Characterization and Evaluation Studies in Apricot Germplasm under High Hills of Himachal Pradesh

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Sixteen apricot accessions in field gene bank of National Bureau of Plant Genetic Resources Regional Station, Shimla were characterized and evaluated for qualitative and quantitative characters along with two checks 'Nugget' and 'Royal' from 2002-04. Morphological variation as expressed by the presence of many qualitative characters showed variability in the apricot germplasm. Highest Coefficient of Variation was observed for pulp-to-stone ratio (88.45%), followed by stone weight (63.21%) and fruit weight (36.78%) indicating enough potential for exploiting the variability for these characters. Correlation analysis showed that fruit length and width had significant positive correlation with fruit weight, while fruit weight had highly significant negative correlation with total soluble solids. Apart from check cultivars, EC552701 (St. Ambroise) and EC140315 (Harogem) were found suitable for planting in the mid and high hills of Himachal Pradesh due to their potential to prolong the fruit availability period besides meeting requirements of table purpose.

Key Words: Apricot, *Prunus armeniaca*, Evaluation, Characterization, Germplasm

Introduction

Apricot (*Prunus armeniaca* L.) is an important fruit crop of mid to high hills and dry temperate regions of western Himalayas, where seemingly wild seedling populations are also found in between 1,000 and 3,000 msl. Wild apricots are known by different names such as '*zardalu*', '*sarha*', '*chulli*' in Himachal Pradesh; '*chuari*', '*zardalu*' in Hindi; '*gurdalu*', '*cherkush*' in Kashmir; '*chult*' in Ladakh; and '*chuaru*', '*chola*', '*kushmaru*' in Uttarakhand (Parmar and Kaushal, 1982). But Sharma (1992, 2000) categorized *chuli*, *sahara* and *zardalu* as three different types of wild apricots warranting botanical variety status to former two and considered the latter as the wild form of apricot. Fruits of commercial cultivars received much attention due to early maturity and abundant availability (Misra, 1983). Although this species had wide range of geographical distribution, yet a particular genotype is ecologically less adapted (Rathore, 1991) for instance, white fleshed, sweet kernelled apricot requires cooler climate and are grown in dry temperate regions from 2,500-3,000 msl, whereas yellow/orange-fleshed, bitter kernelled ones thrive better under the warmer climate of 1,000-1,800 msl. Fruits are used for jam, canning. At the same time, as done in cultivars of above 20% Total Soluble Solids (TSS), flesh is dried and used as an item of food. Besides the above, the sweet kernel, a byproduct in some cultivars, is also used as a substitute to almond used in pastries and confectionery while the bitter kernel for extraction of oil in high hills and dry temperate areas of western Himalayas. Therefore, cultivars need to be identified depending upon the local need. A total of 16 accessions, 12 exotic (from six countries) and four indigenous, maintained at field gene bank of NBPGR Regional Station, Shimla were characterized and evaluated.

Materials and Methods

Present study was carried out at field gene bank of NBPGR Regional Station, Phagli, Shimla (31° 05' 924" N latitude, 77°09'580" E longitude; 1924 msl). The characterized and evaluated germplasm is mentioned in Table 1. Most popular cultivated varieties in high hills such as 'Nugget' and 'Royal' were used as checks. All the plants of the accessions were of 10-12 years age. The plants were grafted on to wild apricot (*chuli*) rootstock. Plants were trained in central leader system. Experimental trees were grown under similar soil and cultural conditions. Observations were recorded on dates of start and end of flowering and fruit harvest (tree-ripe stage), fruit length and width, fruit weight, fruit ground as well as over-color (at the time of harvest), pulp firmness, pulp color, fruit taste, TSS (using Digital Hand-held 'Pocket' Refractometer PAL-1), stone size, stone adherence to pulp, stone length and width, stone weight, kernel taste, pulp-to-stone ratio and productivity status. Descriptor states for qualitative characters were followed as per the descriptor developed by NBPGR (Mahajan *et al*., 2002). Fruit data were recorded from ten randomly selected fruits from each accession and mean values of three years (2002-2004) data were

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Results and Discussion

Data relating to various qualitative characters on 16 accessions (Table 1) showed their diverse nature represented by most of the descriptor states (Mahajan *et al.,* 2002). Round and oblong fruit shape were predominant in the collections. Two-third of the accessions possessed fruits with yellow (pure or mingled) over-colour when ripe. Seven accessions possessed desirable shades of orange-coloured flesh. Most of the accessions possessed either sweet-taste pulp (11 acc.) or free-stone (12 acc.) or both (8 acc.). Barring 5 accessions all yielded bitter kernels. Only three accessions, namely, EC552701 (St. Ambroise), EC140316 (Viva Gold) and EC140315 (Harogem) yielded on par with the superior check, *i.e.*, EC552698 (Nugget). Those high chill requiring cultivars such as EC552699 (Suffaida Parachinar), EC393747 (Shakarpara) and EC552702 (Nari), all possessing sweet kernels, tend to be shy bearers under Shimla conditions indicating their eco-geographical adaptation to dry temperate regions.

Higher coefficient of variation indicated large variation for the traits pulp-to-stone ratio, followed by fruit and stone weight (Table 2) indicating the amenability for exploitation through selection. Large variation for quantitative traits was also reported by many workers (Chaudhary and Singh, 1988; Sharma, 1994, 1995; Srivastava *et al.*, 2006). Such variation observed in the present study might be attributed to the presence of both exotic and indigenous accessions; some are bred for different purposes. More than three weeks difference between the earliest (3rd March; IC349968) and last bloomed (28th March; EC168419) accessions was observed. This observation is of significance since late flowering ones will escape damage from occasional spring frost. Date of fruit harvest also considerably varied from 8th June (EC140316) to 25th June (EC552699). Rathore (1991) suggested planting cultivars ripening at different periods in orchards in order to avoid glut in the market. Both the check cultivars are early in fruiting, *i.e.*, in the first fortnight of June, hence those high/medium yielding accessions maturing late such as EC552701 (St. Ambroise) and EC100224 (Canino) may be worthy enough. All the indigenous collections are early maturing and possessed bitter kernels. Kabu (1978) also reported that bitter kernelled varieties mature earlier than the sweet kernelled ones of Ladakh.

Four accessions namely, EC552701 (St. Ambroise), EC140316 (Viva Gold), EC100224 (Canino), and EC168421 (Sundrop) exhibited higher fruit weight (>40.0 g) than the both the checks. Pulp-to-stone ratio was amazingly highest in EC168421 (121.09) followed by EC140316 (64.51) which is much higher than the superior check, *i.e.*, Nugget. High soluble solids, more than 20 per cent which is an important characteristic in determining suitability for drying (Mehlenbacher *et al.*, 1987) was found highest in EC552702 (27.82% TSS), IC349968 (25.67%) and IC204457 (24.72%) and as such are fit for drying. Moreover, their small fruit weight (<20 g) may not find merit in fresh market.

Firm flesh is desirable for canning and for fresh market, and is essential for transport of the fruit for long distance. Additionally, sweet taste, aroma, free-stone nature, freedom from fruit cracking, uniform maturity are the few essential parameters for a table variety apart from high yield. It is very rare to have one variety with all these desirable traits, for example EC168421 (Sundrop) and EC168419 (Harcot) had firm flesh and high pulp-to-stone ratio, free/semi-clingstone fruits, orange pulp, but showed low productivity. In this context, EC552701 (St. Ambroise) and EC140315 (Harogem) apart from high yield, had sweet taste, firm flesh, free-stone which will satisfy the requirement for fresh market and canning. Additionally, they have an appealing orange over-colour in fruits. EC140315 (Harogem) had deep orange flesh with good aroma highly suitable for dessert purposes and reported to be resistant to brown rot (Rathore, 1991) while EC552701 (St. Ambroise) yields medium to big sized juicy fruits. Even though EC140316 (Viva Gold) had many necessary traits for table purpose including high yield, soft flesh and semi-clingstone may reduce its market value. Moreover, being an early maturing one, it should compete with the check cultivar 'Nugget'. Stone weight had direct significance to kernel yield (Chaudhary and Singh, 1998), the accessions with higher stone weight (>2.25 g) such as EC552701 (St. Ambroise), Trumph Severngi and EC100224 (Canino) may be exploited for oil extraction, in addition to their primary value.

