**±127.06
Epistasis effects		C	C	…….	C	–
		EC387893 × IC326711				
3-Parameter	m	103.37**±0.64	21.39**±0.64	1960.04**±0.64	744.73**±0.64	2.72**±0.64
	[d]	-178**±0.63	-187**±0.63	-154.66**±0.63	27.66**±0.63	0.66±0.963
	[h]	-178**±0.63	1.14±1.18	-398.28**±1.18	52.03**±1.18	1.64±1.18
χ2 (3 d.f)	Epistasis	56.97**±1.18	9.26**	54617.95**	4994.75	8.22**
Observed frequencies	TS	0.315	0.137	7.034**	13.031*	0.048
χ2 (5 d.f). Expected frequencies	3.841					
6-parameter	m	82.40**±0.83	23.50**±0.26	2603.00**±26.03	1066.66**±44.09	1.69**±0.33
	[d]	15.00**±0.81	10.90**±0.79	127.33**±27.77	40.00±26.14	-3.60**±0.02
	[h]	27.76**±3.76	-11.53**±1.85	-968.33118.02	1361.00**±351.73	14.05**±0.02
	[i]	8.39**±3.76	-19.31**±1.84	985.33±118.02	1046.00**±183.96	-3.50**±0.01
	[j]	18.50**±0.92	19.13**±1.80	280.00**±32.39	271.66±296.27	1.37**±0.10
	[1]	30.86**±4.83	14.39**±0.74	3600.00**±161.30	1243.33**±933.66	0.44±0.46
Epistasis effects		C	D	C	C	–
		EC388796 x IC369247				
3-Parameter	m	96.05**±0.964	20.78**±0.64	24.82.06**±0.64	1156.60**±0.64	2.75**±0.64
	[d]	10.29**±0.63	-1.87**±0.63	-111.00**±0.63	45.73**±0.63	0.43±0.63
	[h]	18.38**±1.18	1.14±1.18	-254.60**±1.18	4.07**±1.18	1.64±1.18
χ2 (3 d.f)	Epistasis	67.19**	22.45**	1648**	9733.26**	8.23**
Observed frequencies	TS	0.005	0.086	2.216	13.976**	4.942**
χ2 (5 d.f. Expected frequencies	3.841					

(1)	(2)	(3)	(4)	(5)	(6)	(7)
6-parameter	m	89.60**±0.83	17.17**±0.50	1655.00**±47.69	802.00**±27.15	4.59**±0.33
	[d]	21.50**±0.77	6.21**±0.35	320.00±658.33	-63.33±76.73	-1.02**±0.34
	[h]	49.96**±0.37	13.85**±2.48	1900.00**±655.54	1896.50**±189.10	6.07**±1.33
	[i]	44.60**±3.60	15.04**±2.46	675.00**±314.06	1412.20**±188.02	7.12**±1.33
	[j]	-98.33**±4.79	-13.70**±2.84	3288.00**±658.33	-2532.34**±328.23	9.31**±1.38
	[1]	-98.33**±4.79	-13.70**±2.84	3288.00**±658.33	-2532.34**±328.23	9.31**±1.38
Epistasis effects		D	D	C	D	C
			EC388887 x IC386833			
3- Parameter	m	90.49**±0.64	19.85*±0.64	2373.20**±0.64	997.24**±0.64	3.48**±0.64
	[d]	-2.81**±0.63	-3.43**±0.63	144.40**±0.63	-0.23±0.63	-0.23±0.63
	[h]	1.58±1.18	-3.01**±1.18	-357.40**±1.18	220.24**±1.18	0.51±1.18
$\chi 2$ (3 d.f)	Epistasis	30.71**	28.64**	73666.62**	24476.6**	1.33
Observed frequencies	TS	4.791**	0.568	12.52**	8.255**	0.278
$\chi 2$ (5 d.f). Expected frequencies	3.841					
6-parameter	m	93.86**±0.83	18.14**±0.50	2327.27**±14.05	1052.89**±37.78	–
	[d]	14.43**±0.61	-7.81**±0.46	-632.00**26.55	-418.80**±32.77	–
	[h]	31.38**±2.11	9.35*±2.43	-1285.00**±79.09	-197.12±183.36	–
	[i]	21.48**±1.78	10.30**±2.39	1445.00**±77.35	-309.00±164.00	–
	[j]	11.04**±0.80	-1.48**±0.50	-976.31**±124.67	-472.64**±44.01	
	[1]	88.01**±3058	-24.43±30.02	1581.10**±124.67	-37.30±25.60	
Epistasis effects						
			EC387837 x EC358785			
3-Parameter	m	88.80**±0.64	18.18**±0.64	1004.53**±0.64	1004.53**±0.64	4.90**±0.64
	[d]	6.40**±0.63	1.58**±0.63	8.33**±0.63	113.33**±0.63	-139±0.63
	[h]	-14.62**±1.18	-118±1.18	-357.40**±1.18	-19.09**±1.18	-1.73±0.63
$\chi 2$ (3 d.f)	Epistasis	44.83**	114.99**	73666.62**	61350.90**	9.66**
Observed frequencies	TS	0.015	5.820**	8.157**	1.231	0.107
$\chi 2$ (5 d.f) observed frequencies	3.841					
6-parameter	m	90.26**±0.58	16.82**±0.19	1816.31**±230.02	860.88**±12.07	3.27**±0.13
	[d]	-25.66**±2.90	0.50±0.62	934.00**±81.25	196.00±11.16	0.48*±0.20
	[h]	24.27**±2.90	-3.53*±1.48	545.00**±115.57	-216.10**±60.30	-1.07**±0.10
	[i]	28.59**±2.83	-1.48±1.43	857.41**±111.29	-109.54**±53.19	-5.80**±0.07
	[j]	-14.55**±0.83	-4.01**±0.68	1098.00**±32.62	248.64**±27.29	-0.20±0.75
	[1]	50.40**±4.17	14.31**±2.69	1368.00**±167.30	471.40**±60.90	3.50*±0.17
Epistasis effects		D	D	C	D	D
			IC369247 x IC370846			
3-Parameter	m	94.12**±0.64	23.20**±0.64	1140.41**±0.64	665.03**±0.64	3.56**±0.64
	[d]	5.14**±0.63	-3.50**±0.63	296.95**±0.63	121.66**±0.63	0.55±0.63
	[h]	-1.60±1.18	-1.60±1.18	705.64**±1.18	231.03**±1.18	0.12±1.18
$\chi 2$ (3 d.f)	Epistasis	139.95**	577.90**	554533.80**	10189.15**	0.49
Observed frequencies	TS	0.187	17.63**	43.14**	10.299**	0.074

(1)	(2)	(3)	(4)	(5)	(6)	(7)
$\chi 2$ (5 d.f) observed frequencies	3.841					
6-parameter	m	101.10**±0.57	14.30**±0.14	2308.00**±22.04	900.00**±28.86	–
	[d]	9.66**±0.55	-2.69**±0.43	-247.50**±55.43	45.33±69.19	–
	[h]	55.15**±2.60	7.34**±129	36.33±152.40	1118.00**±186.68	–
	[i]	44.30**±0.26	6.87**±1.11	-2583.00**±141.00	1117.33**±180.68	–
	[j]	18.48**±0.58	-5.58**±0.45	444.16**±60.99	-60.66±75.63	–
	[1]	74.70**±3.40	-2.62±2.18	593.33**±263.94	-1596.00**±315.00	–
Epistasis effects		C	D		D	–
			IC344681 x IC326735			
3-Parameter	m	91.03**±0.64	18.67**±0.64	1833.93**±0.64	815.57**±0.64	3.86**±0.64
	[d]	3.37**±0.63	-173**±0.63	179.53**±0.63	93.00**±0.63	-0.44±0.93
	[h]	-196±1.18	-196±1.18	160.27**±81.18	159.23**±1.18	-0.75±1.18
$\chi 2$ (3 d.f)	Epistasis	69.89**	56.61**	56991.24**	6964.56**	0.26
Observed frequencies	TS	0.056	0.063	11.118**	5.420**	0.290
$\chi 2$ (5 d.f) observed frequencies	3.841					
6-parameter	m	97.03**±0.54	21.16**±0.38	2197.00**±53.50	105.00**±28.86	–
	[d]	3.36**±0.69	-3.40**±0.80	-163.33**±67.16	-180.99**±48.69	–
	[h]	31.27**±2.62	-2.59±0.80	259.00±254.01	75.83±156.02	–
	[i]	31.27**±2.62	-6.98**±2.18	-880.00**±53.50	268.33±151.06	–
	[j]	19.16**±2.58	-2.80**±0.80	-577.00**±71.86	-1433.00**±52.53	–
	[1]	18.01**±3.65	-6.50±3.54	-3.94.00**±356.41	-338.33**±239.53	–
Epistasis effects		C	D	–	–	–

*Significant at <0.05, **significant at P<0.01, C = complimentary epitasis, D = Duplicate epistasis, TS = Transgressive segregants

the traits in all the crosses except to fresh herb yield for cross EC388788 × IC333322, dry herb yield in cross EC388796 × IC326711, length of inflorescence in cross EC387837 × EC358785. The dominance components [h] were found to be significant for all the traits in all crosses except length of inflorescence, fresh herb yield and dry herb yield in cross IC344681 × IC–326735. The additive x additive [i] components of epistasis were found to be significant for all the traits in all the crosses except to EC38887 × IC386833 for dry herb yield, EC387837 × EC358785 for length of inflorescence and IC344681 × IC326735 for dry herb yield. The additive x dominance [j] components of epistasis were found to be significant for all the crosses except to EC369247 × IC370846 for dry herb yield. The dominance x dominance [l] components of epistasis were found to be significant to all the traits in all the crosses except to EC388788 × IC333322 for fresh herb yield, EC38887 × IC386833 for length for inflorescence in crosses to EC369247 × IC370846 and IC344681 × IC326735, indicated that epitasis also played an important role in determining the inheritance of different traits in one or other crosses. Generation mean analysis showed that dominance, additive x additive and dominance x dominance gene action play important role in the inheritance of oil content. Similar results were found by Dani and Kohl (1989) and Kumar *et al.* (2012). The negative additive, dominance x additive and dominance x dominance estimate shows the gene pairs responsible for oil content are in dispersive form (Mather and Jinks, 1977).

Having considered the relative importance of different gene effects for the above traits in present study, a strategy could be developed for efficient breeding programmes aimed at improvement of that trait. As presented above, a trait has exhibited the preponderance of either additive gene effects or non-additive gene effects or both. Those traits showed that complimentary and duplicate types of gene interaction were present confirming the

importance of dominance effects as suggested by Grewall (1988). Thus, considerable non-additive genetic effects observed in this study suggests that selection in advanced generations may be more appropriate because effective selection in early generation of segregating material can be achieved only when additive gene effects are substantial and environment effects are small.

All the crosses exhibited complimentary type of epitasis for the number of inflorescence except cross EC388896 × IC369247 which showed duplicate type of epistasis. For this trait, dominance and dominance x dominance type of gene effect were predominant. The non fixable gene effects were higher than fixable gene effects indicating a greater role of non-additive gene effects, which suggested that this trait can be improved through recurrent selection. These results confirm the findings of Pathak *et al*. (2000); Kumar *et al*. (1994) and Noshin *et al*. (2003) who also reported the involvement of additive type of gene action for this trait. The non-additive type gene effect was found significant in cross EC388788 × IC333322 for the traits number of inflorescence per plant, length of inflorescence, fresh herb yield and cross in EC387893 × IC326711 for the traits number of inflorescence per plant, length of inflorescence, in cross EC388796 × IC369247 for all the traits, cross EC388887 × IC386833 only two traits like number of inflorescence per plant and fresh herb yield and in the cross of EC387837 × EC358785 for all the traits and cross IC369247 × IC370846 for two traits number of inflorescence per plant and dry herb yield per plant and cross IC344681 × IC326735 only for one trait like number of inflorescence per plats. The crosses EC387893 × IC326711, EC388896 × IC369247 and EC387837 × EC338785 showed duplicate type of interaction and the cross EC388788 × IC333322 showed complimentary type of epistasis for the trait length of inflorescence. The non-additive gene effects were predominant for the trait fresh herb yield. All the three type of non-allelic gene interaction were significant in all the crosses except EC388788 × IC333322. Duplicate type of interaction showed in cross EC387893 × IC326711. EC388896 × IC369247 and EC388887 × IC386833 showed complimentary type of epistasis. For dry herb yield, I-type was significant in crosses: EC388788 × IC333322, EC387893 × IC326711, EC388896 × IC369247, EC388887 × IC386833 and EC387837 × EC338785. J type of interaction was significant in EC388788 × IC333322, EC388896 × IC369247, EC388887 × IC386833, IC344681 × IC326735 and (l) type of gene interaction were found in EC388788 × IC333322, EC387893 × IC326711, EC388896 × IC369247, IC369247 × IC370846 and IC344681 × IC326735. In all the significant cases the magnitudes of (h), (i), (j) and (l) were higher than that of additive gene effects. In crosses (i) EC388788 × IC333322, (ii) EC387893 × IC326711 and (iii) IC344681 × IC326735 showed complimentary type of epistasis and duplicate type of epistasis showed in (ii) EC387893 × IC326711,(v) EC387837 × EC338785, (vi) IC369247 × IC370846. The crosses (iii) EC388896 × IC369247 showed complimentary and cross (v) EC387837 × EC338785 showed duplicate type of epistasis. This suggested that duplicate type of gene interaction were present, as also observed Grewall (1988). In crosses having considerable additive genetic affects with less environmental effects selections would be made in early generation of segregating materials.

Transgressive Segregants

Transgressive segregants were also observed during the present study (Table 2). The results indicated significant transgressive segregants for only few traits. The frequencies of transgressive segregants were predicted from GMA and F_2 family. For instance significant transgressive segregants were observed for fresh herb yield in IC369247 × IC370846 (43.14), EC388887 × IC386833 (12.52), EC388788 × IC333322 (11.824), IC344681 × IC326735 (11.18), EC387837 × EC358785 (8.15) and EC387893 × IC326711 (7.037), dry herb yield in EC388896 ×IC369247 (13.976), EC387893 × IC326711 (13.031), IC369247 × IC370846 (10.299), EC388887 ×IC386833 (8.255), IC344681 × IC326735 (5.420), oil content EC388896 × IC369247 (4.942), number of inflorescence in EC388887 × IC386833 (4.791) and length of inflorescence, EC388887 × IC386833 (17.63) and EC387837 × EC338785 (5.820). Of the traits in F_2 population in the present study, early generation selection is effective and should be practiced for future breeding programmers. The results of present investigation demonstrated that the genetic studies can provide information that could be used for predicating the frequencies of transgressive segregants for different traits in basil (Pooni and Kinks, 1978,1979). However, the limitation of GMA is the large amount of practical work required to produce the experimental generation. Therefore, attempts were made to compare the prediction of GMA with F_2 families. The results are in agreement with the results of some earlier workers such as McGinnins

and Shebeski (1968), De Pauw and Shebeski (1973), Sneep (1981),, Singh and Singh (1997). Significant differences between predicted and observed transgressive segregants for most of the traits in F_2 population in basil in the present study has indicated that early generation selection is effective and should be practiced for future breeding programmes. This approach will provide an opportunity for basil breeders to concentrate on a few potential crosses for getting transgressive segregants.

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Heterosis and Combining Ability in Partial Diallel Crosses of Sweet Pepper (*Capsicum annuum* L.)

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The present study was aimed at evaluating various crosses under a partial diallel mating design for quantitative and qualitative parameters to develop suitable F_1S. Heterosis and combining ability studies of 25 hybrids along with their 10 parents were carried out. Analysis of variance for combining ability revealed that variances due to GCA (general combining ability) and SCA (specific combining ability) were highly significant for all the characters studied indicating the importance of additive and non-additive gene effects. Significant relative heterosis was revealed in order of magnitude by total chlorophyll (283.10%) followed by fruit yield/plant (198.11%), ascorbic acid (148.22%) fruit weight (93.13%), number of fruits/plant (60.08%), pericarp thickness (40.74%), fruit circumference (34.23%) and fruit length (12.50%). In view of the best performance in yield, the F_1 hybrid (09/ Cvar1 x DARL 74) may be recommended for commercial utilization followed by (09/ Cvar 5 x DARL 82).

Key Words: *Capsicum annuum*, Combining ability, Heterosis, Partial Diallel Cross

Introduction

Sweet pepper or capsicum is normally considered as a luxury vegetable, consumption being greater in and around the cities (Singh *et al.*, 1993). Being a cool season crop, it is popularly grown in the hills of Uttarakhand, Himanchal Pradesh and Uttar Pradesh. Exploitation of hybrid vigour based on the information of combining ability is an important and efficient breeding approach in crop improvement. Thus, breeding value of an individual genotype becomes one of the significant criteria for selection as parental line to be used in hybrid breeding program. Due to environmental variance, selection of parents on the basis of *per se* performance may not necessarily lead to desirable results (Allard, 1960). The partial diallel mating system is suitable for estimation of combining abilities among crosses. The theory of partial diallel cross for a random set of genotypes was introduced (Kempthorne and Curnow, 1961). The number of crosses is reduced relative to the complete diallel, thus, allowing the evaluation of a greater number of parents or genotypes, which enhances the efficiency of the design for the estimation of variances and of combining abilities of the parents. F_1 hybrids in capsicum are gaining increasing popularity among farmers throughout the world. Hybrids play an important role in enhancing the yield potential (Mamedow and Pyshnaja, 2001).The present investigation therefore was undertaken to identify potential parental combinations in order to have superior hybrids of excellent quality coupled with high yields.

Materials and Methods

Ten diverse genotypes *viz.*, 09/Cvar 1, 09/Cvar 2, 09/ Cvar 3, 09/Cvar 4, 09/Cvar 5, 09/Cvar 6, DARL 73, DARL 74, DARL 7 and DARL 82 were crossed in a partial diallel mating design. A total of 25 hybrids were found successfully with S= 5 and K=3 (symmetrical circulant matrix A). This means that in each array, five crosses were made (S=5) and sampling was to begin after 3rd array i.e. from the fourth array. The experimental material consisting of 25 F_1S with their 10 parents was sown in February, 2012 and transplanted in the field in the month of April, 2012 in a randomized block design with three replications at Defence Institute of Bio Energy Research, Pithoragarh. Net plot size was 3 m x 2 m = 6 m^2. The inter-row and inter-plant distance was 50 cm x 50 cm. Observations were recorded on five randomly selected plants in each replication for fruit length (cm), fruit circumference (cm), fruit weight (g), fruits/plant (no.), fruit yield/plant (kg), pericarp thickness (mm), plant height (cm), ascorbic acid (mg/100g) and total chlorophyll (mg/100g), anti-oxidant activity (µg/100g). The pericarp thickness was measured with the help of Vernier Caliper and the mean values were calculated. Sweet pepper fruits with thicker pericarp not only withstand long distance transportation, but also have invariably longer shelf life (Choudhary *et al.*, 2011).