Correlation coefficients for six quantitative characters, *viz.*, fruit length and width, stone length, width and weight and TSS (Table 3) indicated that fruit length and width had significant positive correlation with fruit weight while fruit weight showed highly significant negative correlation with total soluble solids. Although stone and fruit weight had positive correlation with each other they were statistically

Table 1. Important qualitative characteristics in apricot accessions studied

S. No	Accession	Cultivar	Source country	Fruit shape	Fruit ground colour	Fruit over colour	Pulp colour	Pulp firmness	Fruit taste	Stone size	Stone adherence to pulp	Kernel taste	Productivity status*
1	EC552699	Suffaida Parachinar	Iran	Ovate	Light green	Orange-yellow	Cream	Medium	Sweet	Medium	Free	Sweet	Low
2	EC168419	Harcot	USA	Round	Light yellow	Yellow	Orange	Firm	Sweet	Medium	Free	Bitter	Low
3	EC393747	Shakarpara	Iran	Oblong	Light yellow	Cream-yellow	Light yellow	Firm	Sweet	Medium	Free	Sweet	Low
4	EC168421	Sundrop	USA	Round	Light yellow	Light orange	Light orange	Firm	Sweet	Medium	Semi-cling	Bitter	Low
5	EC552701	St.Ambroise	USA	Oval	Light green	Orange-yellow	Yellow	Firm	Sweet	Large	Free	Tasteless	High
6	EC280843	Rakovslik	Hungary	Oblong	Light yellow	Yellow	Orange	Soft	Sweet	Medium	Free	Sweet	Low
7	EC100224	Canino	Italy	Ovate	Creamy	Yellow	Yellow	Soft	Sweet	Medium	Semi-cling	Bitter	Medium
8	EC140316	Viva Gold	Canada	Round	Yellow	Orange	Light orange	Soft	Very sweet	Medium	Semi-cling	Bitter	High
9	EC140315	Harogem	Canada	Ovate	Yellow	Deep orange	Deep orange	Firm	Very sweet	Large	Free	Bitter	High
10	EC168342	Vittillo	Italy	Oblong	Light green	Yellow	Cream	Firm	Sub acidic	Large	Semi-cling	Sweet	Low
11	Trumph Severngii	Trumph Severngii	USSR	Oblong	Light green	Yellow	Yellow	Medium	Sweet	Medium	Free	Bitter	Medium
12	EC552702	Nari	–	Oblong	Yellow	Yellow	Light yellow	Medium	Very sweet	Medium	Free	Sweet	Low
13	IC204457	BDJ-311	India	Round	Light yellow	Yellow	Yellow	Medium	Sub acidic	Smal	Free	Bitter	Low
14	NIC058127	–	India	Oblong	Yellow	Yellow	Yellow	Medium	Sub acidic	Small	Free	Bitter	Low
15	IC349968	–	India	Round	Light yellow	Light orange	Light orange	Medium	Sub acidic	Small	Free	Bitter	Low
16	IC349933	Zardalu	India	Round	Light yellow	Yellow	Light orange	Soft	Sub acidic	Small	Free	Bitter	Low
Check 1: EC552698 (Nugget)			Italy	Round	Light green	Orange with vermillion blush	Deep yellow	Firm	Sweet	Medium	Free	Sweet	High
Check 2: EC552703 (Royal)			USA	Oval	Yellow	Yellow- orange	Yellow	Firm	Sweet	Large	Free	Tasteless	Medium

*Productivity status: Low: <5 kg/plant; Medium: 5-15 kg/plant; High: >15kg/plant

Table 2. Pooled mean values of quantitative characters in apricot accessions studied

S. No.	Accession	Date of start of flowering	Date of end of flowering	Date of fruit harvest	Days to fruit harvest	Fruit length (mm)	Fruit width (mm)	Fruit weight (g)	Total soluble solids (%)	Stone length (mm)	Stone width (mm)	Stone weight (g)	Pulp-to-stone ratio
1	EC552699	16th March	22nd March	25th June	95	42.54	36.17	23.37	17.27	13.62	10.44	1.23	18.00
2	EC168419	14th March	28th March	15th June	79	39.37	35.85	29.25	17.23	22.44	16.25	0.60	47.75
3	EC393747	16th March	25th March	15th June	82	47.45	42.10	25.27	17.87	13.41	9.66	1.23	19.54
4	EC168421	8th March	19th March	12th June	85	29.87	26.78	40.29	14.37	16.44	10.80	0.33	121.09
5	EC552701	15th March	25th March	16th June	83	40.80	39.86	43.27	15.27	28.86	21.88	3.20	12.52
6	EC280843	10th March	17th March	12th June	87	36.44	28.60	39.40	17.40	14.90	8.35	1.28	29.78
7	EC100224	10th March	17th March	21st June	96	42.69	39.80	40.58	15.77	23.87	20.92	2.25	17.03
8	EC140316	8th March	21st March	8th June	79	36.88	41.21	41.27	16.13	18.99	12.29	0.63	64.51
9	EC140315	9th March	14th March	14th June	92	38.27	35.28	24.80	14.20	23.42	18.02	0.91	26.25
10	EC168342	21st February	3rd March	14th June	103	34.93	33.77	31.32	14.84	21.85	13.18	1.07	28.27
11	Trumph Severngii	3rd March	12th March	14th June	94	43.02	42.08	35.97	15.83	25.92	21.61	2.39	14.05
12	EC552702	7th March	13th March	23rd June	102	32.10	29.19	19.32	27.82	18.63	15.02	1.52	11.71
13	IC204457	11th March	20th March	9th June	81	26.90	20.54	17.94	24.72	19.29	14.77	1.63	10.01
14	NIC058127	10th March	16th March	8th June	84	32.98	27.47	16.21	18.54	14.10	11.00	0.86	17.84
15	IC349968	20th February	3rd March	9th June	98	27.04	21.45	18.40	25.67	15.21	12.15	0.57	31.28
16	IC349933	23rd February	13th March	10th June	89	28.21	23.50	10.87	20.04	12.57	8.22	0.40	26.17
Nugget (Check 1)		11th March	20th March	4th June	76	37.37	36.44	38.75	14.03	21.70	18.37	0.94	40.22
Royal (Check 2)		12th March	19th March	14th June	87	44.11	41.93	37.57	16.30	29.91	26.02	3.54	9.61
Mean					89.31	36.22	32.73	28.59	18.31	18.97	14.04	1.26	30.31
Maximum value					103	47.45	42.10	43.27	27.82	28.86	21.88	3.20	121.09
Minimum value					79	26.90	20.54	10.87	14.20	12.57	8.22	0.33	9.61
SE					1.997	1.57	1.86	2.63	1.05	1.24	1.45	0.19	6.70
CV (%)					10.51	17.38	22.74	36.78	22.87	26.45	32.59	63.21	88.45

Table 3. Correlation matrix for quantitative characters in 16 apricot accessions

Character	Fruit length	Fruit width	Fruit weight	Total soluble solids	Stone length	Stone width
Fruit width	0.91**					
Fruit weight	0.54*	0.63**				
Total soluble solids	–0.47	–0.60*	–0.67**			
Stone length	0.61*	0.60*	0.58*	-0.36		
Stone width	0.64**	0.64**	0.53*	-0.27	0.95**	
Stone weight	0.66**	0.55*	0.43	-0.11	0.77**	0.78**

*Significance at 5% level; **Significance at 1% level

insignificant indicating that there is a scope for selecting genotypes having fruits with high pulp-to-stone ratio.

Genotypes, EC552701 (St. Ambroise) and EC140315 (Harogem) appeared to be suitable for dessert and canning purpose in mid to high hills of Himachal Pradesh. Planting these cultivars along with check cultivars can be encouraged in orchards since they have the potential to prolong the fruit availability period in addition to other traits.