The chemical analyses of fresh fruits included determination of ascorbic acid by 2, 6 dichlorophenol indophenols titration method (AOAC, 1970) and total

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chlorophyll (Witham *et al.,* 1971). The dried fruits of parents and F_1 hybrids were analyzed for antioxidant activity using DPPH method (Hatano, 1988). Data were analyzed and found significant. The mean values of different genotypes for various characters were statistically analyzed using SPAR-1 programme of Doshi and Gupta (1981). SPAR I (developed by Indian Agricultural Statistical Research Institute, New Delhi, India) software was used for statistical analysis. Heterosis was expressed as percent deviation of the F_1 from mid parent (relative heterosis) and calculated by the formula given by Alllard (1960). Mid Parent Heterosis = F_1 Value – Mid Parent Value/ Mid Parent Value x 100.

Results and Discussion

Analysis of variance (ANOVA) for combining ability revealed that variances due to GCA (general combining ability) and SCA (specific combining ability) were highly significant for all the characters studied indicating the importance of additive and non - additive gene effects (Table 1). For almost all characters both additive and non-additive gene action influenced the performance of the hybrids. The non-additive effects played a more important role than additive effects. The magnitudes of GCA and SCA effects are indicative of the relative importance of additive and non-additive gene actions in the inheritance of a trait, respectively. Patil *et al.* (2010) studied combining ability analysis in chilli (*Capsicum annuum* L.) and found the same results. The magnitude of σ^2 GCA (variance of general combining ability) was lower than σ^2 SCA (variance of specific combining ability) for all the characters. The large GCA: SCA variance ratio suggests the importance of additive gene effects, while a low ratio signifies presence of dominant and/or epistatic gene effects. The lower σ2g/σ2s ratio indicates that the predominance of non-additive (dominance or epistasis) gene action is important for all the traits (Table 1). The involvement of non-additive gene effects suggests the improvement of these characters through hybrid breeding. Similar studies were carried out in Yelllow Sarson by Singh and Mishra (2001) and by Torres and Geradi (2007) in rice, Hasanuzzaman *et al.* (2012) in chilli, Chaudhary *et al.* (2013) in chilli and Nascimento *et al.* (2014) in pepper.

In the present investigation, potentiality of the parents was assessed by general combining ability effects (Table 2). Considering the GCA effects, the general combiners were DARL 82 (0.755) for fruit length, DARL 77(2.219) for fruit circumference, 09/Cvar 4 (18.859) for fruit weight, 09/Cvar3 (3.111) for fruit number, 09/Cvar 3 (0.318) for fruit yield per plant, DARL 82 (-6.496) for plant height, 09/Cvar 5 (45.731) for ascorbic acid, 09/ Cvar5 (2.358) for total chlorophyll, DARL 77 (-0.815) for antioxidant activity, 09/Cvar 4 (0.421) for pericarp thickness. High GCA effects are mostly due to additive gene effects or additive x additive gene effects. The negative estimates of GCA effects are desirable for reduce plant height and anti oxidant activity. Good general combiners for number of fruits/plant and yield of chilli were reported by a number of workers (Zewdie and Bosland, 2001; Prasath and Ponnuswami, 2008 and Payakhapaab *et al.*, 2012).

Among 10 parents used in the study, the parent 09/ Cvar 4 for fruit length, DARL 82 for fruit circumference and fruit yield per plant, 09/Cvar 5 for fruit weight and fruit number, 09/Cvar6 for ascorbic acid, pericarp thickness and plant height (dwarfness), 09/Cvar 3 for total chlorophyll and 09/Cvar 2 for antioxidant activity were found best as *per se* performance (Table 3). In order of merit DARL 82, DARL 73 and 09/Cvar 5 were found to be the best performing lines for yield/plant.

Significant relative heterosis was revealed (Table 4) in order of magnitude by total chlorophyll (283.10%) followed by fruit yield per plant (198.11%), ascorbic acid (148.22%), fruit weight (93.13%), number of fruits per plant (60.08%), pericarp thickness (40.74%), fruit width (34.23%) and fruit length (12.50%). The heterosis response observed in most of the hybrids further supported the predominant role of non-additive component in the inheritance of the character studied. Sood and Kaul (2006) also studied a diallel set of six pure lines in capsicum. For fruit length heterosis percentage ranged from -28.91 to 38.55 and the cross 09/ Cvar 2 x DARL 74 exhibited the maximum heterotic percentage (38.55%) followed by 09/ Cvar 3 x DARL 82 (30.20%). For the character fruit circumference, cross 09/ Cvar 2 x DARL 73 showed highest heterosis percentage (34.23) followed by 09/ Cvar 2 x DARL 77 (30.02). For fruit yield 09/ Cvar 1 x DARL 74 exhibited the highest heterosis percentage (198.11) followed by 09/ Cvar5 x DARL 82 (160.51). Cross 09/ Cvar1 x DARL 74 was found superior heterotic cross having relative heterosis 60.08 percent followed by 09/ Cvar 4 x DARL 73 (56.38%) for number of fruits per plant. For plant height 09/ Cvar 3 x DARL 74 exhibited the maximum negative heterosis (-37.40%) followed by 09/ Cvar4 x DARL 77 (-32.745) which is

Table 1. ANOVA for combining ability for quantitative and qualitative characters

Source	df	Fruit length (cm)	Fruit circum-ference (cm)	Fruit weight (g)	Fruit number (no)	Fruit yield (kg)	Plant height (cm)	Ascorbic acid (mg/100g)	Total chlorophyll (mg/100g)	Anti Oxidant activity (µg/100g)	Pericarp thick-ness (mm)
GCA	9	1.381**	20.40**	1465.88**	42.02**	0.558**	281.9**	7527.96**	30.4**	1.215**	0.6326**
SCA	24	1.458**	10.54**	729.93**	54.27**	0.095**	406.8**	11207.91**	27.71**	1.688**	1.477**
Error	48	0.645	1.224	56.99	1.208	0.0192	20.262	50.69	.0134	.00209	0.0432
Variance of GCA	σ^2 GCA	-0.057	0.739	55.19	-0.918	.0347	-9.369	275.99	0.2027	-0.354	-0.0633
Variance of SCA	σ^2 SCA	1.131	1.310	224.31	17.39	.0253	128.85	3719.07	1.923	1.229	0.4781
Average degree of variance	$\sqrt{\sigma^2}$ GCA/ σ^2 SCA	-4.45	1.548	2.01	-4.352	0.853	-3.708	3.670	3.080	-1.863	-2.748

**, Significant at 1% level.

Table 2. Estimates of general combining ability (GCA) for different characters

Parents	Characters									
	Fruit length (cm)	Fruit circum-ference (cm)	Fruit weight (g)	Fruit number (no.)	Fruit yield (kg)	Plant height (cm)	Ascorbic acid (mg/100g)	Total chlorophyll (mg/100g)	Antioxidant activity (µg/100g)	Pericarp thick-ness (mm)
09/Cvar 1	-0.159	0.286	-0.934	-0.508	-0.328**	7.469**	-50.803**	0.462**	0.155**	-0.117
09/Cvar 2	0.364	1.055	2.590	-3.157**	0.075	-1.292	-7.751	-2.293**	0.576**	0.149
09/Cvar 3	-0.512	-1.010	0.953	3.111**	0.318**	-4.43**	-22.736**	-1.538**	0.313**	-0.203
09/Cvar 4	0.671	0.874	18.859**	1.665	0.278**	4.982**	30.849**	0.564**	-0.151**	0.421
09/Cvar 5	-1.155	-1.993*	-17.522**	-0.476	-0.145**	3.645**	45.731**	2.358**	0.358**	0.063
09/Cvar 6	-0.314	-2.230*	-7.071*	1.463	-0.192**	0.734	5.576	2.126**	-0.328**	-0.273
DARL 73	-0.097	0.355	-7.549*	0.338	-0.047	-0.845	-2.342	-1.468**	0.327**	-0.042
DARL 74	0.158	-0.328	5.108	0.470	0.102	-3.853**	4.800	0.860**	-0.125**	0.089
DARL 77	0.289	2.219*	-7.198*	-1.657	0.001	0.087	7.925	-0.807**	-0.815**	0.060
DARL 82	0.755	0.862	12.763**	-1.250	-0.062	-6.496**	-11.224	-0.267**	-0.311**	-0.145
(Gi-Gj)	0.851	1.957	135.41	10.06	0.017	75.47	2079.31	1.514	1.277	0.274

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

Table 3. *Per se* performance of parental lines for different characters

Parents	Characters (per se performance)									
	Fruit length (cm)	Fruit width (cm)	Fruit weight (g)	Fruit/plant (no)	Fruit yield/ plant (kg)	Plant height (cm)	Ascorbic acid (mg/100g)	Total chlorophyll (mg/100g)	Antioxidant activity (µg/100g)	Pericarp thickness (mm)
09/Cvar 1	8.70	23.00	95.00	15.33	0.780	60.00	133.00	5.30	2.42	3.52
09/Cvar 2	7.60	17.40	49.00	15.67	0.540	91.20	83.00	11.01	1.48	2.66
09/Cvar 3	7.67	17.00	77.33	21.33	0.380	93.87	72.00	14.17	2.04	2.32
09/Cvar 4	11.07	24.67	59.00	13.33	0.640	68.80	127.00	0.94	3.73	2.95
09/Cvar 5	10.13	20.53	108.67	22.00	1.050	56.87	154.00	7.90	5.07	3.33
09/Cvar 6	8.40	19.40	66.23	15.33	0.740	52.67	200.00	8.55	7.53	4.15
DARL 73	9.27	19.00	58.33	12.67	1.140	65.33	180.00	3.93	2.38	3.10
DARL 74	9.00	21.67	79.33	18.00	1.040	66.93	90.00	0.84	2.34	2.01
DARL 77	10.80	22.43	100.00	14.00	1.010	68.97	163.00	7.38	1.70	3.55
DARL 82	9.93	25.20	76.67	11.10	1.190	68.13	127.33	3.47	2.23	2.94
CD @ 1%	2.309	3.178	5.688	3.932	0.397	4.811	5.565	0.332	.0415	0.594
CD @ 5%	1.936	2.665	4.770	3.297	0.333	4.035	4.667	0.279	0.034	0.498
SEM	0.656	0.903	1.616	1.117	0.113	1.367	1.581	.0946	.0118	0.169

a desirable character. For antioxidant activity, 09/ Cvar 4 x DARL 74 (-70.15% heterosis) expressed highest antioxidant activity followed by 09/ Cvar 6 x DARL 77 (-67.81% heterosis). For ascorbic acid content, 09/ Cvar 3 x DARL 74 was found superior heterotic cross (148.22%) followed by 09/ Cvar 3 x DARL 74 (134.56%) and 09/ Cvar1 x DARL 74 (95.51%). For the character total chlorophyll, the cross combination 09/ Cvar 4 x DARL 82 was found superior having heterosis percentage (283.10) followed by 09/ Cvar1 x DARL 74 (172.63%). Heterosis for green fruit yield and its components in chilli was also studied by Patel *et al.* (2010). Heterosis studies for earliness, fruit yield and yield attributing traits in bell pepper was studied by (Sood and Kumar, 2010a; Sood and Kumar, 2010b; Shrestha *et al.*, 2011; Sharma *et al.,* 2013).

In the present study, three type of cross combinations were involved such as high x high, high x low and low x low, of which high x low combinations exhibited high heterosis, while high x high combinations showed less heterosis and low x low combinations showed considerable heterosis. The reason may be additive x additive and additive x dominance gene interactions. Negative significant heterosis may be due to inhibitory gene action and suppression of multiple allele by dominant gene.

From the present investigation, it is concluded that the general combiners for different characters can be used in future breeding programme for the development of varieties. To achieve higher yield through F_1 hybrid, the parental lines chosen should possess one or more of the important character like fruit yield/plant, fruit weight, number of fruits/plant along with bio-chemical parameters like ascorbic acid and antioxidant activity. The cross combinations had high heterosis for most of the yield contributing traits. These hybrids offer high scope for the exploitation of heterosis for improving horticultural traits. These cross-combinations could be utilized as hybrid breeding and can also be released as hybrids after further field testing. In view of the best performance in yield, the F_1 hybrid (09/Cvar1 x DARL 74) may be recommended for commercial utilization followed by (09/ Cvar 5 x DARL 82).

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Table 4. Per se performance of parental lines for different characters in hybrids and Heterosis percentage over mid parent value (Relative Heterosis %)

Hybrids	Characters									
	Fruit length (cm)		Fruit width (cm)		Fruit weight (g)		Fruit/plant (no)		Fruit yield/plant (kg)	
	per se performance	Relative heterosis (%)	per se performance	Relative heterosis (%)	per se performance	Relative heterosis (%)	per se performance	Relative heterosis (%)	per se performance	Relative heterosis (%)
09/Cvar 1 x 09/Cvar4	9.20	-6.88	21.40	-10.19**	88.33	14.71**	22.00	53.63**	1.780	150.70**
09/Cvar 1 x 09/Cvar5	9.43	0.11	19.17	-11.90**	86.67	-14.18**	24.67	32.20**	1.830	100.00**
09/Cvar 1 x 09/Cvar6	7.50	-12.28**	17.33	-18.25**	57.67	-28.45**	13.33	-13.04**	1.190	56.57**
09/Cvar 1 x DARL 73	8.17	-9.02	21.73	3.47	60.00	-21.73**	15.00	7.14	1.430	57.14**
09/Cvar 1 x DARL 74	10.63	20.11**	20.60	-7.78	110.00	26.20**	26.67	60.08**	2.370	198.11**
09/Cvar 2 x 09/Cvar5	10.20	15.12**	21.07	11.07**	101.67	28.95**	18.00	-4.46	1.430	123.40**
09/Cvar 2 x 09/Cvar6	10.13	20.02**	21.20	15.21**	95.00	64.87**	23.90	54.19**	1.350	60.71**
09/Cvar 2 x DARL 73	10.47	24.50**	24.43	34.23**	96.67	80.15**	19.37	36.69**	1.260	59.49**
09/Cvar 2 x DARL 74	11.50	38.55**	22.47	15.05**	110.00	71.44**	15.87	-5.76	1.340	49.72**
09/Cvar 2 x DARL 77	8.13	-11.63**	20.57	30.02**	70.00	-6.04	16.50	11.26**	1.130	101.78**
09/Cvar 3 x 09/Cvar6	8.20	1.99	19.67	8.07	57.67	-19.05**	17.27	-5.78	0.850	11.84
09/Cvar 3 x DARL 73	10.00	18.06**	21.50	19.44**	83.67	23.35**	13.50	25.92**	0.830	5.06
09/Cvar 3 x DARL 74	10.43	25.21**	20.80	7.60	72.67	-7.22	18.33	39.81**	0.620	-10.79
09/Cvar 3 x DARL 77	9.30	51.21**	18.47	-6.29	78.00	-12.02**	16.27	0.24	0.740	-5.73
09/Cvar 3 x DARL 82	7.63	30.20**	21.77	3.17	71.67	-6.92	14.30	32.28**	0.730	-7.00
09/Cvar 4 x DARL 73	12.13	19.27**	25.10	14.92**	113.33	93.19**	20.33	56.38**	1.646	84.94**
09/Cvar 4 x DARL 74	9.46	5.77	22.00	-5.04	100.00	44.59**	17.66	12.77**	1.410	67.86**
09/Cvar 4 x DARL 77	8.66	18.79**	21.33	-2.33	60.00	-24.52**	20.00	46.11**	1.233	49.45**
09/Cvar 4 x DARL 82	7.80	-25.71**	23.66	-5.13	58.33	-14.01**	18.10	47.99**	1.348	47.32**
09/Cvar 5 x DARL 74	11.20	19.65**	22.16	5.02	103.33	9.92	22.60	13.00**	1.835	51.65**
09/Cvar 5 x DARL 77	10.40	-0.57	22.33	3.95	70.66	-32.28**	24.50	36.11**	1.353	20.80
09/Cvar 5 x DARL 82	7.13	-28.91**	23.33	2.05	100.00	7.90	23.33	40.12**	1.935	160.51**
09/Cvar 6 x DARL 74	12.50	30.20**	22.50	7.60	115.00	30.35**	20.00	36.42**	1.736	98.40**
09/Cvar 6 x DARL 77	7.43	-18.91**	18.33	-17.80**	76.66	7.29	16.00	21.02**	0.790	-18.13
09/Cvar 7 x DARL 82	8.56	-10.83**	19.76	-10.58**	60.00	-11.11**	12.33	3.78	0.536	-55.99**

** Significant at 1 % level

contd....

Table 4. contd....

Hybrids	Characters									
	Plant height (cm)		Ascorbic acid (mg/100g)		Total chlorophyll (mg/100g)		Antioxidant activity (µg/100g)		Pericarp thickness (mm)	
	per se performance	Relative heterosis (%)	per se performance	Relative heterosis (%)	per se performance	Relative heterosis (%)	per se performance	Relative heterosis (%)	per se performance	Relative heterosis (%)
09/Cvar 1 x 09/Cvar4	62.87	-2.38	136.00	4.61	3.50	8.01	2.73	-11.36	2.29	-29.32**
09/Cvar 1 x 09/Cvar5	56.33	-3.61	180.33	25.78**	5.19	21.36**	4.29	14.70	4.13	-33.23**
09/Cvar 1 x 09/Cvar6	61.67	-8.65	100.67	-39.53**	4.99	-29.29**	2.33	-53.21**	2.42	7.55
09/Cvar 1 x DARL 73	58.33	-6.91	94.33	-39.91**	3.27	-29.22**	2.51	4.58	2.53	-26.88**
09/Cvar 1 x DARL 74	57.00	-10.17**	218.00	95.51**	8.37	172.63**	1.33	-44.11**	2.41	-7.24
09/Cvar 2 x 09/Cvar5	72.67	-1.85	163.00	37.55**	9.94	5.10	2.53	-22.86	2.64	-19.39
09/Cvar 2 x 09/Cvar6	65.67	-8.71	236.00	66.78**	8.05	-17.68	3.10	-31.11**	3.93	-22.58
09/Cvar 2 x DARL 73	86.67	10.73**	209.00	58.33**	7.18	-3.88	2.22	15.02	4.29	36.45**
09/Cvar 2 x DARL 74	65.00	-17.87**	100.00	15.60	3.70	-37.50**	2.10	9.94	2.68	15.02
09/Cvar 2 x DARL 77	66.67	-16.84**	104.00	-15.44	8.11	-11.75	2.32	45.91**	2.63	-13.82
09/Cvar 3 x 09/Cvar6	69.33	-5.38	209.00	53.67**	7.20	-26.38**	2.15	-47.94**	2.39	-18.83
09/Cvar 3 x DARL 73	63.00	-20.85**	314.00	148.22**	7.45	-17.67	1.67	-24.43	3.04	9.59
09/Cvar 3 x DARL 74	50.33	-37.40**	190.00	134.56**	8.60	14.66	1.45	-33.78**	2.83	40.74**
09/Cvar 3 x DARL 77	55.33	-32.04**	102.00	-13.19	8.53	-20.72	3.21	71.65**	2.95	-3.74
09/Cvar 3 x DARL 82	60.00	-25.92**	104.67	5.02	5.24	-40.58**	1.56	-56.66**	3.27	12.16
09/Cvar 4 x DARL 73	47.83	-28.77**	293.00	90.25**	4.95	102.86**	1.57	-48.85**	3.15	7.92
09/Cvar 4 x DARL 74	56.00	-17.48**	172.00	58.52**	7.45	0.078	1.68	-70.15**	2.23	27.01**
09/Cvar 4 x DARL 77	46.33	-32.74**	93.00	-35.86**	5.20	25.00**	1.66	-38.75**	2.01	-31.38**
09/Cvar 4 x DARL 82	48.00	-29.89**	95.00	-25.29**	8.43	283.10**	2.08	-2.11	3.08	-31.86**
09/Cvar 5 x DARL 74	63.73	4.30	136.00	11.47	8.44	93.14**	1.47	-60.24**	2.66	-80.34**
09/Cvar 5 x DARL 77	63.66	2.84	154.00	-2.83	7.10	-7.06	1.48	-56.50**	2.76	-22.67
09/Cvar 5 x DARL 82	62.40	-0.82	236.00	67.78**	4.40	-22.53	1.43	-60.87**	2.98	-12.10
09/Cvar 6 x DARL 74	66.30	9.01	100.00	-44.98**	8.15	2.38	1.49	-67.81**	3.64	-13.37
09/Cvar 6 x DARL 77	57.50	-4.80	105.00	-35.84**	4.28	-28.78**	2.01	-58.70**	3.38	7.30
09/Cvar 7 x DARL 82	56.66	-15.09**	94.00	-39.02**	4.09	10.59	2.31	0.52	3.11	2.98

** Significant at 1 % level

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National Herbarium of Cultivated Plants (NHCP): Importance of Voucher Specimens of Introduced Germplasm

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Herbarium specimens representing plant genetic resources introduced from abroad, are a distinctive component of the National Herbarium of Cultivated Plants (NHCP). These specimens represent diversity augmented in crops and wild species mostly not native to the Indian region. Herbarium specimens, bearing the unique identity number assigned to germplasm introduced into the Indian region, were screened, checked with primary and secondary data records for identity, source locality/area, and its availability as *ex situ* germplasm. Additional data on area of origin/ diversity of species was used to delineate specimens of value in PGR and represented as cultigens, cultivars, both popular and historic, as well as local morphotypes and ecotypes of crops, as well as wild relatives of crops.

Key Words: Crop wild relative, Cultivar, Herbarium, Introduced, Plant genetic resources, Voucher specimens

Introduction

The National Herbarium of Cultivated Plants (NHCP) is a specialized herbarium located in the National Bureau of Plant Genetic Resources (NBPGR), New Delhi focusing on representation of taxa of use or of potential importance in plant genetic resources (PGR) programmes *viz.* crop species, their wild relatives and wild economic plants. The NHCP provides reference material for identification of taxa, baseline information on locality of availability, climatic and habitat preferences of taxa, and ancillary information on source localities. Any herbarium associated with PGR has the distinctive feature of having in its holdings not only native diversity but also of exotic germplasm augmented through exploration or introduction of germplasm in the form of seeds or planting material (Nayar *et al.*, 2011). Thus, these specimens are reference material of taxa not native to the Indian region. Germplasm introduced through the NBPGR is associated with a unique identity number. Herbarium specimens of taxa bearing the germplasm identity numbers are, therefore, vouchers of materials procured from diverse localities and sourced from different germplasm collections and curators.

Herbarium specimens of a taxon, represented over time and space, have a collective value, providing a record of the diversity that is significant as germplasm; individually important specimens include vouchers from exploration programmes and experimental studies. The holdings of the NHCP cover a period of nearly seven decades; it includes the herbarium specimens of the Plant Introduction Scheme (PI) under the Botany Division of the Indian Agricultural Research Institute (IARI) commencing activities of germplasm augmentation through systematic introductions since 1946 upto 1977. Subsequently, this activity was undertaken by a separate institute for PGR, i.e. at the NBPGR. The present analysis attempts to delineate important herbarium specimens (represented in the NHCP) and associated data on introduced germplasm that make these valuable as reference material to a wide user-base.

Materials and Methods

A total of 298 taxa representing 482 germplasm accessions are present in the herbarium bearing Exotic Collection (EC) numbers assigned by the NBPGR to germplasm introduced for research purpose into India (Table 1). The germplasm was raised in experimental conditions at appropriate locations and herbarium specimens for inclusion in the NHCP were prepared from experimental farms (Plant Introduction fields/ Post-entry Quarantine Nursery, PEQN, Issapur Farm, New Delhi) at the Headquarters in Delhi, and regional stations of the NBPGR (Uttarakhand, Odisha, Andhra Pradesh, Himachal Pradesh and Kerala) or crop-based institutes. Herbarium specimens of exotic germplasm,

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Table 1. Herbarium specimens of introduced germplasm in NHCP

S. no.	Crop category	Total species	Specimens of introduced accessions	Specimens of Plant Introduction herbarium (PI)	Germplasm accessions conserved (GB/ FGB)
1	Cereals/ millets (C/M)	38	71	26	13
2	Grain legumes (Gl)	19	43	4	9
3	Fruits (Fr)	13	14	3	10
4	Vegetables (Vg)	14	38	11	11
5	Oilseeds (Os)	13	21	5	8
6	Pseudocereals (Ps)	3	6	3	3
7	Spices/ condiments (S/C)	5	5	3	-
8	Fodder/ forage grasses (FoGr)	35	53	6	2
9	Fodder/ forage legumes (FoLg)	124	190	63	7
10	Ornamentals (Orn)	11	11	11	8
11	Medicinal/ aromatic plants (M&AP)	23	30	24	5
	Total	**298**	**482**	**167**	**22**

FGB: field genebank; GB: genebank

have information on both the source area/ institution which provided the germplasm as well as the area and period during which it was raised in experimental cultivation.

These specimens were validated for their identity, and checked with source data on introduction and collection. Additional information on native region of the taxa of PGR importance as well as its availability in the genebank (as seeds or in the field) was verified to delineate significant voucher specimens of introduced germplasm (Table 2).

Digital scans (jpeg images) of herbarium specimens were created using flat-bed scanner (high resolution HP Scanjet 3500C) at a resolution of 300 dpi. These images of herbarium specimens were linked to database for quick access on a family-wise and genus-wise basis, as well as by unique identity numbers assigned to herbarium specimens (HS numbers) and those assigned to the introduced germplasm (EC numbers).

Results and Discussion

A total of 482 germplasm accessions bearing EC numbers, belonging to 298 species, and represented as herbarium specimens in the NHCP, were introduced from 39 countries. There is an overall preponderance of taxa represented in genebanks, thus indicating that they may have desirable traits. Introductions from United States of America (United States Department of Agriculture, USDA), followed by Australia (Commonwealth Scientific and Industrial Research Organisation, CSIRO), and from Portugal (Botanical Garden of Coimbra), accounted for over 50% of the specimens. Nearly 20% of the accessions were from international organizations *viz*. paddy and other selected species from International Rice Research Institute (IRRI), Philippines, wild species of cereals and grain legumes from International Centre for Agricultural Research in the Dry Areas (ICARDA), Syria, *Vigna* from International Institute of Tropical Agriculture (IITA), Nigeria, and vegetable legumes and tomato from The World Vegetable Centre (AVRDC), Taiwan. Of the total herbarium specimens of introduced accessions, only 20% were from countries of their origin *viz*. local forms of *Punica* from temperate erstwhile Union of the Soviet Socialist Republic (USSR), dry fruit type of *Ziziphus* from Korea, *Vitis* from North America, *Glycine* from China, *Solanum*/ *Lycopersicon*, *Sesbania* and *Arachis* from South America, *Vicia* from Portugal, *Nigella* and *Plantago* from Iran, etc. Specimens of crop germplasm collected under collaborative exploration programmes (24) from areas adjoining India *viz*. under Indo-Nepal collaborative programme from Nepal (1960s), and under collaborative International Board for Plant Genetic Resources (IBPGR)/ NBPGR exploration programmes was another source of exotic material especially of *Solanum* and *Abelmoschus* from Nepal, Bangladesh and Sri Lanka (1989-90). The trend of exchange and circulation at the global level of a limited germplasm base among researchers (Arora

Table 2. Information used for delineating important specimens belonging to introduced germplasm in the NHCP

S. no.	Nature of data	Characteristics	Reference
1.	Herbarium specimen	Unique identity number of specimen (HS no.) Identity of taxon and nomenclature	Nomenclature check http://www.ars-grin.gov/cgi-bin/npgs/html/index.pl
		Suitable representation of vegetative and reproductive parts for determining and confirming identity of taxon	The Plant List www.efloras.com
		Quality digital image of specimen	:
2.	Source data of specimen	1. Source area of exploration/ raising experimental material from seed or propagule	NHCP database
		2. Collector	
3.	Source information on germplasm under introduction	Source institute/ organisation, country and region of supply of germplasm Unique germplasm no. allotted by original source of collection, and collector no. and date Associated data *viz.* cultivar, localized landrace, etc.	www.nbpgr.ernet.in/qeq/ec-search.aspx http://www.ars-grin.gov/cgi-bin/npgs/html/index.pl Rana *et al*., 2006 http://www.ersa.edu.au/case_data_avh checklists of crop varieties, heirloom lines, etc
4.	Germplasm unique identity number	EC (Exotic Collection) number allotted by NBPGR	www.nbpgr.ernet.in/qeq/ec-search.aspx
5.	Native region	Centre of origin/ diversity of the taxon	Zeven and de Wet 1982; http://www.ars-grin.gov/cgi-bin/npgs/html/index.pl
6.	Use/ potential use of the taxon	As crop species, in breeding programmes, or as promising species with domestication potential Categorisation into crop/ wild species, crop-use category	Nayar *et al*., 2003 http://www.ars-grin.gov/cgi-bin/npgs/html/index.pl
7.	Collection and conservation status	Gap analysis of taxa based on herbarium specimens and germplasm collections Availability in genebank as seed Conserved in field genebank	http://gisweb.ciat.cgiar.org/GapAnalysis/; NBPGR genebank data

et al., 1975; Tyagi *et al*., 2006) was further supported by this analysis.

The NHCP includes herbarium of the erstwhile Plant Introduction Division (PI) of the IARI, New Delhi. Taxa represented in NHCP, categorised according to use, were well represented in the PI as well as the NHCP herbaria for cereals and millets, vegetable crops as well as herbage grasses and legumes (Table 1). Grain legumes were the priority for addition in the NHCP, besides species of herbage use belonging to *Crotalaria*, *Lathyrus*, *Vicia* and *Vigna*. Among grasses in *Eragrostis*, *Megathyrsus*, *Panicum*, *Paspalum* and *Sorghum* were represented. In contrast, for medicinal and aromatic plants, as well as ornamentals, larger representation in PI herbarium was a reflection of increasing focus on indigenous diversity during subsequent periods. This analysis, therefore, highlights the value of herbarium specimens in representing changing trends in PGR.

Voucher herbarium specimens have value as cultivars of crops, selections bred for valuable traits and landraces (Table 3). These are distinct variants with observable traits, which may or may not be recognised as distinct taxonomic entities under the genus or species. However, these are significant from the point of view of PGR study and utilization. These specimens are maintained as representatives of infraspecific variants in the NHCP. Furthermore, these local variants or selections from wild species, were often distinguishable by additional features such as colour of leaves, leaf thickness often not observable on the specimen and needing photographic record or additional descriptive data along with specimen for reference. Examples of these were, *mantegazzianus* type of *Amaranthus caudatus,* a local cultivar of Argentina bearing condensed and rounded inflorescence spikes in place of long feathery and often drooping inflorescence and earlier considered a distinct subspecies (Zeven and de Wet, 1982; Hanelt, 1986); Westerwoldicum, a form of ryegrass (*Lolium multiflorum* subsp. *multiflorum*) developed by selected harvesting for earliness in the Netherlands, and used in systematic breeding of annual ryegrass (De Haan, 1955; Humphreys *et al*., 2009); *Sorghum sudanense,* taxonomically considered part of the wild and weedy species, *S.* x *drummondii* selected and

Table 3. Significant herbarium specimens of introduced species in NHCP

S. No.	Botanical Name	EC No.	HS No.	Crop Categ.	Remarks
1.	*Aegilops crassa* Boiss.	EC 573228	HS 20750	CM	GB
2.	*Aegilops kotschyi* Boiss.	EC 573277	HS 20751	CM	GB
3.	*Aegilops lorentii* Hochst. (=*A. biuncialis* Vis.)	EC 573205	HS 20745	CM	GB
4.	*Aegilops searsii* Feldman & Kislev ex K.Hammer	EC 383069	HS 20749	CM	GB
5.	*Aegilops speltoides* Tausch	EC 573334	HS 20743	CM	GB
6.	*Aegilops triuncialis* L.	EC 575781	HS 20748	CM	GB
7.	*Avena sativa* L.	EC 056175	HS 08484	CM	GB; cv. Kent
8.	*Hordeum agriocrithon* A.E.Åberg	EC 015585	HS 05196	CM	GB
9.	*Hordeum murinum* L.	EC 015582	HS 03189	CM	GB
10.	*Hordeum vulgare* L. subsp. *spontaneum* (K.Koch) Thell. (=*H. spontaneum* K.Koch)	EC 015580	HS 03192	CM	GB
11.	*Triticum monococcum* L.	EC 541168	HS 20755	CM	GB
12.	*Triticum monococcum* L. subsp. *aegilopoides* (Link) Thell. (=*T. boeoticum* Boiss.)	EC 577242	HS 20752	CM	GB
13.	*Triticum turgidum* L.	EC 272647	HS 20754	CM	GB; cv. Ambral
14.	*Lolium multiflorum* Lam. (=*L. westerwoldicum* Breakw.)	EC 013440	HS 03339	FoGr	Selection
15.	*Panicum coloratum* L. var. *markarikariense* Gooss. (=*P. markarikariense* (Gooss.) Rensb.)	EC 180404	HS 08725	FoGr	Local drought tolerant variant of fodder value
16.	*Phalaris aquatica* L. (=*P. tuberosa* L.)	EC 002409	HS 03551	FoGr	GB
17.	*Phalaris minor* Retz.	EC 001835	HS 03558	FoGr	GB
18.	*Sorghum bicolor* nothosubsp. *drummondii* (Steud.) de Wet ex Davidse (=*S. sudanense* (Piper) Stapf)	EC 000716	HS 04798	FoGr	Selection from wild plants
19.	*Lathyrus aphaca* L.	EC 309558	HS 08528	FoLg	GB
20.	*Lathyrus chrysanthus* Boiss.	EC 309562	HS 08642	FoLg	GB
21.	*Lathyrus pseudocicera* Pamp.	EC 309554	HS 08533	FoLg	GB
22.	*Sesbania bispinosa* (Jacq.) W.Wight	EC 493681	HS 17890	FoLg	GB
23.	*Sesbania cannabina* (Retz.) Pers.	EC 466696	HS 16608	FoLg	GB
24.	*Sesbania tetraptera* Hochst. ex Baker	EC 435749	HS 17897	FoLg	GB
25.	*Vicia lutea* L. subsp. *vestita* (Boiss.) Rouy (=*V. muricata* Ser.)	EC 001939	HS 04069	FoLg	GB
26.	*Punica granatum* L.	EC 104350	HS 07199	Fr	cv. Achik Dona
27.	*Punica granatum* L.	EC 062811	HS 08079	Fr	cv. Gulsha Rose Pink
28.	*Ziziphus jujuba* Mill.	EC 280769	HS 19178	Fr	FGB; cv. Moodeung/Ja 5
29.	*Vitis acerifolia* Raf.	EC 452210	HS 19168	Fr	FGB
30.	*Vitis aestivalis* Michx.	EC 452212	HS 19170	Fr	FGB
31.	*Vitis amurensis* Rupr.	EC 452213	HS 19169	Fr	FGB
32.	*Vitis arizonica* Engelm.	EC 452207	HS 19177	Fr	FGB
33.	*Vitis cinerea* (Engelm.) Engelm. ex Millardet	EC 452214	HS 19173	Fr	FGB
34.	*Vitis cinerea* Engelm.) Engelm. ex Millardet var. helleri (L.H.Bailey) M.O.Moore (=*V. berlandieri* Planch.)	EC 452209	HS 19166	Fr	FGB
35.	*Vitis ficifolia* Bunge	EC 452206	HS 19165	Fr	FGB