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employing Ward's method. The clustering was based on the squared Euclidean distances and the average linkage between groups was taken as the average of the distance between all pairs of cases with one member of each group (Lal *et al.*, 2007).

Results and Discussion

Variability Analysis

The variance analysis showed that genotypes differ significantly among themselves for all the characters under study (Table 1). The phenotypic coefficients of variation (PCV) were invariably higher than their corresponding genotypic coefficients of variation (GCV) due to environmental influence. The estimates of PCV and GCV indicated the existence of fairly high degree of genetic variability for plant height, peduncle length, number of peduncles and pods per plant, pod weight and pod yield per plant. Plant height, number of peduncles per plant, number of days to flower, pod length, pod weight and pod yield per plant were least affected by environment. This observation draws support from the very high values of heritability recorded for these traits. Higher estimates of heritability coupled with the higher genetic advance for plant height, number of peduncles per plant, number of days to flower and pod yield per plant indicated that heritability of these traits is mainly due to additive effects and selection may be effective. High heritability accompanied with low genetic advance for average pod weight, number of seeds per pod and number of branches per plant indicated advancement of non-additive gene action and the high heritability is being exhibited due to favourable influence of the environment rather than genotypes. Johnson *et al.* (1955) also suggested that high GCV along with high heritability and genetic advance gave better picture for the selection of the genotypes. Similar results were also reported by Venkatesan *et al.* (2003) in cowpea.

Correlation Analysis

Genotypic correlation coefficients were higher than corresponding phenotypic correlation coefficients, indicating the inherent association among the traits (Table 2). Highly significant genotypic correlation coefficient was observed for number of branches per plant, number of peduncles per plant, pod length, pod weight and number of seeds per pod with pod yield per plant. The number of branches per plant had positive correlation with number of peduncles per plant, number of days taken to flower, pod length, number of seeds per pod, pod weight and pod yield. The number of peduncles per plant showed positive correlation with number of days taken to flower, pod length, number of seeds per pod, pod weight and pod yield. However, the number of days taken to flower exerted positive correlation with number of seeds per pod, number of pods per plant and pod yield per plant. Pod length had positive correlation with number of seeds per pod, pod weight and pod yield per plant. The number of seeds per pod exerted positive correlation with pod weight and pod yield per plant. Pod weight showed positive correlation with pod yield per plant. Bapna *et al.* (1972) also obtained similar results.

Direct and Indirect Analysis

The pod weight exerted the maximum positive direct effect on pod yield followed by number of pods per plant and pod length (Table 3). Thus, selection pressure on these traits may lead to an overall increase in pod yield per plant. Number of branches per plant showed the maximum negative direct effect on pod yield followed by number of seeds per pod. Considerable positive indirect effect of pod weight was recorded through pod length, and number of seeds per pod. A positive indirect effect of number of pods per plant was observed through number of peduncles per plant and peduncle length. Highest indirect

Table 1. Variability, heritability and expected genetic advance for cowpea genotypes

Characters	Range	Grand mean	Variability		Heritability (%)	Genetic advance	Genetic advance as % of mean
			PCV	GCV			
Plant height (cm)	42.3-351.5	185.56	39.87	38.30	92.30	140.64	75.79
Branches plant^{-1} (no.)	3.3-6.0	4.56	20.16	12.15	36.30	0.69	15.13
Peduncles plant^{-1} (no.)	33.1-72.3	51.97	23.07	18.67	65.50	16.18	31.13
Peduncle length (cm)	10.6-38.6	24.83	28.05	21.68	59.70	8.57	34.51
Days to flower (DAF)	40.6-68.3	48.74	15.71	14.86	89.50	14.12	28.96
Pod length (cm)	10.4-23.8	14.67	18.48	16.31	77.90	4.35	29.63
Seeds pod^{-1} (no.)	9.3-15.7	12.93	14.29	9.22	41.60	1.58	12.22
Pod weight (g)	2.13-8.40	4.03	33.67	32.64	94.00	2.63	65.10
Pods plant^{-1} (no.)	19.0-37.5	28.02	23.55	13.82	34.40	4.68	16.70
Pod yield (g) plant^{-1}	53.4-213.4	110.23	35.78	31.70	78.50	63.78	57.86

PCV & GCV–Phenotypic coefficient of variation and genotypic coefficient of variation, respectively

Table 2. Correlation coefficients at phenotypic (r_p) and genotypic (r_g) levels

Characters	Plant height (cm)	Branches plant^{-1} (no.)	Peduncles plant^{-1} (no.)	Peduncle length (cm)	Days to flower (DAF)	Pod length (cm)	Seeds pod^{-1} (no.)	Pod weight (g)	Pods plant^{-1} (no.)	Pod yield plant^{-1} (g)
Plant height (cm)	(r_p) (r_g)	0.259 0.410*	0.162 0.180	0.044 0.036	0.205 0.211	-0.021 -0.021	0.162 0.223	0.129 0.134	0.068 0.076	0.119 0.124
Branches plant^{-1} (no.)		(r_p) (r_g)	0.684** 0.684**	0.071 0.039	0.232 0.453**	0.396* 0.812**	0.389* 0.335*	0.597** 0.851**	0.489** -0.103	0.742** 0.806**
Peduncles plant^{-1} (no.)			(r_p) (r_g)	0.012 0.047	0.347* 0.468**	0.587** 0.846**	0.436** 0.448**	0.701** 0.794**	0.486** 0.253	0.913** 0.934**
Peduncle length (cm)				(r_p) (r_g)	0.244 0.282	-0.066 -0.052	-0.073 -0.156	-0.105 -0.133	0.121 0.189	-0.020 -0.042
Days to flower (DAF)					(r_p) (r_g)	0.231 0.256	0.271 0.420*	0.229 0.257	0.182 0.384*	0.325* 0.411*
Pod length (cm)						(r_p) (r_g)	0.398* 0.615**	0.771** 0.898**	0.065 0.109	0.737** 0.957**
Seeds pod^{-1} (no.)							(r_p) (r_g)	0.485** 0.590**	0.114 -0.245	0.460** 0.554**
Pod weight (g)								(r_p) (r_g)	-0.080 -0.278	0.828** 0.895**
Pods plant^{-1} (no.)									(r_p) (r_g)	0.442** 0.177

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

Table 3. Direct (diagonal) and indirect effect of yield contributing traits at phenotypic (P) and genotypic (G) levels

Characters		Plant height (cm)	Branches plant^{-1} (no.)	Peduncles plant^{-1} (no.)	Peduncle length (cm)	Days to flower (DAF)	Pod length (cm)	Seeds pod^{-1} (no.)	Pod weight (g)	Pods plant^{-1} (no.)	Pod yield plant^{-1} (g)
Plant height (cm)	G	**0.052**	-0.072	0.009	0.001	0.014	-0.006	-0.009	0.113	0.023	0.124
	P	**-0.028**	0.010	0.053	0.001	0.004	-0.002	-0.005	0.068	0.019	0.119
Branches plant^{-1} (no.)	G	0.021	**-0.175**	0.034	0.001	0.030	0.229	-0.014	0.712	-0.032	0.806**
	P	-0.007	**0.037**	0.224	0.001	0.005	0.045	-0.011	0.313	0.137	0.742**
Peduncles plant^{-1} (no.)	G	0.009	-0.120	**0.049**	0.001	0.031	0.239	-0.018	0.665	0.078	0.934**
	P	-0.005	0.025	**0.328**	0.001	0.007	0.066	-0.013	0.368	0.137	0.913**
Peduncle length (cm)	G	0.002	-0.007	0.002	**0.004**	0.019	-0.015	0.006	-0.112	0.058	-0.042
	P	-0.001	0.003	0.004	**-0.005**	0.005	-0.007	0.002	-0.055	0.034	-0.020
Days to flower (DAF)	G	0.011	-0.079	0.023	0.001	**0.067**	0.072	-0.017	0.216	0.118	0.411*
	P	-0.006	0.009	0.114	-0.001	**0.021**	0.026	-0.008	0.120	0.054	0.325*
Pod length (cm)	G	-0.001	-0.143	0.042	0.001	0.017	**0.282**	-0.025	0.752	0.033	0.957**
	P	0.001	0.015	0.192	0.001	0.005	**0.113**	-0.012	0.404	0.018	0.737**
Seeds pod^{-1} (no.)	G	0.012	-0.059	0.022	-0.001	0.028	0.174	**-0.040**	0.494	-0.074	0.554**
	P	-0.005	0.014	0.143	0.001	0.006	0.045	**-0.029**	0.254	0.032	0.460**
Pod weight (g)	G	0.007	-0.149	0.039	-0.001	0.017	0.253	-0.024	**0.838**	-0.085	0.895**
	P	-0.004	0.022	0.230	0.001	0.005	0.087	-0.014	**0.525**	-0.022	0.828**
Pods plant^{-1} (no.)	G	0.004	0.018	0.012	0.001	0.026	0.031	0.010	-0.232	**0.308**	0.177
	P	-0.002	0.018	0.159	-0.001	0.004	0.007	-0.003	-0.042	**0.281**	0.442**