S. No.	Botanical Name	EC No.	HS No.	Crop Categ.	Remarks
36.	*Vitis girdiana* Munson	EC 452211	HS 19172	Fr	FGB
37.	*Vitis riparia* Michx.	EC 452208	HS 19171	Fr	FGB
38.	*Cicer pinnatifidum* Jaub. & Spach	EC 015562	HS 05241	Gl	GB
39.	*Lathyrus cicera* L.	EC 309561	HS 08644	Gl	GB
40.	*Phaseolus vulgaris* L.	EC 405211	HS 10242	Gl	GB
41.	*Pisum sativum* L.	EC 334161	HS 16042	Gl	GB; cv. Dwarf Gray Sugar
42.	*Vigna radiata* (L.) R.Wilczek	EC 398899	HS 10116	Gl	GB
43.	*Vigna radiata* (L.) R.Wilczek	EC 398938	HS 10117	Gl	GB
44.	*Vigna unguiculata* (L.) Walp.	EC 367710	HS 15486	Gl	GB
45.	*Vigna unguiculata* (L.) Walp.	EC 472257	HS 15487	Gl	GB
46.	*Vigna unguiculata* (L.) Walp.	EC 501045	HS 15491	Gl	GB; cv. Green Pixie
47.	*Anacyclus pyrethrum* (L.) Link	EC 281897	HS 10013	M&A	GB
48.	*Abelmoschus moschatus* Medik.	EC 316073, EC 329390	HS 17955, HS 17956	M&A	GB
49.	*Digitalis grandiflora* Mill. (=*D. ambigua* Murray)	EC 333802	HS 10023	M&A	GB
50.	*Digitalis purpurea* L.	EC 207361	HS 10022	M&A	GB
51.	*Datura stramonium* L. var. *tatula* (L.) Torr. f. *bernhardii* (C.E.Lundstr.) Danert (=*D. bernhardii* C.E.Lundstr.)	EC 019706	HS 02902	M&A	Selection made in USA
52.	*Cotoneaster franchetii* Bois	EC 024577	HS 18523	Orn	FGB
53	*Cotoneater salicifolius* Franch.	EC 027475	HS 19164	Orn	FGB
54.	*Crataegus coccinea* L. forma *wendlandii* hort. ex Lavallée	EC 024499	HS 18123	Orn	FGB
55.	*Rosa brunoni* Lindl. (=*R. moschata* non Herrm.)	EC 018586	HS 08346	Orn	FGB
56.	*Rosa luciae* Franch. & Rochebr. ex Crép. (=*R. wichuraiana* Crép.)	EC 033173	HS 19871	Orn	FGB
57.	*Rosa multiflora* Thunb.	EC 031218	HS 19625	Orn	FGB
58.	*Rosa* x *damascena* Mill.	EC 025987	HS 19970	Orn	FGB
59.	*Spiraea douglasii* Hook.	EC 024706	HS 18520	Orn	FGB
60.	*Helianthus annuus* L.	EC 494379, EC 494423	HS 16034, HS 16033	Os	GB
61.	*Brassica napus* L.	EC 389916	HS 17030	Os	GB; cv. Profit of canola
62.	*Brassica napus* L.	EC 400804	HS 16019	Os	GB; cv. Westar of canola
63.	*Brassica nigra* (L.) W.D.J.Koch	EC 289661	HS 17035	Os	GB
64.	*Brassica rapa* subsp. *dichotoma* (Roxb.) Hanelt (cv-grp. Brown sarson)	EC 191597, EC 333596	HS 17004, HS 17006	Os	GB
65.	*Crambe hispanica* subsp. *abyssinica* (Hochst. ex R.E.Fr.) Prina (=*C. abyssinica* Hochst. ex R.E.Fr.)	EC 499724	HS 16029	Os	GB
66.	*Eruca vesicaria* subsp. *sativa* (Mill.) Thell. (=*E. sativa* Mill.)	EC 400072	HS 16032	Os	GB
67.	*Sinapis alba* L.	EC 390162	HS 16049	Os	GB
68.	*Amaranthus caudatus* L. (=*A. caudatus* subsp. *mantegazzianus* (Pass.) ined.; *A. mantegazzianus* Pass.)	EC 013953	HS 04651	Pc	Local variant
69.	*Amaranthus caudatus* L. (=*A. edulis* L.)	EC 150188	HS 07061	Pc	GB
70.	*Amaranthus hypochondriacus* L.	EC 169611, EC 359422	HS 07091, HS 09743	Pc	GB

S. No.	Botanical Name	EC No.	HS No.	Crop Categ.	Remarks
71.	*Solanum lycopersicum* L. var. *lycopersicum* (=*Lycopersicon esculentum* Mill.)	EC 001129	HS 09095	Vg	cv. Burwood Prize
72.	*Solanum lycopersicum* L. var. *lycopersicum* (=*Lycopersicon esculentum* Mill.)	EC 315490	HS 09086	Vg	cv. Mountain Delight
73.	*Solanum lycopersicum* L. var. *lycopersicum* (=*Lycopersicon esculentum* Mill.)	EC 130053	HS 09105	Vg	GB
74.	*Solanum lycopersicum* L. var. *lycopersicum* (=*Lycopersicon esculentum* Mill.)	EC 315478	HS 09109	Vg	GB
75.	*Solanum melongena* L.	EC 169769	HS 07089	Vg	GB
76.	*Solanum melongena* L.	EC 316224	HS 18316	Vg	GB; collection from Nepal
77.	*Solanum peruvianum* L. (=*Lycopersicon peruvianum* (L.) Mill. var. *peruvianum*)	EC 315457	HS 09101	Vg	GB
78.	*Solanum pimpinellifolium* L. (=*Lycopersicon pimpinellifolium* (L.) Mill.)	EC 274046	HS 09099	Vg	GB

cv: cultivar; FGB: field genebank; GB: genebank. Crop category: CM, cereals and millets, FoGr, fodder grasses, FoLg, Fodder legumes, Fr, fruits, Gl, grain legumes, M&A, medicinal and aromatic plants, Orn, ornamentals, Os, oilseeds, Pc, pseudocereals, Vg, vegetables.

bred for forage purpose (Boonman, 1993); and *Panicum coloratum* var. *markarikariense*, a salt-tolerant ecotype, native of the floodplains with low rainfall (Markarikari area of Botswana) in southern Africa and distributed widely as drought-tolerant germplasm (http://www.fao.org/ag/AGP/AGPC/doc/GBASE/data/pf000277.htm) and having bluish green, glaucous and fleshy leaves as compared to var. *coloratum* (http://www.tropicalforages.info/key/Forages/Media/Html/Panicum_coloratum.htm).

Cultivars/ local types/ old and heirloom lines of crop plants were some of the other reference specimens available in the NHCP, viz. *Avena sativa* cv. Kent (http://www.ars-grin.gov/cgi-bin/npgs/html/index.pl), a popular check variety for oats cultivation in the Indian subcontinent; *Pisum sativum* cv. Dwarf Gray Sugar, an edible snow pea under continuous cultivation for over 200 years (http://casfs.ucsc.edu/documents/for-the-gardener/peas.pdf); and *Lycopersicon esculentum* cv. Burwood Prize, an heirloom cultivar from Australia (http://naldc.nal.usda.gov/download/36965/PDF); and local germplasm of *Punica granatum* from the Middle East region such as Achik Dona and Gulsha Rose Pink represented sources of material used in breeding for traits such as high yield and red colour of fruits.

Wild relatives of major crops are better represented as introduced germplasm more so than crops, particularly of seed producing species viz. *Oryza*, *Triticum*/ *Aegilops*, *Avena*, *Hordeum*, *Secale*, *Panicum* and *Setaria* (29) among cereals and millets, grain legumes such as *Arachis*, *Cicer*, *Lathyrus* and *Lens* (7). Besides these, species of herbage value (116), among vegetables species of *Solanum/ Lycopersicon* (5), selected species of medicinal importance, viz. *Nigella*, *Plantago* and *Datura* (9), and, among fruits, *Vitis* (8) are also represented. These were mostly wild species native of other megadiversity regions and hence introduced for their potential importance in breeding and selection. The important ones (both PI and NHCP collections) are also conserved in the genebank (Table 1).

Wild taxa of cereals and millets were mainly native of the Central Asian/ West Asian/ Mediterranean/ European regions (number of accessions represented in NHCP given in parenthesis)- *Aegilops* (wild relative of *Triticum*, 9), wild and weedy species of *Avena* (2: *A. fatua*, 1, and *A. sterilis* subsp. *ludoviciana*, 1); in *Hordeum vulgare*, the progenitor taxon, subsp. *spontaneum* (1), weedy form subsp. *agriocrithon* (1), *H. bulbosum* (3) and *H. murinum* (1), besides *H. stenostachys* (1), a wild species of the South American region; *Oryza* was represented by collections belonging to different genomes viz. AA: *O. rufipogon*-*O. nivara* (6), *O. barthii* (1) and *O. longistaminata* (1), BB/ BBCC: *O. eichingeri* (8) and *O. punctata*-*O. minuta* (2); CC: *O. officinalis* (4); CCDD: *O. latifolia* (3); EE: *O. australiensis* (1); FF: *O. brachyantha* (3); and HHJJ: *O. ridleyi* (1); progenitor species of *Secale cereale*, *S. vavilovii* (1); and of *Panicum*, extending to the Indian region, *P. antidotale* (3). Introduced species of wild

relatives of crop taxa represented species that were not only a priority for utilization, but for systematic study as well.

Solanum/ Lycopersicon (tomato group), native of the South American region, was represented by the wild species, *L. cheesmaniae* (1) and *L. pimpinellifolium* (4), and were the closest relatives of tomato and potential sources of resistance to drought and disease; and *L. chilense* (2), *L. hirsutum* (4) and *L. peruvianum* (5), belonging to its secondary genepool, were sources of disease, pest and drought resistance. *Solanum* (brinjal group), was represented by the wild species *S. sisymbriifolium* (1), native of South America and a potential source of disease and pest resistance. Some of the introduced species of wild and weedy relatives of crops also extended their distribution as weeds of disturbed areas, viz. *Nigella sativa*, *Plantago lanceolata*, *Trifolium dubium* and *T. tomentosum* (Pradheep *et al*., 2011) and *Solanum sisymbriifolium* (Kohli *et al*., 2012), naturalized in the Indian region. These also served as reference specimens of taxa contributing naturalized weeds.

Many of the wild species in NHCP represented taxa that were well collected and represented in the germplasm in the genebank and herbarium specimens globally (http://gisweb.ciat.cgiar.org/GapAnalysis/). *Triticum monococcum* subsp. *aegilopoides* and *Vicia hyaeniscyamus* present in NHCP were poorly represented in genebank/ herbarium collections worldwide (http://www.fao.org/docrep/005/y4586e/y4586e08.htm for medicinal plants).

A total of 35 species belonging to 19 genera of grasses were of fodder/ forage value, native to the Central Asian/ Near East/ Mediterrranean and European regions and others of the North/ Central/ South American regions and African regions. Legumes used as fodder and forages/ vegetables and cover crops accounted for 124 species belonging to 14 genera. Majority of the taxa were temperate species native to the Central Asian, Near East, Mediterranean centres and extending to the European region (Zeven & de Wet, 1982) and introduced as germplasm from USA, South America or Australia. The source area and source institute/ country of diversity introduced in herbage grasses and legumes thus by and large represent germplasm. Specimens of taxa of herbage value, therefore, had a collective value representing diversity augmented through collection missions organised at the international level by CSIRO, Australia, FAO, USDA and other agencies to New World, Europe, Africa and the Mediterranean and Near East regions (Whyte, 1958), and systematic selection and breeding work, undertaken during early part of the 19th century in Europe and Mediterranean areas (Humphreys *et al*., 2009; Small, 2011) and introduced to other regions.

Conclusion

Nearly 70 herbarium specimens were delineated for their specific importance out of a total of 482 specimens of introduced germplasm represented in the NHCP; besides, all wild species, both closely related ones and others that were more of herbage value were significant additions for taxonomic and systematic study of crop taxa. Secondly, the analysis brought out the different parameters to be documented to work out that the PGR value of herbarium specimens as and when they are added, thereby ensuring that all distinctive characters are represented in the form of specimens, images, photographs and study of micro-morphological characters. Lastly, a collective value could be estimated for specimens belonging to related species or closely related genera; in the present analysis species (41) of the *Medicago-Trigonella-Trifolium* complex was one such example.

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Germplasm Collection and Diversity Analysis in Yardlong Bean (*Vigna unguiculata* subsp. *sesquipedalis*) from Coastal Andhra Pradesh and Odisha

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Diversity in yardlong bean (*Vigna unguiculata* subsp. *sesquipedalis*), an under-utilized vegetable legume was collected from parts of North coastal Andhra Pradesh (Srikakulam and Viziznagaram districts) and adjoining regions of Odisha (Koraput and Gajapati districts). Substantial variation was observed among the 39 accessions collected. Most of collections had pods which were light green (28), some were light green with purple tip (6), and a few were dark green (4); one accession (IC582551, Jeypore, Koraput, Odisha) had purple pods with green tip. Variation in pod length ranged from 24-75 cm; fresh pod weight (10 pods) from 60-140 g and seeds/pod from 6.2-17. Pod length had the highest dispersion index (158%), followed by100-seed weight (127%), fresh pod weight (89%) and seeds/pod (83%). Accessions IC582850 and IC582863 had the longest pods (75 cm). A pure line selection from IC582850 (Jeypore, Odisha) is released for cultivation as 'Arka Mangala'. This pole type, photo-insensitive variety with green, smooth pods and a crop duration of 3-4 months recorded a pod yield of 25.7 t/ha with an increase of 24% and 30% pod yield over the check varieties 'Lola' and 'Vyjayanthi', respectively.

Key Words: Andhra Pradesh, Arka Mangala, Odisha, Pod trait diversity, Yardlong bean

Introduction

Yardlong beans are important vegetable legumes throughout the tropics and sub-tropics of Asia. Botanically classified as *Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdc. are believed to have been selected and developed for their long tender pods in South-East Asia, from vegetable types of *Vigna unguiculata* introduced there from India (Steele and Mehra, 1980). Known by several names, such as string bean, long-podded cowpea, asparagus bean, snake bean, Chinese long bean, pea-bean, bora, juro-kusasagemae (Japanese), dowgauk (Chinese) or sitaw (Filipino), yardlong beans are cultivated for their strikingly long drooping pods (30-90 cm) that are relished as a vegetable. Besides the tender pods, the young leaves and seeds are also eaten. Referred to as 'poor man's meat' in the Philippines, yardlong bean is commercially important in parts of Indonesia, Thailand, Philippines, Taiwan and China, while being a minor vegetable throughout its range of distribution. It is estimated that area under yardlong bean in China alone exceeds 250,000 ha annually (Rubatzky and Yamaguchi, 1997), while in Thailand it is grown on about 18,560-20,160 ha annually (Sarutayophat *et al.*, 2007). Yardlong beans are mainly a warm-season crop and capable of surviving extreme humidity and heat. They can be planted in a wide range of climatic conditions but are very sensitive to cold temperatures. Although cowpeas originated in Africa, this vegetable form has been introduced there only in recent times. It is now grown as a minor garden crop in many sub-tropical countries of Africa (especially West Africa) and America (*e.g.* Caribbean). It is popular in these countries also due to its beautiful, large violet flowers and the long drooping pods.

In India, yardlong bean is a less known under-utilized vegetable grown in the peninsular region particularly Kerala, Tamil Nadu, coastal Andhra Pradesh and Odisha. It is also cultivated to some extent in West Bengal, Assam and the North Eastern Hill (NEH) region. It is a highly self-pollinating, vigorous climbing annual, growing up to a height of three to four meters. It produces very long, slender and succulent pods that may be white, light green, dark green, brownish red or purple. Nutritionally, the tender green pods are rich in crude protein (3.5-5%), besides being a good source of vitamin

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A (941 IU) and C (13 mg), iron (2.5 mg), calcium (80 mg), phosphorus (74 mg) and dietary fibre (2 g) making it an excellent vegetable (Singh *et al.,* 2001). In Kerala's climate, yardlong beans may be cultivated throughout the year and significant research on this crop has been undertaken by the Kerala Agricultural University. Several high yielding varieties such as Lola, KMV-1, Mallika, Sharika, Vellayani and Vyjayanthi have been released for the long pods ranging from 40-60 cm. Even so, the yardlong bean is still a relatively minor legume crop, but its importance both as a vegetable and as a legume cannot be over-emphasized.

The Indian region is the secondary centre of diversity for cowpeas and over 3,000 accessions are conserved in the National Genebank (NGB) at the National Bureau of Plant Genetic Resources (NBPGR), New Delhi. However, only a few of these are specifically designated as 'yardlong bean', collected from a few pockets in Odisha. Farmers in the North coastal region of Andhra Pradesh (Srikakulam and Vizianagaram) and adjoining regions of Odisha (Koraput and Gajapati) are known to cultivate yardlong beans for local consumption. However, these areas have so far not been adequately explored for this species, and hence, not much is known about its cultivation practices and extent of diversity. An exploration was, thus, undertaken to augment the few collections and fill these gaps in knowledge. The results of this study are reported in the following account.

Materials and Methods

Characteristics of the Surveyed Region

Vizianagaram and Srikakulam form the northern most districts of Andhra Pradesh located between 17º15´-19º 10´ N and 83º-84º 50´E. This region is rugged with hills and valleys with hill tops ranging from 300 – 1000 masl. The region falls under the upper Godavari region of the Eastern Ghats, with the soil varying from deltaic alluvial to red sandy loams and sandy clays. The vegetation comprises mainly dry deciduous forests with a few pockets of moist deciduous patches at high altitudes. Tribal groups including *Savara, Jatapu, Kuttiya, Gadaba, Yerkula, Konda Dora, Samanthas* and *Konda Kapus* reside in this area. The major rivers passing through are Nagavali and Vamsadhara. The climate is characterized by high humidity throughout the year. The South-West monsoon which follows the summer lasts up to mid October, while the North-West monsoon from mid October lasts to the end of November. Annual rainfall averages 1,000-1,100 mm**.** Maximum and minimum temperatures during the South West monsoon range from 33-35°C and 26-27°C, respectively.

Koraput and Gajapati districts of Odisha adjoining Andhra Pradesh are characterized by a warm/hot humid climate, an average rainfall of 1,200-1,710 mm and a temperature range from 34°C to as low as 7.5°C in the highlands. Soils are mainly red, mixed red and yellow, sandy loams and clay loams. More than 70% of the total population in the region comprises Scheduled Tribes with as many as 52 tribal groups including *Khonds, Bhatadas, Parojas, Bhumias* and *Bondas*. The topography consists of high land plateau with a number of hills and hillocks with an average height of 100-1000 masl. The whole area is drained by five major rivers namely Vamsadhara, Nagavali, Indravati, Kolab and Mackanad and several tributaries and small perennial streams.