effect of pod length was exhibited via pod weight. Path coefficient analysis revealed the importance of characters such as number of pods per plant, pod weight and pod length in selection of superior genotypes for pod yield. Similar results were also obtained by Lal *et al.* (2007) in cowpea.

Hierarchical Cluster Analysis

Multivariate hierarchical clustering was carried for ten different quantitative characters (Fig. 1). Distance between all pairs of genotypes was calculated using squared Euclidean distance method and genotypes were clustered based on Ward's method. From the dendrogram, it can be

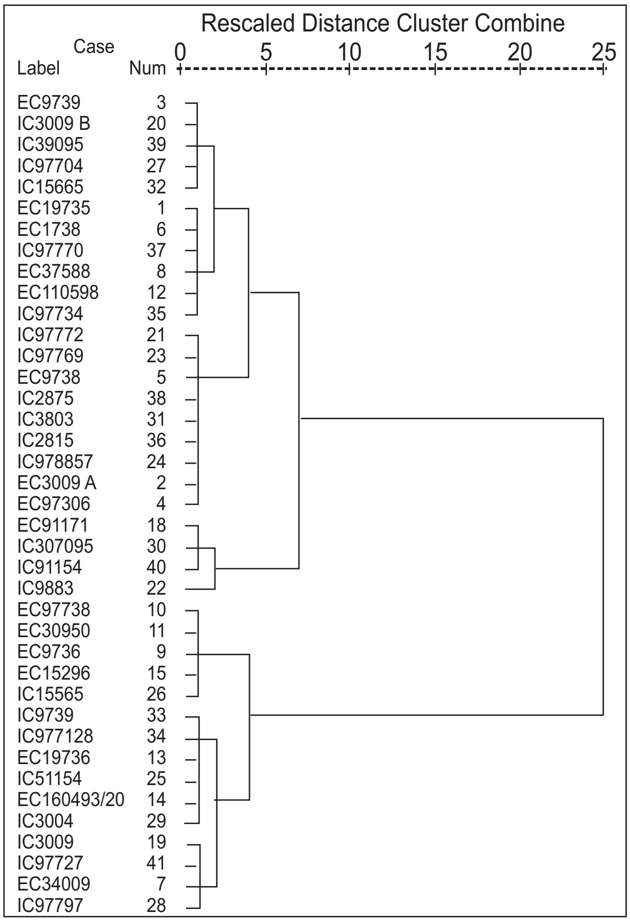

Fig. 1: Multivariate cluster analysis of 41 cowpea genotypes using Ward's Method

concluded that 41 genotypes were mainly divided at first node into 2 clusters with 24 and 17 genotypes in different groups. Cluster with 24 genotypes was again divided into 2 groups at second node with 20 and 4 genotypes. Similarly, 20 genotypes further divided into 2 groups at third node with 11 and 9 genotypes and 11 genotypes again divided into 2 groups at the fourth node with 6 and 5 genotypes, respectively. However, cluster of 17 genotypes further divided into 2 groups at second node with 12 and 5 genotypes and 12 genotypes again equally divided into 2 groups at third node with 6 genotypes in each group, respectively. Since these clusters are group of individuals possessing similar characters mathematically gathered into the same cluster, these individuals are supposed to exhibit higher external heterogeneity. Genotypes included in the same clusters with a high order of divergence will be expected to provide the best breeding material for achieving the maximum genetic advance for yield *per se,* provided other factors do not operate to limit the realization of this potential. It is rather encouraging that the divergence revealed in the present genotypes due to these characters will offer a good scope of improving pod yield through rational selection. A crossing programme involving parents selected on the basis of genetic divergences of yield components may likely to produce transgress segregates for yield potential. These results were in close conformity with the findings of Hazra *et al.* (1992) and Lal *et al.* (2007).

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Genetic Diversity in Bread Wheat Germplasm under Reclaimed Sodic Soil Condition

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The genetic diversity in 300 wheat genotypes was assessed under reclaimed sodic soil condition for grain yield and its component traits using non-hierarchical Euclidean cluster analysis which grouped the genotypes in 11 different clusters. Cluster VII had highest intra-cluster D^2 values indicating maximum intracluster diversity. This cluster was also most distantly related to cluster VI than the other cluster combinations indicating most diverse genotypes for their further utilization in wheat improvement programme. Cluster VII showed highest mean values for grain yield per plant and tillers per plant.

Key Words: Wheat, Genetic divergence, Clusters analysis, Reclaimed sodic soil

Introduction

The salt affected lands occur in practically all climatic regions but the areas affected by soil salinity are not well defined and thus, global estimates vary widely (Flowers *et al.*, 1986). Of nearly 160 million hectares of cultivated land under irrigation worldwide, about one-third is already affected by salt, which makes salinity a major constraint to food production. It is considered as single largest soil toxicity problem in tropical Asia (Greenland, 1984). In India, nearly 7.0 million hectare area is affected by salts that cover the maximum area in the states of Uttar Pradesh, Gujarat and Haryana. The combination of salt affected soils and poor quality groundwater in wheat growing areas of the country severely limit wheat productivity. The salinity aspect was addresed at Cental Soil Salinity Research Institute (CSSRI), Karnal and the salt affected land was reclaimed for research purspose to generate suitable material for salt affected areas.

The germplasm is the reservoir of genetic variability and it needs to be churned properly for developing genotypes for different agro-climatic and soil conditions. For crop improvement purposes, the most widely used methodology is hybridization followed by selection in which diverse parents are used. The importance of genetic diversity for selecting parents for recombination breeding in an autogamous crop such as bread wheat to recover transgressive segregates has also been repeatedly emphasized (Cox and Murphy, 1990) and therefore, characterization of genetic divergence for selection of suitable and diverse genotypes should be based on sound statistical procedures such as D^2 statistic and non-hierarchical Euclidean cluster analysis (Mahalanobis, 1936; Spark, 1973). Keeping these in view, the wheat germplasm lines were evaluated with the objective to determine the magnitude of variability among the wheat germplasm for yield and component traits and to identify genetically diverse and agronomically desirable genotypes for their further exploitation in wheat improvement programme aimed at enhanced grain yield in salt affected conditions.

Materials and Methods

Three hundred genotypes maintained at the Division of Crop Improvement, CSSRI, Karnal (Haryana), constituted the material for the present study that included released varieties, genetic stocks, germplasm lines, doubled haploids and advanced breeding lines developed at various centres (Table 1). The material was evaluated under reclaimed sodic soil that is near to normal condition (pH value of 8.2) in augmented design with 12 blocks accomodating 25 test genotypes and 5 checks, namely, KRL 19, HD 2009, PBW 343, HD 4530 and *Kharchia* 65 in each block. The plot size was single row of 1 m with 23 x 5 cm spacing. All the recommended agronomic practices were followed to raise a good crop. The data were recorded on five randomly selected plants for plant height (cm), tillers per plant, spike length (cm), number of spikelets per spike, grain number per spike, 1000-grain weight and grain yield per plant (g) whereas the days to heading and days to maturity were recorded on plot basis. The data was analysed for adjusted mean values of 300 test genotypes for various traits in relation to the checks and estimates of error mean squares were obtained following Federer (1956) and used for subsequent statistical analysis. The non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973) was done to estimate the intra and inter-cluster distances and to group the genotype into different clusters.