Germplasm Collection

The potential areas for collection of yardlong bean germplasm were determined in consultation with Acharya N.G. Ranga Agricultural University (ANGRAU), State Horticulture Department, Andhra Pradesh, Odisha University of Agriculture & Technology (OUAT), Odisha, and Indian Institute of Horticultural Research (IIHR), Bengaluru. A farmer field was taken as a basic unit of germplasm collection. Random samples from the populations along with purposive samples of specific material were collected and stored in cotton bags. Seed samples were also collected from kitchen gardens, tribal shandys and farm stores. A unique collector number was assigned to each accession and passport information was documented along with geographical coordinates of the collection sites (latitude, longitude, elevation) which were recorded using Global Positioning System (Garmin 12, USA). Discussions with local farmers were conducted to obtain both ethnobotanical information and details on cultivation, processing and consumption practices. Fresh pod weight was recorded using a portable top pan balance at the collection site. Pod length and seeds/ pod were measured along with seed traits *viz.*, length, width and thickness.

Statistical Analysis

The statistics mean, median, standard deviation, minimum, maximum were used to summarize the distribution of data for each quantitative trait. Phenotypic dispersion index (Bramley, 2005) and phenotypic coefficient of variation (PCV) were used to quantify the

observed diversity. Pearson's coefficient of correlation was used to estimate the strength of association between the quantitative traits. PCV is the commonly used statistic to estimate dispersion. Its valid use however requires a trait to be normally distributed, which may not always be the case. Although we have reported the PCV in our results, we preferred to quantify and report diversity by the dispersion index, also called spread, defined as [(max - min)/median)]*100. This index, unlike PCV, does not require the trait to be normally distributed and provides a more realistic feel of the relative magnitude of diversity for a trait as it is based on the observed range (maximum – minimum) of the trait. The PCV, being based on the standard deviation, tends to provide an underestimation of underlying diversity. DIVA-GIS version 7.1.6 was used to understand spatial distribution and diversity available in pod and seed traits recorded *in situ*.

Results and Discussion

Cultivation, Processing and Consumption Practices

Thirty nine accessions of yardlong bean were collected from 17 villages in Srikakulam and Vizianagaram districts of Andhra Pradesh (AP) and 11 villages in Gajapati and Koraput districts of Odisha spanning an altitude of 28-903 m. Yardlong beans in the area are known by several names such as *Podugu chikkudu, Kampa chikkudu, Nela Chikkudu, Gaddi chikkudu, Lolugu chikkudu, Ankur chikkudu* in Telugu, and *Jhudunga, Barboti, Bodhi, Tupsilamba, Daspallia, Lamba, Dhala bodhi, Tupsigeda, Nalibodi, Alladi, Raisa, Jhuler, Ramba, Safed lamba* in Oriya. *Chikkudu* traditionally refers to the lablab bean in AP, and various names for yardlong bean, in the vernacular, are derived with the addition of different adjectives as '*podugu*' (long), *nela* (ground, trailing), *gaddi* (wild), *Kampa* (pole/pillar), *Lolugu* (village in Ghara mandal of Srikakulam district) where there is abundant cultivation of the crop), *Ankur* (name of seed company). Similarly in Odisha too, local names reflected the description of the pod *viz., Lamba, Tupsilamba* (long) and *Daspallia* (ten seeded).

The crop, usually sown in June-July with the onset of rains are harvested in November-December. In Odisha, the crop is sown a month later than in adjoining AP, and consequently harvested during December-January. The accessions were either climbing or trailing; and raised either as a pure/sole crop, as a mixed/inter-crop with other vegetables as okra, cowpeas, cucurbits, leafy greens or ginger or as a fringe crop on paddy bunds (Fig. 1). Climbing types were usually trailed onto erect bamboo supports with wooden sticks for trellising and to ensure straight pods for harvesting maximum yield. The pods, hanging in pairs, started to form about 40-45 days after sowing, the first pods became ready for harvest around 55-60 days after sowing. Fresh pods were picked every day or every alternate day depending on the growth rate of the pods and the genotype. Regular picking ensured continuous production over a period of three to four months, sometimes even extending to six months, depending on the genotype. The pods were picked at maximum length of the pods and before the seeds matured and expanded.

Pods were picked early in the morning after evaporation of surface moisture. A bit of stem was left attached to the pod while picking to avoid any injury at the severed end which was reported to accelerate post harvest disease/decay. Thereafter, pods were spread flat to prevent sweating and cleaned to remove debris as leaves, broken/diseased pods, flowers etc. Pods were sorted by length and loosely bundled for market. Fresh pods were handled carefully as they bruised easily. High quality pods were well-formed, straight, of uniform colour, fresh, tender and firm. Crispness was tested by bending the pods which snapped audibly.

The pods formed towards the end of the season were allowed to dry to provide seed for the next planting and freely exchanged with neighbouring villages. Although some farmers separated the varieties based on seed coat colour, usually a typical field was mixed; this diversity allowed farmers to get some yield despite environmental uncertainties and minimal inputs. Anthracnose and cowpea aphid borne mosaic virus were observed in pockets in fields in Gajarainivalasa, Satyavada, Baleru

Fig. 1. Yardlong bean as fringe crop in paddy fields

Sunigiri and Ramabhadrapuram in Srikakulam and Vizianagaram (AP) and Tahajang area in Koraput, Odisha but no appreciable yield losses were reported by farmers. The local types were said to yield less but over a longer period as compared to varieties being supplied by seed companies. The fresh produce was sold in local markets and village shandys (Fig. 2). Yardlong beans do not have a long shelf life and must be consumed within a couple of days of harvest. Post harvest acceptability is reduced due to rapid wilting of the pods on storage after picking.

The crisp, tender pods are eaten both fresh and cooked. The flesh of these stringless beans is softer than the vegetable cowpeas or snap beans and takes less time for cooking. At their best when young and slender at pencil thickness, they are usually cut into short sections for cooking purposes, being used in curries, stir fried alone or along with other vegetables. They are also made into *pakodis/bhajjis* after mixing in chickpea flour batter or used in cooked/fresh salads. A popular method is to chop them into very short cubes and fry them in an omelette. The women are intimately involved with all aspects of the yardlong bean cultivation. The beans are a vital constituent of their daily cookery and they are very interested and innovative in creating new recipes.

Fig. 2. Yardlong bean being sold in Jepore market

Diversity

All collections had indeterminate growth habit whether trellised or not, and variation was observed for fresh pod weight, pod length, pod colour and seed size, colour and weight. Most of the pods were light green (28; 72%), whereas some were light green with purple tip (6; 15.4%), and a few were dark green (4; 10%); one accession (IC582551, Jeypore, Koraput, Odisha) had purple pods with green tip (Fig. 3). Seeds were all kidney shaped and variously colored - red, dark red, red with a white tip, white with red or brown patches and black (Fig. 4). Descriptive statistical analyses on pod and seed traits recorded during the collection are presented in Table 1. Variation in pod length ranged from 24-75 cm; in fresh pod weight (10 pods) from 60-140 g and seeds/pod from 6.2-17. Hundred seed weight varied from 7.3-23.2 g. Pod length had the highest dispersion index (158%), followed by100-seed weight (127%), fresh pod weight (89%) and seeds/pod (83%). Accessions IC582850 and IC582863 had the longest pods (75 cm) followed by IC582861 (45 cm), IC582862 (40 cm), IC582872 (39 cm) and IC582841 (39 cm). Highest fresh pod weight was observed in IC582872 and IC582850 (140 g) followed by IC582873 (135 g) and IC582882 (120 g). Pod length was significantly correlated with seeds/pod and seed length. Seed length, seed width and seed thickness were significantly inter-correlated (Table 2). Hundred seed weight showed a significant correlation with seed length. The DIVA-GIS analysis corroborated the rich diversity

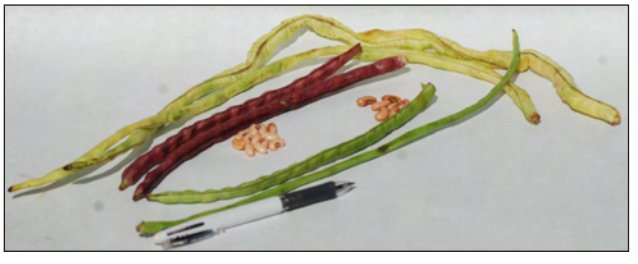

Fig. 3. Variation in pod colour and size

Fig. 4. Variation in seed colour

Table 1. Descriptive statistical analysis of pod and seed characteristics

	Mean	Median	Standard Deviation	Minimum	Maximum	Dispersion Index (%)	PCV (%)
Fresh weight (g)	93.0	90.0	21.2	60.0	140.0	88.9	22.8
Pod length (cm)	36.2	32.2	13.5	24.0	75.0	158.4	37.3
Seeds/pod	12.8	13.0	3.0	6.2	17.0	83.1	23.8
*Seed length (mm)	9.7	9.8	1.2	6.3	11.8	55.8	12.3
*Seed width (mm)	5.1	5.1	0.6	3.1	6.0	55.8	12.0
*Seed thickness (mm)	3.4	3.5	0.6	1.6	4.3	77.2	17.5
*100-seed weight (g)	12.6	12.6	3.9	7.3	23.2	126.6	30.7

*Dry seeds; PCV = Phenotypic coefficient of variation

Table 2. Inter-relationships between pod and seed traits

	Fresh wt	Pod length	Seeds/pod	Seed Length	Seed Width	Seed Thickness
Pod length (cm)	0.26					
Seeds/pod	0.19	0.45*				
Seed length (mm)	0.30	0.44*	0.04			
Seed width (mm)	0.24	0.28	0.04	0.59*		
Seed thickness (mm)	0.32	0.15	-0.30	0.44*	0.84**	
100-seed weight (g)	0.29	0.20	-0.04	0.52*	0.49*	0.47*

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

available within the yardlong bean accessions in the areas explored. High Shannon diversity index (2.1-3.0; Fig. 5) was observed for fresh pod weight, pod length and seeds/pod from North-coastal Andhra Pradesh and adjoining Koraput region of Odisha.

Pod quality, a critical attribute in determining consumer preference/acceptability is judged on the basis of pod colour, length, succulence, firmness, crispness, tenderness and sweetness. However, desirable qualities differ in different markets. For instance, people in central Thailand prefer firm pods while those in the North-East favour fairly soft pods (Kongjaimun, 2013). Consumers in Thailand and Hong Kong prefer light green and extra long pods, and those in Brunei prefer dark green, short pods, while the European and Canadian markets prefer dark green, and medium pod length (Bounnhong, 1997). In coastal Andhra Pradesh green pods were largely common whereas in adjoining parts of Odisha, as in Kerala, both green and purple types were available in local markets. Purple types are known to retain the colour even on cooking, thus, lending colour to the cooked dish. Purple pods are believed to contain anthocyanins which are useful as antioxidants. Antitoxidant activity

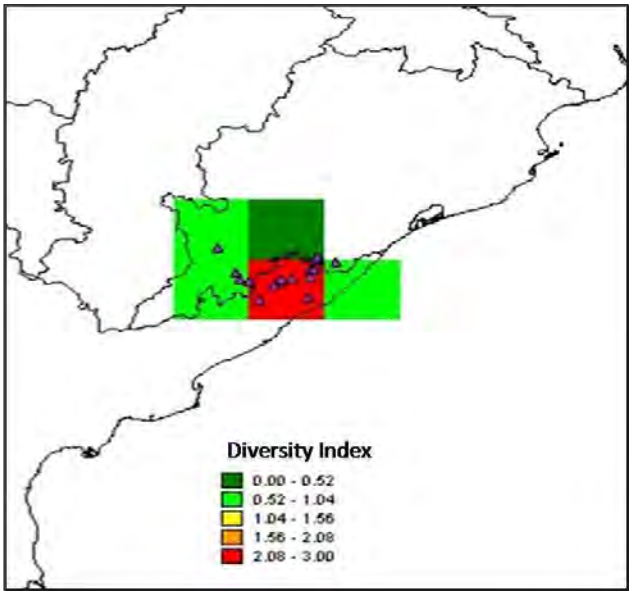

Fig. 5. Diversity Index

(AOA) is reported to be highly heritable in cowpea, with a strong relationship between AOA and seed coat colour (Nzaramba *et al.*, 2005), the pigmented varieties possessing favourable factors that enhance AOA. Purple

podded plants were also observed to be more tolerant to pests and disease as well as water stress conditions and to have a thicker skin, so possibly disliked by insect pests (Waluyo and Hardinaningsih, 2013).

The spacing between adjacent seeds in a pod contributes to a typical difference between yardlong beans and cowpeas. In the former, seeds are distributed throughout the length of the pod, thus making it fleshier, whereas in the latter, seeds are crowded next to each other in the pod. This is clearly suggestive of divergent selection during domestication and evolution of the crop. Present observations supported this. Seeds/pod was minimum in IC582867 (6.2) with a pod length of 28 cm, while IC582850 and IC582863 with a maximum pod length of 75 cm each had 17 seeds/pod dispersed along the entire length of the pod.

The few studies on yardlong bean in India have focused mainly on collections from Kerala with considerable diversity in local types with high genotypic and phenotypic coefficient of variation for pod yield/ plant, clusters/plant, pods/plant, pods/cluster and pod weight, and therefore scope for improvement through selection (Vidya and Oomen, 2002; Vidya *et al*., 2002; Resmi and Gopalakrishnan, 2004; Lovely and Radhadevi, 2006; Kumar and Devi, 2009). Globally, however, there is a good deal of focused research on several aspects of yardlong bean including genetic diversity (Gillaspie *et al.,* 2005; Sarutayophat *et al.,* 2007; Benchasri and Bairaman, 2010; Ullah *et al.,* 2011, , Mahmudul Huque *et al.,* 2012), genetics of pod/seed traits, domestication and QTL mapping (Kongjaimun *et al.,* 2012, 2013), host plant resistance (Brito *et al.,* 2011; Benchasri *et al.,* 2012;), optimum time for harvesting pods (Ofori and Klogo, 2005); and as a potential new crop (Coker *et al.,* 2007).

Given the many factors that currently constrain vegetable production, including climate change, increased urbanization and pressure on arable land, coupled with the growing interest in this under-utilized vegetable worldwide in recent years, it is appropriate to focus research on this vegetable that comfortably fits into most cultivation and production practices with little additional efforts, particularly in high rainfall states. The long pod character of yardlong bean has the potential for developing bush-type cowpea by hybridizing with grain type cowpea. The bush-type vegetable cowpea with semi-erect growth habit with long-succulent pods and long peduncles (40-50 cm long) protruding over canopy and holding pods above ground has an advantage of requiring no staking, thus reducing cultivation costs (Singh *et al*., 2003).

Substantial diversity is available in the collected germplasm, and their systematic evaluation would reveal their potential for contribution to yardlong bean/cowpea genetic improvement. In an effort to popularize this promising underutilized vegetable, a pure line selection from IC582850 (Jeypore, Koraput, Odisha) was released for cultivation as 'Arka Mangala' (Fig. 6). The variety recorded a pod yield of 25.7 t/ha with an increase of 24% and 30% pod yield over the check varieties 'Lola' and 'Vyjayanthi', respectively. A pole type photo-insensitive variety with green, smooth pods and crop duration of 3-4 months, it is suitable for both *kharif* and *rabi* seasons. This variety was taken up for trials in Kerala (KVK conducted farm experiments at Mookkannur and Ayur panchayaths of Ernakulam district) and has reportedly performed well in comparison to 'Lola', the prevailing variety, even being better resistant to diseases and pests (http://kvkernakulam.org.in/news100.html).

Fig. 6. Arka Mangala

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SHORT COMMUNICATION

Development of Microsatellite Markers from Enriched Genomic Library of ISH 100 (*Saccharum* hybrid) for Genetic Variability of Sugarcane

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Microsatellite primers were developed from the interspecific hybrid ISH 100 of sugarcane to study patterns of population genetic structure across the species. About 26 SSR primers were screened, out of which 13 exhibited polymorphism (50%). These 13 SSR primers were assessed on 8 individuals sampled from one population. The number of alleles per locus ranged from 2 to 6 and observed heterozygosity ranged from 0.16 to 0.60. The genetic diversity among the population depicted from this study can be used for genetic diversity analysis of sugarcane.

Key Words: ISH 100, Microsatellite, Population genetic structure, Sugarcane

Sugarcane is a monocotyledonous crop plant that is cultivated in the tropical and sub-tropical regions of the world, primarily for its ability to store high concentration of sucrose in the internodes of the stem. In 2010, Food and Agricultural Organization of the United Nations estimated that sugarcane is cultivated in about 23.8 m ha, in more than 90 countries with a worldwide harvest of 1.69 billion tons. Modern sugarcane varieties cultivated for sugar production are complex interspecific hybrids (*Saccharum* spp.) that have arisen through intensive selective breeding of species within the genus *Saccharum*, primarily involving crosses between the species *S. officinarum* L. and S. *spontaneum* L. (Cox *et al*., 2000). Commercial hybrid cultivars of sugarcane descended from interspecific hybridization between *S. officinarum* and *S. spontaneum* (Banumathi, 2010). ISH 100 is an interbreed of Co7202 {CoC671 × (*S. officinarum* (57NG110) × *S. robustum*)}. Genetic make-up of ISH 100 makes it an ideal candidate for phytogeographic and population genetic diversity analysis. This hybrid has good representation of different genomes. In sugarcane a number of microsatellite markers are available but the density of microsatellite and other markers in available microsatellite maps is still not adequate. Compared to other crops, sugarcane breeding programs have historically been slow in progress because of the low efficiency and technical difficulties in crossing and selection processes (Chen *et al*., 2009). Therefore it is important to develop large number of useful polymorphic microsatellite markers (Singh *et al*., 2013). Thus, in the present study microsatellite markers were developed from ISH 100 and were tested for polymorphism, on parents of mapping population.

Genomic DNA of ISH 100 was extracted from fresh leaves, using CTAB method (Hoisington *et al*., 1994) and was digested using *Eco*R1. The recombinant plasmids were produced by ligating restriction fragments from *Saccharum* DNA into the *Hin*d III site of pUC19 plasmid. The fragments were enriched for microsatellite motifs CA, GA, ATG and TAG prior to ligation. Ligated products were introduced into *E. coli* strain DH5α (Electro Max J, Invitrogen) by electroporation. 2 µl of ligation mix was used for each of the libraries. After transformation and recovery incubation in SOC broth (Invitrogen), glycerol was added to a level of 20% of the final volume. Libraries were stored at approximately -70^{o}C. To isolate colonies for sequencing, cells from the glycerol stock were spread on X-gal/IPTG/ampicillin-LB agar plates. The capture protocol sometimes results in inserts that were less than 300 bp long. These smaller inserts were less likely to have sequences flanking a microsatellite that were long enough for primer design. Additionally, non-recombinants did not develop blue precipitate fully, and it was possible to select two colonies simultaneously if they were not well separated on the plate. Sterilized toothpicks were used to transfer white

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colonies from the spread stock plates on X-gal/IPTG/ ampicillin LB plate. The plate was incubated overnight, and colonies were selected from this plate. Some colonies have subsequently developed faint blue pigmentation; that generally contained recombinant plasmid with an insert of proper size.

The DNA fragments were cloned into the *Hin*d III (AAGCTT) cut site of the pUC19 plasmid. To obtain desired sequences Primer A (forward): 5'- AGG AAA CAG CTA TGA CCA TG -3'. Primer B (reverse): 5'- ACG ACG TTG TAA AAC GAC GG -3'were found to be effective. Typical annealing temperature for these primers was 57^{o}C; they also worked well at 58^{o}C. The clones from which sequences obtained were identified, were prepared for overnight culturing and subsequent mini-prepping. Cultures were grown overnight at 37^{o}C in a 96-deep well plates using 2X LB broth. Purification of plasmid DNA was accomplished using Millipore MultiScreen MAFB NOB Plates. DNA sequencing was accomplished using Applied Biosystems's Big Dye Terminator v3.1 Sequencing Standard Kit, followed by electrophoresis on an Applied BioSystems Model 3730 DNA Sequencer.

Once appropriate microsatellites were found, PCR primers were designed from the unique flanking regions using Designer PCR, version 1.03 (Research Genetics, Inc.). To test the primer, PCR reaction comprised : initial denaturation at 94^{o}C for 3 minutes, denaturation at 94^{o}C for 40 seconds, annealing at 55-57^{o}C for 40 seconds, extension at 72^{o}C for 30 seconds and final extension at 72^{o}C for 4 minutes. Initially products were separated on 3% agarose gels stained with ethidium bromide to check amplification.

Twenty six primer pairs (Table 1) were found to consistently amplify PCR products of expected size and were selected for fragment analysis. These 26 loci were amplified as above and products were visualized using an Applied Biosystems Avegene. Of the 26 loci checked, one failed to produce consistent results and 12 were monomorphic across the samples. The remaining 13 loci were used to assay 8 genotypes of sugarcane. SSR markers were scored on the basis of their band size, either present (1) or absent (0) for each SSR loci. Polymorphic information content (PIC) value was estimated with Power Marker v3.23 (Liu *et al*., 2005). The calculations of population genetic parameters, including alleles, observed and expected heterozygosity between the two populations, were estimated with the program POPGENE1.32 (Tech, 2000). The number of alleles per locus ranged from 2 to 6 with an average of 3.69 (Table 2). The expected and observed heterozygosity ranged from 0.40 to 0.83 and from 0.16 to 0.60, respectively (Table 2).

Thus, in the present investigation 13 SSR markers were isolated and characterized. The markers identified from ISH 100 can be used for mapping population, gene tagging and genetic diversity analysis. The ISH 100 was developed from a cross of S. *officinarum* and

Table 1. Characteristics of 13 microsatellite loci developed from inter-specific hybrid (ISH 100) of sugarcane

S.No	Primer	Forward sequence	Reverse sequence	Fragment size (bp)	Repeats motif	Annealing temp. (Ta) ^{o}C	Gene bank ID
1	A8	TATGGAGAGAGCAACCTATCA	GACGGAAGATTGGGATTC	220-610	(CA)25	56.9	28374217
2	A12A	TCAAAGTGGCTACAGAATAGGT	CAGCAAGGTTCCAAGTACC	170-310	(CA)15	56.7	28374214
3	A119	CCTATCGAATTGTGCTACTC	GCATGTGTATTGTGTTAGAGAA	118-180	(CA)16	54.8	28374210
4	A132	GGCCTTCGATTAACCGAT	ACAGGACGCTGCTTCTTG	194-310	(GT)17	57.7	28374215
5	B105	GGTGGCTAACAGACAGGG	TTGCTGCCGAGAGTCATA	118-500	(CT)16	56.9	28374220
6	B107	TTATCCCTTTCGTTCAGTAGAG	ATTTTGCGTAGGGTCTGAG	281-390	(CT)26	57.3	28374222
7	B112	TTATTTGTCCAACCTGCTTCTG	CATGGATGCTTTTGCGTTAG	118-190	(CT)22	56.9	28374225
8	B119	CACCCAGCAGTTATTGGA	CAGCAATCAAGTGTTCACTG	194-380	(CA)7,(CT)11	56.6	28374228
9	B126	ACCACCACCACTTTGTCTT	GGATTGCTAAAGCATTGGT	281-400	(CT)25	57.3	28374233
10	C1	ACCACCACCACTTTGTCTT	CGTGAGAAGGTAGGGAAACA	118-194	(ATC)13	56.7	28374240
11	C9	CCAAACCACATTGTAGCAG	CTTCTTGTCATCATCACTTGAG	194-234	(GAA)7	56.6	28374252
12	C123	GCGCCTATTTAATACCAGA	CTTTCCCTATACCCATGATAG	194-281	(ATC)12	56	28374247
13	C130	AAGGGAAGAGCAGGAGAG	CGGGAGGTCAAAATGTTA	234-281	(ATG)13	56.8	28374248

Table 2. Genetic properties of the newly developed 13 microsatellites of inter-specific hybrid (ISH 100) of sugarcane

Primer	Number of alleles	Expected heterozygosity (H_O)	Observed heterozygosity (H_E)	Inbreeding coefficient (F_{IS})	Polymorphism information content (PIC)
A8	5	0.19	0.8	0.56	0.33
A12A	5	0.18	0.81	0.35	0.44
A119	3	0.41	0.58	0.73	0.39
A132	4	0.45	0.54	0.13	0.30
B105	4	0.36	0.63	0.4	0.38
B107	2	0.46	0.53	-0.42	0.32
B112	4	0.27	0.72	0.26	0.42
B119	6	0.16	0.83	0.37	0.40
B126	3	0.3	0.69	0.39	0.43
C1	3	0.35	0.64	0.45	0.43
C9	2	0.6	0.4	1	0.37
C123	4	0.23	0.76	0.17	0.51
C130	3	0.37	0.62	0.81	0.39

S. spontaneum and the F_1 of this cross was again crossed with two of the commercial hybrids having representation of different species of sugarcane. The ISH 100 was studied extensively in our laboratory at molecular cytogenetic level using genomic *in situ* hybridization technique (unpublished data) and we have observed that this hybrid has the chromosomes of different species of sugarcane as *S. spontaneum, S. officinarum, S. robustum* and *S. sinense*. The hybrid has a good representation of different genomes and therefore, the markers developed from ISH 100 may be utilized across different species of sugarcane for genetic diversity analysis.

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Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXVIIIth meeting held on January 31st, 2014 at the National Bureau of Plant Genetic Resources, New Delhi, approved the registration of following 23 germplasm lines out of 74 proposals considered. The information on registered germplasm is published with the purpose to disseminate the information to respective breeders for utilization of these genetic stocks in their crop improvement programmes. Upon request, the developer(s)/author(s) is/are obliged to distribute the material for crop improvement programme of National Agricultural Research System.

1. PHULE G-00109 (IC0598237; INGR14001), a Chickpea (*Cicer arietinum*) Germplasm with Resistance to Wilt

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PHULE G-00109 (IC0598237; INGR14001) is a chickpea (*Cicer arietinum*) germplasm with resistance to wilt developed by hybridisation followed by pedigree selection of IG-9216 x ICCV-10 at ICRISAT, (AP).

Associated characters and cultivated practices

- Resistant to *Fusarium* wilt disease
- Medium maturity (102 days)
- High average yield (2113 kg/ha)
- Bold seed size (25 g/100 seeds).

Morpho-agronomic Characteristics of Phule G-00109

Entry	Year	Yield (kg/ha)	Maturity days	Plant height (cm)	Plant spread (cm)	Fruiting branches per plant	Pods/plant	100 seed wt. (g)
PG-00109	2004-05	2114(3)*	100	34.9	15.1	11.1	32.1	25.6
	2005-06	1882(3)*	107	49.4	14.6	15.5	38.4	26.1
	2006-07	2250(5)*	98	38.7	16.0	12.5	37.1	23.8
Mean		2113	102	41.0	15.2	13.0	35.8	25.1

*Figures in parentheses indicates number of test locations

Recommended cultivation practices: Seed rate: 85 Kg/ha; Spacing: 30x10 cm, fertilizer dose 25:50:30 NPK kg/ha, Suitable for rainfed and irrigated conditions.

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2. NIC7133, SD5-1278 (IC013884; INGR14002), a Safflower (*Carthamus tinctorius* L.) Germplasm with Resistance to Fusarium Wilt (*Fusarium f.* sp. *carthami*)

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A safflower landrace from Uttar Pradesh, IC13884 (NIC7133[SD5-1278]) was identified for resistance to *Fusarium* wilt caused by *Fusarium oxysporum* f.sp. *carthami*. The accession was received from NBPGR Regional Station, Akola during 1990-91 at the Germplasm Maintenance Unit (GMU) of Safflower at Solapur, assigned the alternate ID GMU 4983 and maintained. Subsequently, the accession is being maintained at Directorate of Oilseeds Research (DOR), Hyderabad since the year 2000.

It has undergone screening against *Fusarium* wilt pathogen (*Fusarium oxysporum* f. sp. *carthami*) under wilt sick plot conditions since 2003-04 and has exhibited consistent resistant reaction to wilt (Disease intensity: 0-10%) for 3 consecutive years (2003-04 to 2005-06) when the susceptible check 'Nira' showed 88.3-100% wilt incidence across locations (Tandur and Solapur) and years (Table 1) (Anonymous, 2004, 2005, 2006; Suresh *et al*, 2009). The resistance against wilt was confirmed through pot culture during 2010-11 (Anonymous, 2011) and *in vitro* screening by using fusaric acid method (Anonymous, 2012) during 2011-12 (Anjani *et al*, 2012) (Table 2).

The accession has serrate lower leaf margins, yellow colour of corolla turning to orange at faded stage, spiny outer involucral bracts, base to apical branching pattern, medium plant height, medium sized capitula, seeds with thick hull and oil content ranging from 26-28%.

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Table1. Field evaluation of NIC 7133[SD5-1278] / GMU 4983 in wilt sick plot

Year	Centre	Disease incidence (%)	
		GMU 4983	Nira (Susceptible check)
2003-04	AICRP (Safflower) Tandur	0	98.0
2004-05	AICRP (Safflower) Tandur	<10	100.0
2005-06 (UDN)	AICRP (Safflower) Tandur	0	88.3
	AICRP (Safflower) Solapur	<10	98.7

Table 2. Laboratory confirmation of *Fusarium* wilt resistance of NIC 7133[SD5-1278] / GMU 4983

Year	Centre/Method	GMU 4983	Nira (Susceptible check)
2010-11	DOR, Hyderabad, Pot culture	<10% wilt incidence	>80% wilt incidence
2011-12	AICRP (Safflower) Solapur [*In vitro* Fusaric acid method]	Survival 15 days (resistant reaction)	Survival 3 days (susceptible reaction)

3. DPC-16 (IC0598621; INGR14003) a Unique Pistillate Line of Castor (*Ricinus communis* L.) with Unique Morphotype of Flower, Stem Colour and Zero Bloom with Hermaphrodite Flower at Tip

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DPC-16, a pistillate line with a unique morphotype i.e. hermaphrodite flower at the tip of the pistillate spike, was developed at Directorate of Oilseeds Research, Hyderabad. Castor, a member of *Euphorbiaceae*, is a sexually polymorphic species with unisexual flowers, either male or female mostly arranged as monoecious and occasionally pistillate spikes. The plant consists of several series of determinate branches each terminated by a raceme. The development of raceme along any one axis is sequential; thus it is possible to have racemes at all stages of development. The basic sex forms in castor are monoecious and pistillate. Monoecious (M**)** is the most natural occurrence of annual and perennial castor. The spike has basal 1/3 to 1/2 male flowers while the top portion has female flowers. In between these, few whorls have both male and female flowers in an interspersed fashion. Pistillate (P) occurs as a rare recessive mutant with the spike having female flowers throughout the spike. Interspersed Staminate Flower (ISF) is a variant of pistillate form with male flowers interspersed, throughout the female flowers on the spike which helps in maintenance of pistillate line. Sex reversion from pistillate to monoecious is the most common problem encountered in the seed production plots.

Three types of pistillate mechanism N, S and NES types were utilized for development of pistillate lines in castor. The N type is governed by recessive sex switching gene and maintained by sib mating. In USA, N type of pistillate lines *viz*., Nebraska 145-4, CNES-1 were used for development of castor hybrids (Classen and Hoffman, 1950). S type pistillate line was obtained by selection within sex reversals at the Weizmann Institute, Israel and governed by dominant and epistatic effects (Shiffriss, 1960). NES type is governed by a recessive sex-switching gene in combination of environmentally sensitive genes for ISF expression. NES type is a combination of both N and S type as it carries the homozygous recessive gene for pistillateness and environment sensitive genes for ISF (Kulkarni and Ankineedu, 1966). Among the three types of pistillate lines-N, S and NES, S type is the most commonly used in heterosis breeding in India while the diverse source NES is underexploited due to the lack of suitable combiners (Lavanya *et al*., 2006).

Efforts initiated at the Directorate of Oilseeds Research to enhance the genetic diversity of pistillate lines using NES source led to identification of the genetic stock DPC-16 in a segregating population of the cross NES-6 x TMV-5 with the unique trait of a single hermaphrodite flower at the tip of the spike (Lavanya, 2002 and Lavanya, 2009). Heritability of the trait was observed up to 80-90 % in a population of nearly 60-100 plants every year. The trait was further stabilized by selfing the pistillate line with hermaphrodite flowers in ten generations. The proposed stock has other distinct morphological characters like red stem, zero bloom, medium long (25-30 cm), semi-compact spike with spiny capsules (Table 1). The stem color of the plants was very distinct without any bloom and initially coined

Table 1. Chief botanical and morpho-agronomic traits of DPC-16

Trait	DPC-16
Stem color	Red
Presence of bloom	Zero (absent)
Type of internodes	Elongated
Number of nodes up to primary spike	12-16
Leaf shape	Flat
Branching pattern	Divergent
Spike shape	Cylindrical
Spike compactness	Semi compact
Sex expression	Pistillate; hermaphrodite flower at the top
Capsule: spininess	Spiny
100-seed weight (g)	Medium (21-30)
Seed shape	Oval
Seed base color	Brown
Seed mottling	High
Seed caruncle	Inconspicuous

as "purple" and later modified as "red" stem color as per the RHS color chart (Ref. No. RHA 187A). The genetic stock has a potential to use in the heterosis breeding as a diverse source of pistillate line and will also be further useful in the study of sex polymorphism in castor and development of genetic stocks for distinct sex expression.

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4. RG 2818 (IC0346622; INGR 14004) a Castor (*Ricinus communis* L.) Germplasm with Resistance to Wilt (*Fusarium oxysporum* f. sp. *ricini*)

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RG2818 (IC346622) was selected from the original heterogeneous population of KA68/01 collected from Tamil Nadu State of India. It had undergone nine generations of self-pollination. It was tested for resistance against *Fusarium* wilt and evaluated for agronomic and yield traits along with other germplasm collections at the Directorate of Oilseeds Research, Hyderabad.

RG2818 was screened against *Fusarium* wilt (*Fusarium oxysporum* f. sp. *ricini)* in wilt sick plots at DOR, Hyderabad and SK Nagar, Gujarat for six

Table 1. Reaction of RG 2818 against *Fusarium* wilt (*Fusarium oxysporum* f.sp. *ricini)*

Year of screening	Method of screening	Wilt incidence (%) in RG 2818		Wilt incidence (%) in susceptible checks*	
		DOR, Hyd.	S.K. Nagar	DOR, Hyd.	S.K. Nagar
2002-03	Wilt sick plot	5.0	0.0	95.8 (Aruna)	91.9 (GAUCH-1)
2003-04	Wilt sick plot	0.0	0.0	88.5 (VP-1)	98.5 (GAUCH-1)
2003-04	Confirmation of resistance under artificial epiphytotic conditions in glasshouse using root-dip inoculation technique.	7.1	0.0	71.4 (Kranti)	97.5 (GAUCH-1)
2004-05	Wilt sick plot	8.3	0.0	86.4 (VP-1)	100 (JI-35)
2004-05	Confirmation of resistance under artificial epiphytotic conditions in glasshouse using root-dip inoculation technique.	0.0	0.0	84.6 (JI-35)	100 (GAUCH-1)
2006-07	Wilt sick plot	0.0	16.7	100 (VP-1)	96.7 (JI-35)
2007-08	Wilt sick plot	16.6	0.0	100 (JI-35)	100 (JI-35)
2010-11	Wilt sick plot	0.0	0.0	93.8 (Kranti)	100 (JI-35)

*The entries in parentheses are wilt susceptible checks

years. *Fusarium oxysporum* f.sp. *ricini* inoculum was being maintained in wilt sick plots by adding wilt inoculum at regular intervals. Susceptible check was grown after every 10 rows of test entries in wilt sick plots to ensure uniform disease expression across the sick plot. Resistance reaction of RG2818 was further confirmed twice under artificial epiphytotic conditions in glasshouse using root dip inoculation method (Raoof and Nageshwar Rao, 1996) at DOR, Hyderabad and S.K Nagar. It consistently exhibited resistant reaction (0-16.7% wilt incidence) whereas the susceptible checks exhibited 71.4-100% wilt disease incidence (Table 1). The scale proposed by Mayee and Datar (1986) was used to rate the reaction against wilt. Any genotype showing <20% wilt incidence is rated as resistant.

RG2818 is has red stem with high node number and bloom. Its raceme is cylindrical in shape, loose and covered with more male flowers than pistillate ones. Capsules are green, big, spiny and non-dehiscent. In addition to wilt resistance, RG2818 is a high yielding accession, with yield capacity around 200g/plant. It is a medium maturity duration type.

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5. CJ-3 (IC0598611; INGR 14006), a Physic nut (*Jatropha curcas* L.) Germplasm with High yield, Early Flowering (125 Days) and High Oil Content (38.01%)

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Oil from *Jatropha curcas* as a source of biodiesel a renewable liquid fuel and its biochemical properties are near equivalent to petro-diesel after transesterification (Paramathma *et al.,* 2007 and 2012). The parent TNMC-7 (*Jatropha curcas*) has unique characters such as green pithy soft stem, with 170-183 days to first flowering (Annonymous 2004-05 and 2005-06) with a seed yield of 0.258, 1.225 and 1.384 kg/plant in the first, second and third years respectively.