Results and Discussion

The analysis of variance showed significant differences

Table 1. Origin of genotypes/ culitvars/ advaced generation lines used as experimental material

Centre	Entries (Total)	Name of the entries
Perth, Australia	54	BT-Schomburgk, Camm, Carnamah, Cunderdin, Ducula 4, Gamenya, Gutha, Kulin, Perenjori, Schomburgk, Spear, Westonia, 96W639-D-1-8, 96W639-D1-40, 96W639-D-1-53, 96W639-D-1-56, 96W639-D2-1, 96W639-D2-8, 96W639-D2-11, 96W639-D2-12, 96W639-D2-17, 96W639-D2-22, 96W639-D3-2, 96W639-D3-4, 96W639-D3-9, 96W639-D3-18, 96W 639-D3-19, 96W639-D3-29, 96W639-D4-10, 96W639-D4-24, 96W639-D5-2, 96W639-D5-5, 96W639-D5-6, 96W639-D5-9, 96W639-D5-10, 96W639-D5-15, 96W639-D5-17, 96W639-D5-20, 96W639-D5-21, 96W639-D5-26, 96W639-D5-30, 96W639-D5-31, 96W639-D5-33, 96W 639-D5-42, 96W639-D5-43, 96W 639-D5-44, 96W639-D6-2, 96W639-D6-5, 96W639-D6-12, 96W639-D6-18, 96W639-D6-29, 96W639-D6-34, 96W639-D6-36, 96W639-D6-37
CIMMYT, Mexico	04	BWIR7, BWMA8, WC1, WC6
CSAUA&T, Kanpur	24	K 78, K2008, K2021, K0101, K0103, K0111, K0123, K0124, K0142, K0209, K0224, K8027, K8034, K9107, KLP0265, KLP0268, KLP0317, KLP0318, KLP0319, KYZ0162, KYZ0165, KYZ0176, KYZ0294, KYZ0295
NDUA &T, Faizabad	22	NW1012, NW1014, NW1067, NW1076, NW2036, NW2069, NW2083, NW2095, NW(S)01-9, NW(S)02-4, NW(S)02-5, NW(S)02-6, NW(S)02-8, NW(S)02-11, NW(S)02-15, NW(S)03-1, NW(S)03-2, NW(S)03-3, NW(S)03-4, NW(S)03-5, NW(S)03-6, NW(S)03-7
CSSRI, Karnal	22	KRL1-4, KRL3-4, KRL35, KRL99, KRL100, KRL104, KRL105, KRL107, KRL113, KRL115, KRL117, KRL118, KRL119, KRL120, KRL121, KRL122, KRL123, KRL124, KRL125, KRL126, KRL127, KRL128
IARI, New Delhi	22	HD2189, HD2285, HD2329, HD2643, HD2687, HD2733, HD2781, HD2855, HD2859, HD2861, HD2864, HD2865, HD2866, HD2868, HD2885, HD2886, HDR77, PS701, PS703, PS705, PS708, PS711
IARI, Regional Station, Shimla	21	HS240, HS277, HS295, HS365, HS375, HS418, HS420, HS431, HS433, HS436, HS440, HS445, HS449, HS450, HS451, HS453, HS454, HS 455, HS 456, HS457, HS460
IARI, Regional Station, Indore	20	HI 977, HI1418, HI1454, HI1479, HI1500, HI1514, HI1516, HI1527, HI1530, HI1531, HI1532, HI1533, HI1535, HI1536, HI4672, HI8381, HI8498, HI8634, HI 8637, HI8638
IARI, Regional Station, Pusa	12	HP1731, HP1744, HP1761, HP1867, HP1871, HP1873, HP1875, HP1876, HP1877, HP1878, HP1879, HP1880,
IARI, Regional Station, Wellington	08	HW 3080, HW 4028, HW 5001, HW 5015, HW 5018, HW 5023, HW 5028, HW 5070
VPKAS, Almora	20	VL 616, VL 738, VL 802, VL 804, VL 829, VL 824, VL 830, VL 832, VL 852, VL 858, VL 859, VL 860, VL 861, VL 862, VL 864, VL 865, VL 866, VL 867, VL 868, VL 869
BHU, Varanasi	18	AKJ03-1, AKJ03-2, AKJ03-3, AKJ03-5, AKJ03-6, AKJ03-7, HUW206, HUW234, HUW468, HUW510, HUW524, HUW533, HUW549, HUW564, HUW567, HUW574, HUWJ2, HUWJ13
GBPUA&T, Pantnagar	14	UP2338, UP2425, UP2565, UP2584, UP2590, UP2592, UP2594, UP2596, UP2618, UP2619, UP2620, UP2623, UP2624, UP2625
RAU, Durgapura	13	Raj 1482, Raj 1555, Raj 3077, Raj 3765, Raj 3777, Raj 4037, Raj 4065, Raj 4067, Raj 4069, Raj 4077, Raj 4078, Raj 4085, Raj 4086
CCSHAU, Hisar	11	WH736, WH755, WH773, WH775, WH779, WH785, WH794, WH1008, WH1009, WH1010, WH1011
JNKVV, Jabalpur	09	MP1150, MP1155, MP1156, MP1160, MP1161, MP1165, MP1168, MP1169, MP4010
PAU, Laudhiana	06	PBW 175, PBW 373, PBW 396, PBW 498, PBW 502, PBW 509
Total	300	

among the blocks and checks for all the traits (Table 2). The traits studied showed wide range among the genotypes under reclaimed sodic soil conditions. The coefficient of variation (%) was also estimated to get the comparative values of variability present for the traits under study and it indicated the maximum variability for grain yield/plant followed by tillers per plant, spike length and grain number/ spike (Table 2). On the other hand, lower CV values were observed for days to maturity and heading, number of spikelet per spike and 1000-grain weight indicating less variability for the trait compared to other traits (Singh and Chatrath, 1993; Singh *et al.,* 2001; Munns and James, 2003; Pawar *et al.,* 2003). However, there is still ample scope for selection of superior genotype for these traits. The best performing genotypes for various traits were screened on the basis of their performance and the promising genotypes for more than two characters were identified for their further utilization in wheat improvement programme. These genotypes were HD 2886 (for early heading, spike length, grain number and 1000-grain weight), HD 2861 (for early heading, plant height and 1000-grain weight), Raj 4077 (for early heading, spike length and 1000-grain weight), HW 5015 (for plant height, grain number and yield per plant) and NW 2069 (for spike length, grain number and yield per plant).

Based on Non-hierarchical Euclidean cluster analysis, all the 300 genotypes were grouped into 11 clusters (Table 3) as the sequential F test revealed the appropriateness

Table 2. Analysis of variance, general mean, range and coefficient of variation for nine characters under reclaimed sodic soil conditions

Traits	Mean sum of squares (MSS)			Mean	Range	Coefficient of variation (%)
Source of variation	Blocks	Checks	Error			
Degree of freedom	11	04	44			
Days to heading	133.01**	146.98**	2.47	94.7	78 - 116	6.05
Days to maturity	13.54**	23.75**	2.64	140.7	136 - 145	1.06
Plant height (cm)	333.04**	3012.45**	34.21	90.7	67.5 - 134.2	10.79
Spike length (cm)	8.91**	38.15**	0.22	11.3	6.8 - 15.6	12.74
Spikelets/ spike	6.50**	20.14**	0.75	19.7	15 - 26	8.61
Tillers/ plant	7.19**	2.76**	0.72	5.6	3.2 - 9.0	14.87
Grains/ spike	92.29**	356.09**	31.87	62.0	36 - 87	12.60
1000-grain weight (g)	37.91**	41.67**	5.80	39.7	26.9 - 45.6	9.79
Grain yield/ plant (g)	39.16**	21.15**	3.11	10.3	2.0 - 16.8	26.60