J.integerrima was as male donor parent with moderate resistance to pest and diseases, dwarf (1.342–1.564 m), petal colour pink, with long peduncle (Paramathma *et al*, 2007) and flowering in 150-163 days, small single seeded capsule, with poor yield of 15-20 g/plant/year (Rathakrishnan and Paramathma, 2009). In order to improve seed yield, stem quality and flowering inter specific hybridization was made between two diverse species of *J. curcas* (TNMC-7) and *J.integerrima.* The F_1 progenies were back crossed with TNMC-7 as female parent and CJ-3 was selected at Forest College and Research Institute, TNAU, Coimbatore.

Morpho-agronomic characters: The unique traits of CJ-3 (13143; IC0598611) posses semisolid stem, with pigmentation of Pale green and brown mottle, early (125-135 days), non-seasonal, continuous flowering for eight months (Paramathma 2012), reticulate, tri lobbed, rarely 4 lobbed pod, Seed testa colour - Black 202, Group A, posses 38.01% seed oil and seed yield of 0.442, 2.047 and 2.612 kg/plant/year from first, second and third year respectively (Viswanathan *et al.,* 2012).

Associated characters and cultivated practices for CJ-3 (INGR14006)

The culture CJ-3 also susceptible to mealy bug and root rot disease and it is at early stage of MLT trials. Two kg of seeds are required for planting one ha. The seeds may be soaked in water for 12 hours and the treated seeds should be sown in 10x20 cm poly bags. After 90 days, field planting has to be done with pits of size 30x30x30 cm at a spacing of 3x2 m (1660 seedling/ha) by adding 10 g/pit of *Pseudomonas fluorescence*t. Two split dose of urea, super phosphate and potash @ 20:120:60 g/seedling have to be applied. Life saving irrigation needed immediately after planting and afterwards at an interval of 20-30 days. First pruning has to be done at a height 45 cm from the ground level.

Table 1. Salient characteristics of morpho-agronomic description of CJ3

Description of variety and Name	CJ-3
Plant height (cm)	290.4
Collar diameter (cm)	11.36
No. of primary branches	2.87
No. of secondary branches	12.07
Branching pattern	Dichotomous branching
Stem pigmentation	Pale green with brown mottle
Stem surface	Rough
Types of inflorescence	Cymose - Panicle
Anthesis	7.00 am
Petal color	Green
Leaf color	Light green
Leaf shape	Cordate with rudimentary tri-lobbed
Leaf surface	Smooth
Leaf tip	Acuminate
No. of fruiting bunches	40.33
Seed beak	Prominent
Pod reticulation	Three lobbed, rarely 4 lobed
Testa colour	Black 202, Group A
Peduncle	Long pendulous
Pod size	Medium (Length: 2.44 cm, Width: 2.34 cm)
Pod shape	Elongated
Seed shape	Ovate
Seed size	Medium (Length: 2.04 cm, Width: 1.54 cm)
Days to 50% flowering (days)	125-135
Maturity (days)	175-185
Maturity group (early, medium and late)	Early
Reaction to major disease under field conditions	Susceptible to root rot
Reactions to major pests (under field conditions)	Susceptible to mealy bug
Oil content (%)	38.01%
Seed yield (station/demonstration trials) kg/plant	0.442/1st year,2.047/ 2nd year, 2.612/3rd year

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6. SD23/6 (IC208366; INGR14007), a Pea (*Pisum sativum*) Germplasm with Resistance to Four Isolated Strains of Powdery Mildew (*Erysiphe pisi*) viz. *rangway, trilkinath, stingri* and *kangra*

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7. SD23/57 (IC208378; INGR14008), a Pea (*Pisum sativum*) Germplasm Resistance to Four Isolated Strains of Powdery Mildew (*Erysiphe pisi*) *viz. rangway, trilkinath, stingri* and *kangra*

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8. G-389 (IC0596521; INGR14009), a Garlic (*Allium sativum* L) Germplasm for earliness

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Generally garlic varieties developed by different organization takes about 130-270 days to attain physiological maturity. Now a day's there is no variety available for growing during *Kharif* season having early maturity in India. In this chain NHRDF has recently identified a new garlic genotype "G-389" which is being harvested within 72-80 days during *Kharif,* late *Kharif* and 85-95 days in *Rabi* season, about 40-50 days earlier than other garlic varieties grown in India. This variety was developed through mass selection at Nashik. Plant height is up to 45-60 cm with 7-8 green leaves/plant. Neck thickness ranged between 0.75-1.0

cm. Colour of bulb is white with pinkish tinge. Bulbs are compact attractive and diameter of bulb is 2.80-3.50 cm, size index 9-12 cm^2, cloves varies from 18 to 25 and 50 bulb weight is about 450-600 g. The length of clove 1.25-2.0 cm, width 0.75-0.90 cm and size index of clove is 1.5-2.0 cm^2. Average yield 60-75 q/ha with good storage capacity.

Morpho-agronomic characteristics: The plant is medium tall in height; pseudo-stem and leaf are green in colour, erect and slightly narrows than other varieties. The experiment was carried out at RRS, Nashik and (pooled data presented in Table-1), revealed that the highest plant height (43.94 cm), leaf breadth (0.83 cm), number of cloves/bulb (22.17), bulb diameter (3.23 cm), weight of 20 cloves (0.23 g) and gross yield (68.06 q/ha) were recorded in G-389 where plant height, leaf breadth and weight of 20 cloves were found at par in Amleta local check, however, highest number of leaves (6.70/plant) was recorded in local check Amleta and found at par with G-389. A crop should produce sufficient number of leaves to harness light energy and synthesize adequate photoassimilate for biomass production. It is also reported that increase in bulb weight was associated with increase in plant height, leaves per plant, bulb diameter, higher number of cloves per bulbs and cloves weight. (Singh *et al.,* 2011; Singh *et al.,* 2012; Islam *et al.,* 2004; Singh and Chand, 2003). The genotype "G-389" took minimum period (76 days) for physiological maturity *i.e.* for harvesting the crop (Anonymous, 2010) followed by the local check Amleta which took 99 days for maturity of the crop. Thus it is concluded that the G-389 recorded about 23 days early maturity and also gave about 18% higher yield over the local check and promise for its cultivation successfully during *Kharif* season.

Associated characters and cultivation practices: The highest total soluble solids (38.83 %) and dry matter content (40.84 %) were recorded in G-389 though it showed non-significant differences. In general cool growing period gives more yields. It can be grown better on fertile, well drained loamy soils. The optimum soil pH range is 6–7. About 500-700 kg cloves are required for one hectare, care should be taken to select bigger cloves preferably from the outer side of the bulbs. 25 t FYM, 100 kg N, 50 kg P, 50 kg K and 40-50 kg S/ha through chemical fertilizers has been recommended. Because of small cloves it is planted with spacing of 10 x 7.5 cm to get optimum bulb yield. Garlic needs irrigation at an interval of 10-12 days during vegetative growth and 8-10 days during maturation. Drip irrigation can also be used for high yield and quality bulbs. Pendimethalin @ 3.5 liter or oxiflurofen (goal) @ 2.5 liter/ha + 1 hand weeding gives good control of broad leaved weeds. Spray of Multi K (13:0:45) at 50 and 65 days after planting improve the quality of the bulbs. 10-15 days before harvesting, irrigation should be stopped otherwise it can be splitted re-sprout and decrease yield and market values.

The crop is considered ready for harvesting when the tops turn light yellowish or brownish and show signs of drying. Curing is additional process of drying to remove the excess moisture and to allow the bulbs to become compact and go into dormant stage and within a week in the field to dry the bulbs thoroughly, after that cured for 7-10 days in shade either with tops or after cutting the tops by leaving 2.0-2.5 cm from bulbs and send in the market after proper sorting and grading for sale. It can be stored in bundles along with foliage or in hessian bag or leno bags after foliage cut in ventilated go-downs.

Table 1. Pooled data evaluation of garlic Genotypes for earliness at RRS, Nasik for 2011-12

Treatments	Plant height (cm)	No. of leaves/ plant	Leaf length (cm)	Leaf breadth (cm)	No. of cloves/ bulb	Bulb diameter (cm)	Cloves diameter (cm)	Wt. of 20 cloves (g)	TSS (%)	Dry matter (%)	Gross yield (q/ha)
G-389	43.94	6.27	25.47	0.83	22.17	3.23	0.68	0.23	38.83	40.84	68.06
G-391	39.47	5.34	22.43	0.72	19.24	2.87	0.62	0.20	37.84	39.80	49.66
Yamuna Safed-3 (G-282) (C)*	33.83	5.04	24.67	0.61	----	2.57	----	----	----	----	----
Amleta local (C)	42.40	6.70	25.60	0.78	19.83	2.96	0.68	0.21	38.33	40.17	57.69
S. Em±	1.54	0.28	1.35	0.02	0.33	0.06	0.02	0.01	0.53	0.43	2.03
CD at 5%	4.90	0.91	NS	0.08	1.42	0.18	NS	0.04	NS	NS	8.71

*Note: Clove separation did not take place

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9. DPO-296-4 (IC0598208; INGR14010), a Golden Yellow Leaf Colour Mutant of Isabgol (*Plantago ovata* Forsak) Germplasm

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Isabgol is an important medicinal plant mainly used as laxative worldwide and India is the sole exporter of this crop to the world market. Isabgol husk, the seed epidermis having muco-polysaccharide layers, is widely used against constipation, diarrhoea and intestinal irritation. Isabgol is also an excellent source of dietary fiber and has hypocholaesterolemic activity and is widely accepted as food additive in several processed materials like cookies, ice-cream, bread, etc. (Trautwein *et al.*, 2000). This crop is mainly cultivated in arid and semi-arid regions of Gujarat, Rajasthan and parts of Madhya Pradesh as rain-fed *Rabi* crop where intermittent drought limits Isabgol production. It is an introduced crop and the genetic variability available in India is low. To handle the IPR issue, it is necessary to have sufficient DUS descriptors. PPVFR has released the isabgol DUS guidelines with 15 descriptors and more descriptors are to be added for easy and accurate identification of isabgol variety/germplasm. In this direction, first time, a golden yellow colour leaf mutant (DOP-296-4) has been identified at DMAPR and it can effectively use as one of the descriptors for identification of isabgol genotypes.

DPO 296-4 has golden yellow colour leaves; the leaf pubescence is medium and narrow leaf bread (0.6 to 1.0). It has erect plant growth habit with 5-15 branches and medium height (25-35 cm). The spike arrangement is compact, spike-peduncle is unbranched, spike flower arrangement is compressed with 3-7 cm spike length and about 50 spikes/plants. The 1000-seed weight of spike is low.

DOP-296-4 will be useful to own the Intellectual Property Rights (IPR) the isabgol varieties being released

as it has an important morphological and qualitatively controlled marker characters that should be effectively used as one of the DUS characters. In this context, the golden yellow leaf mutant, DPO 296-4 reported herein may be useful genetic resources that can be incorporated into the high yielding commercial varieties for its easy identification.

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10. SBI 2007-291 (IC0598475; INGR14011), a Sugarcane (*Saccharum* spp. Hybrid) Germplasm with Early High Sucrose

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11. DMR QPM 58 (IC0594368; INGR14012), a Quality Protein Maize (*Zea mays*) Germplasm with Early Maturity

12. DMR QPM-03-124 (IC0594269; INGR14013), a Quality Protein Maize (*Zea mays*) Germplasm with Medium Maturity

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Maize is a major cereal crop for both human and livestock nutrition, worldwide. Several million people, particularly in the developing countries, derive their protein and calorie requirements from maize. Therefore, this vast segment (human population) depends upon cereals for their nutrition and livelihood. Protein from cereals including normal maize, have poor nutritional value because of reduced content of essential amino-acids such as lysine and tryptophan. Quality Protein Maize (QPM) is an improved version of maize that contains higher amount of lysine and tryptophan with lower amount of leucine and isoleucine in the endosperm than those contained in normal/conventional maize. Such balanced combination of amino acids in the endosperm results into its higher biological value ensuring more availability of protein to human and animal than normal maize. Hence, an attempt was made to develop inbred lines with higher concentration of tryptophan and lysine which may be used in the hybrid breeding program. Given below is the information on QPM lines registered as unique germplasm.

DMR QPM 58 (IC 0594368; INGR14012)

DMR QPM 58 (IC 0594368, INGR 14012) is an early maturing QPM line with low anthesis silking interval (ASI), high tryptophan (0.67%) and high protein content (9.40%). This inbred line has been developed after evaluating, selecting and selfing for 5-7 generations of Shakti 1, a quality protein maize OPV.

Morpho-agronomic characteristics: In the present study, a set of elite QPM inbred lines (*o-2* with hard endosperm) along with check entries (normal as well as QPM) was evaluated under Delhi conditions for *per se* performance as well as biochemical traits i.e. protein (%) and tryptophan in protein (%). Data was recorded on various parameters *viz*., phenology, agro-morphology and quality along with DUS-related characteristics. This inbred line has small ($<45^0$) leaf angle with straight leaf

attitude. It showed early anthesis (47 days) as well as silk emergence (48 days) with low ASI of one day. It has purple brace roots, glumes (of tassel) and silk. However, anthers are green. The tassel is dense with straight tassel branches. The tassel angle between main axis and lateral branches as well as leaf width of blade is narrow. The plant height is short (105 cm) with low ear placement. The ear shape is cylindrical with orange round shaped grains. It has medium ear number of rows of grains and small 1000 kernel weight of 122g (Kaul *et al.,* 2012).

DMR QPM-03-124 (IC 0594371; INGR14013)

DMR QPM-03-124 (IC 0594369, INGR 14013) is a medium maturing QPM line with low anthesis silking interval (ASI), high tryptophan (0.65%) and high protein content (8.77%). This inbred line has been derived from Shakti-1, quality protein maize OPV after evaluating, selecting and selfing for 5-7 generations.

Morpho-agronomic characteristics: DMR QPM-03-124 is medium maturing QPM line with 0.65% tryptophan in protein (Kaul *et. al.*, 2012). It showed medium anthesis (52 days) and silk emergence (53 days) with low ASI of one day. This inbred line has small ($<45^0$) leaf angle with straight leaf attitude. It has purple brace roots, glumes (of tassel) and silk. However, anthers are green. The tassel is dense with straight tassel branches. The plant height is short (114 cm). The ear shape is conico-cylindrical with yellow flint grains. It has medium ear placement and medium kernel weight (166g).

References

Kaul J, JC Sekhar, R Sai Kumar and S Dass (2012) Studies on variability in elite inbred lines of quality protein maize. *Maize J.* **1:** 27-29.

13. DMRE 63 (WNZPBTL 9) (IC0594373; INGR14014), a Maize (*Zea mays*) Germplasm with Resistance to Pink Borer

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Maize (*Zea mays* L.) is grown predominantly during *Kharif* season in northern parts whereas continuous cropping is practiced during *Kharif* and Rabi seasons in Southern and Eastern India. The average productivity of maize in our country is much lower than its potential. Lack of proper pest management is one of the reasons for the lower productivity. The lepidopteran stem borers are of great economic importance in most maize growing countries throughout the world and are major constraints in its productivity. Pink stem borer, *Sesamia inferens* (Walker) is a serious pest limiting the production of maize in Rabi season. Hence in order to develop resistant desirable hybrids, pink stem borer tolerant inbred lines are urgently sought.

Morpho-agronomic characteristics: A set of inbred lines was evaluated for Leaf Injury Rating (LIR) in the scale of 1-9 in Rabi seasons (2009-10, 2010-11 and 2011-12) at Winter Nursery Centre, DMR, ANGRAU, Hyderabad. Based on least LIR of 2.0, the desirable lines were identified and evaluated for phenology and DUS traits. DMRE 63 (WNZPBTL 9) (IC0594373, INGR14014) is an early maturing inbred line resistant to pink stem borer (*Sesamia inferens*). The inbred line has wide leaf and tassel angle along with curved leaf attitude of blade, tassel attitude of lateral branches and sparse tassel. It has purple brace roots and anthers. However, tassel anthocyanin colouration of base of glumes, silk and leaf sheath are green in colour. The plant height, tassel length of main axis above lowest side branch and plant ear height are medium with narrow leaf width of blade, short ear length and small ear diameter. The ears are conical in shape and have medium number of yellow kernel rows with non-pigmented shank. It has straight kernel row arrangement, flint grains with round shape and small 1000-kernel weight of 154.2 g, respectively.

14. PS-1 (IC0598201; INGR14015), a Finger Millet (*Eleusine coracana*) Germplasm with Partial Sterility, Useful In Hybridization and Easy Maintenance

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15. PUNE SELECTION-3 (IC0599272; INGR14016), a Papaya (*Carica papaya*) Germplasm with Papaya Ring Spot Virus (PRSV) Tolerance and Higher Yields (30-40 Kg of Fruits)

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Pune Selection-3 a papaya line is having field tolerance to Papaya Ring Spot Virus (PRSV) and yields 30-40 Kg of fruits (Datar *et al.,* 2013; Anonymous, 2012, 2013). The parental material is a land race of papaya named Madhubala which was segregating. From this segregating population PS-3 was selected in the year 2009.Since then it was sibmated and pure line developed by selection at IARI, Regional Station Pune.

Morpho-agronomic Characteristics: Mean height of the plant is 1.96 meters, mean canopy E-W is 2.4 and N-S 2.15 meter, mean stem girth is 34.5 cms, leaf shape is palmate type, petiole colour is green. Days to flower 58-60. The line PS-3 is dioecious in nature with male or female flowers on separate plants. The percentage of plants with male flowers is 25-30. Petal colour in flowers is cream yellow. Height of the fruiting column is 1.1 meters. Mean number of fruits per plant is 25-30. Mean fruit weight is 1.5 Kg. Average yield per plant is 30-40 Kg/plant. Shape of the fruit is oblong with beak at styler end. Mean length of fruit is 24 cms while breadth is 16.5 cms. The flesh colour is pink to red with a TSS of 9-11.

Associated Characters and Cultivated Practices: The papaya line PS-3 is having field tolerance to Papaya Ring Spot Virus (PRSV) It shows mild PRSV symptoms at late stage. The incidence of PRSV in PS-3 and two checks Red Lady and Pusa Nanha over years is given in Table 1 and 2.