** Significant at 1% level

Table 3. Clustering pattern of 300 bread wheat genotypes on the basis of non-hierarchical Euclidean cluster analysis under reclaimed sodic soil condition

Cluster	Number of genotypes	Genotypes
I	32	VL 824, VL 862, VL 867, VL 868, HD 2329, UP 2565, UP 2590, Raj 1555, Raj 3077, MP 1156, MP 4010, WH 775, WH 779, WH 785, KO 123, KO 124, KO 224, NW 2083, HS 365, HI 1516, HI 1479, HUW 510, HW 4028, HD 2285, HP 1871, PBW 175, NW (S) 3-1, Raj 4078, KRL 100, KRL 115, BT-Schomburgk, HD 2643
II	38	HD 2733, KO 209, HI 8498, HI 8381, HI 8634, HI 4672, HI 8638, HI 8627, HUW-567, HUW-533, HUW 549, PS 701, HP-1731, HP-1879, PBW 373, 96W 639-D-1-53, 96W 639-D-1-56, 96W 639-D2-11, 96W 639-D2-12, 96W 639-D2-22, 96W 639-D3-18, 96W 639-D4-24, 96W 639-D5-5, 96W 639-D5-6, 96W 639-D5-9, 96W 639-D5-10, 96W 639-D5-15, 96W 639-D5-17, 96W 639-D5-20, 96W 639-D5-26, 96W 639-D5-43, KRL 119, KRL 124, KRL 125, KRL 126, KRL 128, 96W 639-D5-42, Ducula 4
III	30	VL 860, HD 2687, UP 2584, Raj 4037, Raj 4069, MP 1169, K 78, NW 1012, NW 1014, NW 2036, HS 418, HI 1514, HI 1531, HI 1454, HI 1418, HUW-574, HUW-234, HD 2861, HD 2864, HD 2855, Spear, PBW 509, WH 1011, NW (S) 3-4, NW (S) 2-11, KRL 120, KRL 1-4, AKJ-03-5, Gutha, Schomburgk
IV	33	VL 859, VL 861, UP 2596, UP 2625, Raj 1482, MP 1165, HS 440, HS 451, HS 453, HS 455, HS 460, HI 1532, HI 1535, HU\V 468, HUW 206, HW 3080, HW 5001, BWIR 7, 96W 639-D5-2, 96W 639-D5-21, KRL 107, KRL 121, KRL 127, N\V (S) 02-8, AKJ-03-1, 96W639-D5-44, Cunderdin, Perenjori, Camm, Westonia, Kulin, Raj 4067, HD 2859
V	19	KO 103, K 9107, K 2021, N\V 1076, HS 436, HS 445, HI 1527, PS 703, PS 711, HP 1878, HP 1876, HP 1880, KLP 318, KO 111, NW (S) 3-7, Raj 4086, 96W 639-D5-33, KRL 123, HUWJ 13
VI	14	VL 858, VL 864, VL 865, VL 866, 96W 639-D2-1, 96W 639-D2-8, 96W 639-D3-4, 96W 639-D3-23, 96W 639 D4-10, 96W 639-D5-31, 96W 639-D6-2, 96W 639-D6-34, 96W 639-D6-36, 96W 639-D6-37
VII	16	HD 2865, HI 1500, HP 1867, NW (S) 3-2, Raj 4077, BWMA 8, KRL 104, KRL 3-4, NW (S) 02-4, NW (S) 02-15. KLPO 265, KLPO 268, KYZO 295, K 142, WCl. 96W639-Dl-40
VIII	18	Gameny, HS 449, HS 450, HS 454, HS 456, HS 457, HI 1530, 96W 639-D-1-8, 96W 639-D3-2, 96W 639-D5-30, 96W 639-D6-5, 96W 639-D6-12, 96W 639-D6-18, 96W 639-D6-29, KRL 117, WC 6, 96W 639-D2-17, Carnamah
IX	47	VL 852, VL 830, UP 2592, UP 2619, UP 2620, UP 2624, UP 2425, Raj 3765, Raj 3777, MP 1150, MP 1155, MP 1160, MP 1168, WH 736, WH 794, KO 101, NW 2095, HS 295, HS 420, HS 431, HS 433, HUW-524, HW 3070, HW 5022, HW 5023, H\V 5018, HD 2886, PS 705, PS 708, HP 1873, HP 1761, HP 1875, HP 1744, PBW 498, PBW 502, UP 2338, KLP 317, KLP 319, WH 1009, NW (S) 3-6, Raj 4085, NW (S) 1-9, 96W 639-D3-9, KRL 99, HUWJ 2, KYZ 294, AKJ-03-6
X	27	K 2008, K 8034, NW 2069, HS 240, HS 277, HS 375, HI 1536, HI 1533, HUW-564, KRL 35, HW 5015, WH 755, WH 1008, \VH 1010, NW (S) 3-3, NW (S) 3-5, KRL 105, KRL 113, KRL 122, NW (S) 02-5, NW(S) 026, KYZ 162, KYZ 165, AKJ-03-2, AKJ-03-3, AKJ-03-07, 96W 39-D3-19
XI	26	VL 832, VL 869, VL 616, VL 738, VL 802, VL 804, VL 829, HD 2189, HD 2885, HD 2866, HD 2868, HD 2781, HDR 77, UP 2594, UP 2618, UP 2623, Raj 4065, MP 1161, WH 773, K 8027, NW 1067, HI 977, HP 1877, PBW 396, KRL 118, KYZ 176
Total	300	

of 11 clusters for all the genotypes under consideration. The cluster strength varied from 14 to 47 genotypes in these clusters out of which cluster IX was the biggest accommodating 47 genotypes followed by cluster II with 38 genotypes and cluster IV with 33 genotypes. The pattern of distribution of these germplasm lines into different clusters indicated that the genotypes of same origin were grouped into different cluster that suggested that geographical diversity is not similar to those of genetic diversity and the clusters accomodated the genetically more similar genotypes.

The cluster mean values were estimated for various traits (Table 4) and it was observed that out of 11 clusters, only six cluster had the higher mean values for the traits in desired direction. Cluster VII has shown higher mean values for grain yield per plant, 1000-grain weight and tillers per plant. Cluster X had higher mean for spikelets per spike and grain number per spike whereas, cluster I had shown superiority for early flowering and dwarf plant types. Early maturity and longer spikes were observed in cluster V and cluster XI, respectively.

The intra and inter-cluster distances (Table 5) were estimated to identify the diverse groups of genotypes. The intra-cluster distance ranged from 2.000 to 2.436 and it was

Table 4. Cluster means and coefficient of variance for nine characters under reclaimed sodic soil condition

Cluster No.	Character	Days to heading	Days to maturity	Plant height (cm)	Spike length (cm)	Spikelets / spike	Tillers / plant	Grains / spike	1000-grain weight (g)	Grain yield / plant (g)
I	Mean ± SD	88.51± 3.78	140.09±1.16	83.36±7.85	10.78±1.02	17.62±1.00	5.39±0.62	55.57±8.15	41.55±2.67	8.28±1.72
	C.V. (%)	4.27	0.82	9.41	9.46	5.67	11.50	14.66	6.42	20.77
II	Mean±SD	98.60±3.14	140.66±1.17	90.37±8.05	9.39±0.95	19.28±1.06	5.41±0.51	58.83±5.90	40.69±2.69	9.66±1.45
	C.V. (%)	3.18	0.83	8.90	10.11	5.49	9.44	10.02	6.61	15.01
III	Mean±SD	90.84±3.40	141.64±0.76	85.66±6.14	10.82±0.85	18.32±1.42	6.04±0.64	62.39±6.20	40.97±2.69	11.83±1.97
	C.V. (%)	3.74	0.53	7.16	7.85	7.75	10.59	9.93	6.56	16.65
IV	Mean±SD	96.53±5.00	142.00±0.96	86.26±4.92	11.47±0.94	20.37±1.36	5.31±0.60	67.67±3.91	33.67±2.20	9.13±2.34
	C.V. (%)	5.17	0.67	5.70	8.19	6.67	11.29	5.77	6.53	25.73
V	Mean±SD	92.80±4.29	138.76±0.85	92.06±7.29	11.43±0.96	18.97±1.48	6.27±0.59	60.29±5.18	40.90±2.36	12.63±1.94
	C.V. (%)	4.62	0.61	7.91	8.39	7.80	9.40	8.59	5.77	15.36
VI	Mean±SD	104.21±6.14	139.32±1.21	97.52±7.42	10.98±0.99	20.55±0.84	4.53±0.63	63.09±5.49	37.28±3.94	5.83±2.11
	C.V. (%)	5.89	0.86	7.60	9.01	4.08	13.90	8.70	10.64	36.19
VII	Mean±SD	90.56±4.45	140.85±0.88	107.78±11.98	11.46±1.40	18.78±1.07	6.72±0.71	54.83±8.01	43.37±0.90	13.10±2.33
	C.V. (%)	4.91	0.62	11.11	12.21	5.69	10.56	14.60	2.07	17.78
VIII	Mean±SD	99.08±3.08	114.58±0.94	101.50±7.89	10.50±0.86	20.81±1.14	6.30±1.05	63.57±5.00	36.01±3.49	9.61±1.88
	C.V. (%)	3.10	0.66	7.77	8.19	5.47	16.66	7.86	9.69	19.56
IX	Mean±SD	92.55±3.90	140.11±1.24	86.92±7.22	12.50±1.26	20.87±1.21	5.01±0.52	67.14±4.98	41.54±2.57	11.03±2.11
	C.V. (%)	4.21	0.88	8.30	10.08	5.79	10.37	7.41	6.18	19.21
X	Mean±SD	97.53±4.61	139.97±1.43	93.03±8.96	12.00±1.17	21.73±1.13	6.15±0.63	71.75±5.99	37.23±3.07	12.98±2.10
	C.V. (%)	4.72	1.02	9.63	9.75	5.20	10.24	8.34	8.24	16.17
XI	Mean±SD	95.66±4.89	142.15±1.25	93.65±7.68	12.66±1.02	19.72±1.36	5.20±0.52	56.83±6.60	42.42±2.22	8.37±1.93
	C.V. (%)	5.11	0.87	8.20	8.05	6.89	10.00	11.61	5.23	23.05

Table 5. Estimates of average intra and inter-cluster distances for eleven clusters under reclaimed sodic soil condition

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**(2.208)**	2.471	2.134	3.617	2.656	4.030	3.639	3.986	3.012	4.389	2.816
II		**(2.000)**	2.289	2.862	2.660	2.822	3.491	2.467	2.925	3.390	2.677
III			**(2.031)**	2.900	2.206	**4.435**	2.805	3.044	2.600	3.225	2.658
IV				**(2.051)**	3.675	3.166	4.613	2.308	2.716	2.693	2.909
V					**(2.052)**	4.086	2.433	3.204	2.516	2.678	3.294
VI						**(2.322)**	**5.131**	3.179	3.504	3.864	3.370
VII							**(2.436)**	3.378	3.798	3.850	3.339
VIII								**(2.262)**	3.365	2.471	3.038
IX									**(2.167)**	2.342	2.423
X										**(2.376)**	3.660
XI											**(2.218)**

Values in parenthesis are intra-cluster distances

Table 6. Potent genetic donors in bread wheat identified from cluster VI and VII for different characters under reclaimed sodic soil condition

Genotypes	Cluster	Traits (#)	Days to heading	Days to maturity	Spike Length (cm)	Spikelets / spike	Tillers / plant	Grains / spike	1000-grain weight (g)	Yield/plant (g)
KLPO 268	VII	06		*	*	*		*	*	*
2-K-142	VII	06	*	*		*	*	*	*	
WC 1	VII	05		*	*		*		*	*
Raj 4077	VII	05	*		*	*	*		*	
KYZO 295	VII	04		*	*				*	*
NW(S)3-2	VII	04	*		*		*		*	
VL 866,	VI	04		*	*	*		*		
KLPO 265	VII	03	*						*	*
KRL 104	VII	03					*		*	*
NW(S)02-15	VII	03					*		*	*
HP-1867	VII	03	*				*		*	
96W639-D2-1	VI	03		*		*		*		
96W639-D6-37	VI	03		*		*			*	
96W639-D6-2	VI	02		*		*				
VL 865	VI	02		*	*					
96W639-D6-36	VI	02		*		*				
96W639-D1-40	VII	02					*		*	
BWMA 8	VII	02					*		*	
Best check			HD 2009 (87 days)	HD 2009 (140 days)	KRL 19 (11.9cm)	PBW 343 (20)	Kh. 65 (6.40)	KRL19 (67)	PBW343 (42.3g)	PBW343 (11.4g)

maximum in cluster VII that indicated maximum diversity among the member genotypes of the cluster VII. On the other hand, least value was observed for cluster II (2.000) and cluster III (2.031) that indicated presence of narrow genetic variation within these clusters. The magnitude of inter-cluster distances measure the extent of genetic diversity between the cultivars of the different clusters which ranged from 2.134 between clusters I and III to 5.131 between clusters VI and VII. The maximum inter cluster distance between cluster VI and VII indicated the maximum diversity between these clusters and suggested the selection of genotypes from these clusters for their further utilization in hybridisation programme through combination breeding.

As clusters VI and VII are distantly related, the genotypic performance among the members of these two groups was evaluated and the promising genotypes for various traits were identified. The better performing genotypes than the respective checks were screened and the donor genotypes for two or more characteristics identified (Table 6). Among them, KLPO 268, 2-K-142, WC 1 and Raj 4077 were most promising genotypes for more than four traits and these can be more extensively utilized in wheat programmes aimed to improvement of genotypes for reclaimed sodic soil conditions.

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Variability and Character Association of Yield Components in Rainfed Lowland Rice

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Forty-two released lowland rice varieties including check were evaluated to obtain information on genetic variability, heritability, interrelationship of grain yield and its components. Highly significant differences were observed among the genotypes in all the characters. High PCV and GCV were observed in plant height, grains/panicle, EBT/hill and panicle weight. High heritability with high genetic advance was observed in plant height and grains/panicle. But high heritability with low genetic advance was recorded in days to fifty per cent flowering, 1000-grain weight and grain length. Plant height had significant positive correlation with panicle weight, grains/panicle, 1000-grain weight and negative correlation with single plant yield.

Key Words: Correlation, Genetic variability, Rainfed lowland rice, Yield components

Introduction

Rainfed lowlands are very predominant in India in general and eastern India in particular. Of the 45 million ha of harvested rice area in the country, about 28% are rainfed lowland. It is very fragile due to erratic climatic conditions. The production is very low in these areas and varies from 1.5-2.0 t/ha. In order to increase the productivity, development of good varieties with specific traits should be taken into consideration. In any rice breeding programme, attempts are always being made to break the yield barrier. Grain yield is a very complex character and it is the result of expression of several interrelated polygenic characters. It is therefore, imperative to obtain information from different genetic parameter influencing grain yield. Development of high yielding varieties require a thorough knowledge of existing genetic variation and also the extent of genetic association among the yield contributing characters. Knowledge of association of yield component with yield is of paramount importance to formulate an effective breeding programme. The interrelationships of component characters of yield provide the information about the improvement of desirable characters under selection. The variability and nature of association of different yield characters were studied in native land races of rice by Tomar *et al.* (2000) and in upland rice by Rao and Srivastava (1994).

Materials and Methods

Forty-two released lowland rice varieties including check were transplanted to evaluate their yield attributing characters and yield under rainfed lowland condition. The materials were sown in Randomized Block Design in three replications with Pooja as local check during *kharif* 2005 and 2006 at Central Rice Research Institute, Cuttack. The recommended doses of fertilizer were applied. Five competitive plants in each replication were selected randomly for recording observation on plant height (cm), EBT/hill, panicle length (cm), panicle weight (g), days to fifty per cent flowering (DFF),1000-grain weight (g), grains/panicle, sterile spikelets /panicle, grain length (mm), grain breadth (mm), L/B ratio, single plant yield (SPY) (g).The data were subjected to statistical analysis (Panse and Sukhatme, 1967).The phenotypic and genotypic coefficient of variability, broad sense of heritability and genetic advance at 5% selection intensity were computed by using the formulae suggested by Johnson *et al.* (1955). The phenotypic and genotypic correlation coefficient were calculated as per Al-Jibouri *et al.* (1958).