Table 1. Incidence of PRSV in PS-3, Red Lady and Pusa Nanha over years

Cultivar/line	February 2009	March 2009	February 2010	March 2011	April 2011	April 2012	Mean
PS-3	3.17	4.6	17.7	22.2	6.8	21.5	12.66 (6)
Red Lady	78.33	70.75	100	100	89.6	96.7	89.23 (6)
Pusa Nanha	17.18	–	33.33	–	38.6	39.2	32.07 (4)

Table 2. Yield of papaya fruits Kg./plant in PS-3 , Red Lady and Pusa Nanha over years

Cultivar/line	February 2009	March 2009	March 2011	April 2011	April 2012	Mean
PS-3	36.15	32.53	28.75	33.18	32.62	32.64
Red Lady	18.42	8.85	2.93	3.89	12.95	9.40
Pusa Nanha	22.84	–	–	25.51	0.0	16.11

Cultivation practices: Under Maharashtra conditions it is recommended to plant two months old seedlings in spring (Feb.-April) since the aphid vector population is minimum during Feb. to June. Seedlings should be raised in plastic bags in net house. Since PS-3 is a dioecious line two seedlings should be planted at a hill at one feet distance. Row to Row and plant to plant distance should be 2.1x 2.1 meters. Apply 10 Kg. Cow dung manure+2 Kg. Neem seed cake + 1 Kg. Sterameal per hill. Apply inorganic fertilizers like N, P, K 250g/plant in six splits at two months interval. Similarly spray micronutrients like $ZnSO_4$ 0.25-0.5% and Boron 0.1% at flowering and four weeks later.

References

Datar VV, KK Zote, R Verma, S Tripathi and SPS Tomer (2013) Field evaluation of papaya cultivars/ lines for Papaya ringspot virus. *J. Mycol. Plant. Pathol* **43(4):** 481-483.

Anonymous (2013) Papaya cultivar for PRSV resistance. *Annual Report 2012-13, IARI, New Delhi* pp 84.

Anonymous (2012) Papaya for PRSV resistance. *Annual Report 2011-12, IARI, New Delhi* pp 78.

16. Creeping (IC0391661; INGR14017), a Mango (*Mangifera indica*) Germplasm with Medium Size Fruits, Yellow Coloured Fibreless Pulp, Good Sugar Acid Blend, Good Keeping Quality for Processing and Fruits with Red Blush on the Skin

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Mango is highly heterozygous and due to its propagation by seeds has resulted in extensive variability. There is a very large diversity for the monoembryonic varieties and in India about one thousand varieties are being grown. It is a chance seedling said to have originated in the Trichur region of Kerala (Naik and Gangolly, 1950).

Morpho-agronomic characteristics: It is a semi-vigorous tree having round shaped fruits with attractive yellow colour. It is a monoembryonic variety and the fruits are about 200-220g. The tree canopy is spreading type and the growth is mostly towards horizontal direction (Gangolly *et al.*, 1957; Anon, 1985; Iyer and Subramanyam 1986; Dinesh *et al.*, 2012).It is a regular and high yielder. The pulp is slightly fibrous towards the stone. However the fruits are not very sweet. It has a pulp recovery of >70%. The fruit characteristics are given Table 1.

Traits of interest: It can be used in the breeding programme for incorporating dwarf stature as well as good peel colour and high pulp recovery.

Barcode:

Table 1. Descriptor and descriptor state of IIHR 19977 (IC0391661)

Descriptor	Descriptor state
Tree size	Dwarf
Bearing behaviour	Regular
Leaf colour	Light brownish red
Leaf tip	Acuminate
Panicle colour	Greenish red
Panicle shape	Pyramidal
Yield (Kg/plant)	60-70
Fruit length (cm)	6.40
Fruit breadth (cm)	6.70
Fruit thickness (cm)	5.76
Skin colour	Yellow with red blush
TSS (°Brix)	13.20
Pulp content (%)	71.80
Pulp colour	Dark yellow
Stone weight (g)	16.60

References

Anon (1985) *Indian J. Hort.* **43:** 221-23.

Iyer CPA and MD Subramanyam (1986) Creeping, a promising genotype for introduction of dwarfness in *mango. Indian. J. Hort.* **43:** 321 223.

Naik KC and SR Gangolly (1950) A monograph on classification and nomenclature of South Indian Mangoes. Govt Press, Madras.

Gangolly SR, SLR Singh, KD Singh (1957) Mango. Published by ICAR, New Delhi, India.

Dinesh MR, C Vasugi, KV Ravishankar and YTN Reddy (2012) Mango catalogue. Indian Institute of Horticultural Research, Bengaluru.

17. Kalapadi (IC0391736; INGR 14018), a Mango (*Mangifera indica*) Germplasm with Dwarf Stature, Produces Medium Sized Fruits Having Deep Yellow Coloured Pulp with High TSS and Good Keeping Quality

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The variety is indigenous to certain districts of Andhra state. The history of its origin and distribution is not known. It bears heavy crops regularly. In the coastal districts of Karnataka, the variety is known as Kallapady especially in the Dakshina Kannada districts. It is also known by the name KattiNeelum in the Tanjore district of Tamil Nadu (Naik and Gangolly, 1950).

Morpho-agronomic characteristics: The tree is dwarf statured but in some regions it is observed to be semi-vigorous. The fruits have very prominent lenticels. The young foliage is light brownish in colour. Fruits on ripening become pale yellow with green patches. The fruits are round in shape with a prominent beak. The pulp colour is pale yellow but firm and free from fibre. It has less pulp recovery but good keeping quality (Anon, 1985, 1988; Dinesh et al., 2012). The fruit characteristics are given in Table 1.

Traits of interest: It can be used in the breeding programme for incorporating dwarf stature, excellent fruit quality and good keeping quality.

Barcode:

Table 1. Descriptor and descriptor state of IIHR 342 (IC391736)

Descriptor	Descriptor state
Tree size	Dwarf
Bearing behaviour	Regular
Leaf colour	Light brownish red
Leaf tip	Acuminate
Panicle colour	Greenish red
Panicle shape	Pyramidal
Yield (kg/plant)	50-60
Fruit length (cm)	7.20
Fruit breadth (cm)	6.20
Fruit thickness (cm)	6.13
Fruit weight (g)	150
Peel colour	Greenish yellow
Pulp colour	Pale yellow
TSS (°Brix)	19.5
Pulp content (%)	31.90
Stone weight (g)	23.70

References

Anon. (1985, 1988) Reported at All India Coordinated Fruit Workshop.

Naik KC and SR Gangolly (1950) A monograph on classification and nomenclature of South Indian mangoes. Govt Press, Madras.

Dinesh MR, C Vasugi, KV Ravishankar and YTN Reddy (2012) Mango catalogue. Indian Institute of Horticultural Research, Bengaluru.

18. Janardha Pasand (IC0391715; INGR14019), a Mango (*Mangifera indica*) Germplasm Dwarf in Stature, Produces Medium Sized Fruits Having Yellow Coloured Pulp with High TSS, Good Keeping Quality with Attractive Red Blush All Over the Fruit

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The variety has originated in the East Godavari district of Andhra state. It is a late season variety and has good commercial value in the growing region. It is a regular bearing variety and fruits are borne in clusters (Naik and Gangolly, 1950).

Morpho-agronomic characteristics: This variety is a semi-vigorous tree type having sparse canopy. It is a medium yielder producing medium sized fruits. Fruits are borne in clusters of 2 to 3 fruits. The fruits are oval shaped and are not very sweet to taste. The fruits have thick peel and ripen to attractive red colour. It is one of the best indigenous varieties having excellent peel colour. The fruits taste is flat as the TSS is less and the pulp colour is yellow (Anon, 1982; Dinesh *et al*., 2012).

Traits of interest: It can be used in the breeding programme for incorporating dwarf stature, excellent peel colour and good keeping quality.

Barcode

Table 1. Descriptor and descriptor state of IIHR19962 (IC391715)

Descriptor	Descriptor state
Tree size	Semi-vigorous
Bearing behaviour	Regular
Leaf colour	Light green
Leaf tip	Acuminate
Panicle colour	Crimson
Panicle shape	Conical
Yield (Kg/plant)	45-50
Fruit length (cm)	8.90
Fruit breadth (cm)	6.60
Fruit thickness (cm)	6.63
Fruit weight (g)	256.20
Peel colour	Yellow with red blush
Pulp colour	Dark yellow
TSS (°Brix)	14.60
Pulp content (%)	67.50
Stone weight (g)	26.00

References

Anon (1982) Reported at All India Coordinated Fruit Workshop.

Dinesh MR, C Vasugi, KV Ravishankar and YTN Reddy (2012) Mango catalogue. Indian Institute of Horticultural Research, Bengaluru.

Naik KC and SR Gangolly (1950) A monograph on classification and nomenclature of South Indian Mangoes. Govt Press, Madras.

19. Ati Madhuram (IC0391622; INGR14020), a Mango (*Mangifera indica*) Germplasm with Medium Sized Round Shaped Fruits, Yellow Coloured Fibreless Pulp and Dwarf Stature

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The variety is grown in certain districts of Andhra state. The history of its origin and spread is not known (Naik and Gangolly, 1950). It produces fruits with very sweet taste.

Morpho-agronomic characteristics: It produces round shaped medium sized fruits. Tree has comparatively sparse canopy, when grown with enough moisture tree is vigorous. It is not a very regular bearer. Fruits are medium sized with fiber free pulp and very sweet taste. The pulp recovery is more than 60%. The fruits ripen to pale yellow colour (Anon, 2010; Dinesh *et al*., 2012) (Table 1).

Traits of interest: It has excellent firm pulp with high TSS and high pulp recovery.

Barcode

Table 1. Descriptor and descriptor state of IIHR19898 (IC391622)

Descriptor	Descriptor state
Tree size	Dwarf
Bearing behaviour	Irregular
Leaf colour	Light greenish brown
Leaf tip	Acuminate
Panicle colour	Light red
Panicle shape	Pyramidal
Yield (kg/ tree)	50-60
Fruit length (cm)	8.55
Fruit breadth (cm)	8.00
Fruit thickness (cm)	7.60
Fruit weight (g)	301.25
Peel colour	Yellow
Pulp colour	Yellow
TSS (°Brix)	21.40
Pulp content (%)	67.40
Stone weight (g)	34.60

References

Anonymous, (2010) UNEP-GEF report submitted to National Project Coordinator, India, Bioversity International Centre.

Naik KC and SR Gangolly (1950) A monograph on classification and nomenclature of South Indian Mangoes. Govt Press, Madras.

Dinesh MR, C Vasugi, KV Ravishankar and YTN Reddy (2012) Mango catalogue Published by Indian Institute of Horticultural Research, Bengaluru.

20. Kerala Dwarf (IC0391747; INGR14021), a Mango (*Mangifera indica*) Germplasm with Dwarf Stature, Medium Sized Round Shaped Fruits having Yellow Coloured Pulp

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It is a variety known to have originated in Trichur region of Kerala. Trees are very dwarf statured. It produces round shaped fruits of not very good quality.

Morpho-agronomic characteristics: It produces big sized fruits of about 400g. The young leaves are light green with brownish tinge. The fruits ripen to yellow colour with greenish patches. It does not bear regularly. The variety is ideally suited for high density planting. The pulp recovery is less because of bigger sized stone. Fruits are flat in taste with poor TSS (Naik and Gangolly, 1950; Anon, 1990-91; Dinesh *et al*., 2012) (Table 1)..

Barcode

Table 1. Descriptor and descriptor state of IIHR 20096 (IC391747)

Descriptor	Descriptor state
Tree size	Dwarf
Bearing behaviour	Irregular
Leaf colour	Light greenish brown
Leaf tip	Acuminate
Panicle colour	Dark red
Panicle shape	Pyramidal
Yield (kg/ tree)	20
Fruit length (cm)	9.40
Fruit breadth (cm)	9.50
Fruit thickness (cm)	9.30
Fruit weight (g)	437.50
Peel colour	Yellow
Pulp colour	Pale yellow
TSS (°Brix)	12.50
Pulp content (%)	57.80
Stone weight (g)	38.80

References

Anon (1990-91) Reported at All India Coordinated Fruit Workshop.

Naik KC and SR Gangolly (1950) A monograph on classification and nomenclature of South Indian Mangoes. Govt Press, Madras.

Dinesh MR, C Vasugi, KV Ravishankar and YTN Reddy (2012) Mango catalogue Published by Indian Institute of Horticultural Research.

21. Allahabad Safeda (IC0395191; INGR14022), a Guava (*Psidium guajava*) Germplasm with Medium Sized Fruits, White Coloured Pulp, High TSS, Good Keeping Quality and Soft

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It is a variety that is said to have originated in the Allahabad region. It is a semi-vigorous tree producing round shaped fruits. It is one of the main commercial varieties of guava grown in the country. It performs well in most of the guava growing regions.

Morpho-agronomic characteristics: The tree has smooth stem and it does not grow very tall. It produces round shaped fruits with high TSS, which ripen to pale green colour having smooth surface. Pulp is white in colour and seeds are soft. It is a heavy bearer having consistent pulp. The keeping quality of the fruits is good (Anon, 1985, 1989-90, 1990-91; Dinesh and Vasugi, 2010). It is amenable for high density planting (Table 1).

Traits of interest: Round shaped fruits having smooth surface, high TSS and soft seeds.

Table 1. Descriptor and descriptor state of IC0395191

Descriptor	Descriptor state
Tree size	Semi-vigorous
Bearing behaviour	Heavy
Fruit weight (g)	180-200
Yield/plant (kg) (8 to 10 yrs old)	70.0 to 80.0
Peel colour	Greenish yellow
Surface	Smooth
Pulp colour	White
Pulp consistency	Good
Hundred seed weight (g)	0.90
TSS (º Brix)	11.0
Acidity (%)	0.32
Pectin content (%)	0.81
Keeping quality	Good
Susceptibility to canker	Susceptible

Barcode

References

Anon (1985, 1989-90, 1990-91) Annual progress report of IIHR, Bengaluru.

Dinesh MR and C Vasugi (2010) Guava improvement in India and future needs. *J. Hortic. Sci.* **5:** 94-108.

22. Arka Mridula (IC0395190; INGR14023), a Guava (*Psidium guajava*) Germplasm with Medium Sized Fruits, White Coloured Pulp, High TSS, Good Keeping Quality and High Pectin

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It is selection from the open pollinated progenies of Allahabad Safeda. Fruits are similar to Allahabad Safeda with round shape. The Indian Institute of Horticultural Research released it in the early nineties. It is widely cultivated in Tamil Nadu and Karnataka.

Morpho-agronomic traits: It is a semi-vigorous tree having spreading habit. It is a heavy bearer having amenability for high density planting. It produces round shaped fruits with firm white pulp. Seeds are soft and chewable. The pulp is firm and the fruits on ripening become yellow. The surface of the fruits is smooth and it has good consistency. The TSS is high and acidity is low. It also has good keeping quality. It is rich in ascorbic acid content (Dinesh and Vasugi, 2010) (Table 1).

Traits of interest: Excellent quality fruit having high TSS, soft seeds and firm pulp.

Barcode

Table 1. Descriptor and descriptor state of IC0395190

Descriptor	Descriptor state
Tree size	Semi-vigorous
Bearing behaviour	Heavy
Fruit weight (g)	180-200 g
Yield/plant (kg) (8 to 10 yrs old)	70.0 to 80.0
Yield/ha (tons)	16-18
Peel colour	Yellow
Surface	Smooth
Pulp colour	White
Pulp consistency	Good
Hundred seed weight (g)	0.80
TSS (° Brix)	12.5
Acidity (%)	0.30
Ascorbic acid (mg/100g)	315.0
Pectin content (%)	0.81
Keeping quality	Good
Susceptibility to canker	Good

Reference

Dinesh MR and C Vasugi (2010) Guava improvement in India and future needs. *J. Hortic. Sci.* **5:** 94-108.

23. Red Flesh (IC0395219; INGR14024), a Guava (*Psidium guajava*) Germplasm with Medium Sized Fruits, Pink Coloured Pulp, High TSS, Good Keeping Quality

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It is a variety known to have originated in Uttar Pradesh. It is a vigorous tree having erect growing habit. Although not commercially extensively cultivated it is grown here and there in certain pockets of Andhra Pradesh, Tamil Nadu and Karnataka.

Morpho-agronomic characteristics: It produces oval shaped fruits having deep pink coloured pulp with hard seeds. It is heavy bearer producing small sized fruits. The peel colour on ripening becomes yellow with smooth surface. Pulp is firm and is not very sweet. However, fruits are also not acidic (Anon, 1985; Dinesh and Vasugi, 2010) (Table 1).

Table 1. Descriptor and descriptor state of IC0395219

Descriptor	Descriptor state
Tree size	Semi-vigorous
Bearing behaviour	Heavy
Fruit weight (g)	88-120 g
Yield/plant (kg) (8 to 10 yrs old)	60 to 70
Peel colour	Yellow
Surface	Smooth
Pulp consistency	Good
Pulp colour	Deep pink
Hundred seed weight (g)	1.20
TSS (º Brix)	10.0
Acidity (%)	0.25
Susceptabilityto canker	Susceptible

Traits of interest: Firm pulp having deep pink colour.

Barcode

References

Anon (1985) Annual progress report of IIHR, Bengaluru.

Dinesh MR and C Vasugi (2010) Guava improvement in India and future needs. *J. Hortic. Sci.* **5:** 94-108.

Erratum

The title published in Indian J. Plant Genet. Resourc.(2014) Vol 27(1): 69 was incorrectly cited. The correct title is as follows:

NSS-7809 (IC0283734; INGR13056), a Pearl Millet (*Pennisetum squamulatum*) Germplasm with Popping Traits

Jyoti Kumari[1], Sushil Pandey[1], SK Jha[2], S Chauhan[2], GK Jha[2], C Tara Satyavathi[2], NK Gautam[1] and M Dutta[1]

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Error is regeretted.

GUIDELINES TO AUTHORS

GENERAL

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2. Withers LA and F Engelmann (1998) In vitro conservation of plant genetic resources. In: A Altman (ed.) *Agricultural Biotechnology*. Marcell Dekker Inc., New York, pp 57-58.
3. WOI (1985) *The Wealth of India - Raw Materials. A Dictionary of Indian Raw Materials and Industrial Products-Raw Material* Vol 1: A (Revised). Publications and Information Directorate, Council of Scientific and Industrial Research, New Delhi, 513 p.
4. Engels, JMM and V Ramanatha Rao (eds) (1988) *Regeneration of seed crop and their wild relatives*. Proceedings of a Consultation Meeting, 4-7 December 1995. ICRISAT, Hyderabad, India and IPGRI, Rome, Italy, 167 p.

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