Results and Discussion

The analysis of variance (ANOVA) of this experiment revealed that the genotypes were significant for all the characters (Table 1). Mean values, range, coefficient of variation, PCV, GCV, heritability in broad sense and genetic advance as percentage of mean indicate significant variability in certain characters and there is enough scope for exploitation (Table 2).The values of mean performance of yield and yield attributing characters are presented (Table 4). The plant height varied from 81.8 cm (BPT 5204) to 175.5 cm (Hanseswari), EBT/hill 7.8 (Sudhir) to 20.2 (Swarna), panicle length 21.3 cm (BPT 5204) to Sonamani (31.3 cm), panicle weight 2.1g (Dhusura) to

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Table 1. Analysis of variance for 12 yield attributing characters

Characters	Sources of variation		
	Replication	Genotypes	Error
Plant height (cm)	13.30	2050.89**	8.44
EBT/hill	4.02	14.52**	2.43
Panicle length (cm)	0.49	11.96**	1.35
Panicle weight (g)	0.20	1.40**	0.10
Grains/panicle	19.95	2822.09**	218.56
Sterile spikelets/panicle	11.00	35.12**	9.12
DFF	1.88	158.09**	0.23
1000-grain weight (g)	1.48	69.88**	0.24
Grain length (mm)	0.25	2.75**	0.06
Grain breadth (mm)	0.02	0.42**	0.01
L/B ratio	0.001	1.09**	0.02
SPY (g)	25.29	23.65**	6.16

** Significant at 1% level of probability
EBT/hill: Ear bearing tiller/hill, DFF: Days to fifty per cent flowering, L/B: Grain length/grain breadth ratio, SPY: Single plant yield

4.8 g (Varshadhan), and grains/panicle 41.6 (FR-13A) to 193.0 (Tulsi). 1000-grain weight is an important character and it ranged from 13.7 g (Dhusura) to 31.0 g (Sabita) indicating wide variability. The single plant yield varied from 9.9 (Ketekijoha) to 23.7 (Gayatri). In general, all the traits exhibited higher magnitude of PCV than GCV. Maximum GCV was observed in 1000-grain weight (21.7) followed by grains per panicle (20.3), panicle weight (19.5), plant height (19.09) and L/B ratio (18:5). This high value of GCV indicated that maximum variability exists in these traits and there is enough scope for further improvement. Similar observations were obtained by Rabindra Babu (1996) and Deb Choudhury and Das (1998).

The heritability values expressed high in DFF (99.5) followed by 1000-grain weight (98.9), plant height (98.7), grain length (93.1), L/B (93.3) and lowest in sterile spikelets/panicle (48.7) and single plant yield (48.8). The genetic advance recorded highest in grains/panicle (54.2) followed by plant height (53.4) and lowest in panicle weight (1.2), L/B ratio (1.2) and grain breadth (0.73) etc. High heritability with high genetic advance was observed in plant height and grains/panicle. This is most likely due to additive gene effects and direct selection may be very effective. High heritability with low genetic advance was observed in EBT/hill, panicle length, panicle weight, grain length, grain breadth etc. These characters are governed by non-additive gene action (epistasis/dominance) and GXE interaction. The high heritability being exhibited was due to favourable influence of the environment rather than genotypic. In these cases, simple selection might not be effective. As such progeny of family testing should be practised for improvement of these traits. High heritability with moderate genetic advance was observed in days to fifty per cent flowering. This trait could be included in the breeding systems as composite characters. The estimates of PCV were higher than GCV value except DFF which indicates the influence of environment but variation was very less, because of low influence of environment on these characters. Heritability estimates along with genetic advance are more helpful in predicting gain under selection than heritability estimate alone. (Sinha *et al.*, 2004; Johnson *et al.*, 1955).

The estimates of genotypic correlation coefficients are essential in evaluating the possibility of simultaneous improvement of many characters or improvement of a single complex trait on the assumption of correlated response to selection. In the present study, the correlation

Table 2. Range, mean and genetic parameter of 12 yield attributing characters in lowland rice varieties

Characters	Range	Mean ± SE	PCV	GCV	Heritability (%) broad sense	Genetic advance	Genetic advance (as % of mean)
Plant height (cm)	81.8-175.5	136.6 ± 1.6	19.2	19.09	98.7	53.42	39.08
EBT/hill	7.8-20.2	11.44 ± 0.9	22.21	17.53	62.29	3.2	28.5
Panicle length (cm)	21.3-31.3	25.18 ± 0.6	8.78	7.43	72.3	3.2	13.07
Panicle weight (g)	2.1-4.8	3.37 ± 0.1	21.7	19.5	80.7	1.2	36.14
Grain/panicle	41.6-193.0	145.5 ± 8.5	22.7	20.3	79.8	54.2	37.30
Sterile spikelet/panicle	10.3-29.0	18.12 ± 1.7	23.26	16.24	48.7	4.2	23.25
DFF (days)	122.3-151.6	132.9 ± 0.2	5.5	5.6	99.5	14.9	11.2
1000-grain weight (g)	13.7-31.0	22.2 ± 0.2	21.8	21.7	98.9	9.9	44.50
Grain length (mm)	6.7-10.9	8.3 ± 0.1	11.78	11.36	93.1	1.9	22.50
Grain breadth (mm)	1.9-3.3	2.57 ± 0.05	14.9	14.4	93.2	0.73	28.70
L/B ratio	2.2-4.3	3.3 ± 0.09	18.7	18.1	93.3	1.2	35.90
SPY(g)	9.9-23.7	15.3 ± 1.4	22.6	15.8	48.8	3.5	22.60

EBT/hill: Ear bearing tiller/hill, DFF: Days to fifty per cent flowering, L/B: Grain length/grain breadth ratio, SPY: Single plant yield

Table 3. Correlation coefficient of yield and its attributes in lowland rice

Character		PH	EBT/H	PL	PW	G/P	SS/P	DFF	1000-GW	GL	GB	L/B	SPY
PH	P	**1.000**	-0.082	0.098	0.312**	0.194*	-0.110	0.089	0.262**	0.108	0.354**	-0.192**	-0.301**
	G		-0.111	0.112	0.353	0.212	-0.151	0.089	0262	0.119	0…374	-0.200	-0.405
EBT/H	P		**1.000**	-0.109	-0.067	0.120	-0.147	0.027	-0.215*	-0.129	-0.102	-0.019	0.020
	G			-0.071	-0.030	0.157	-0.342	0.038	-0.263	-0.158	-0.118	-0.030	0.051
PL	P			**1.000**	-0.105	0.048	0.050	0.046	-0069	0.030	-0.257**	0.213*	0.110
	G				-0.118	0.083	0.036	0.059	-0.076	0.032	-0.319	0.264	0.169
PW	P				**1.000**	0.385**	-0.213*	0.238**	0.479**	0.217*	0.479**	-0231**	0.076
	G					0.464	-0.257	0.268	0.536	0.225	0.576	-0.301	0.047
G/P	P					**1.000**	-0.275**	0.306**	-0.042	-0.048	-0.012	-0.045	0.070
	G						-0.427	0.336	-0.052	-0.035	0.014	-0.060	0.200
SS/P	P						**1.000**	-0.265**	-0.031	-0.008	-0.120	0.096	-0.083
	G							-0.372	-0.030	0.051	-0.140	0.147	-0.035
DFF	P							**1.000**	0.149	0.032	0.025	-0.014	0.112
	G								0.151	0.033	0.031	-0.018	0.157
1000-GW	P								**1.000**	0.551**	0.555**	-0.089	-0.022
	G									0.576	0.581	-0.096	-0.016
GL	P									**1.000**	-0.092	0.663**	-0.136
	G										-0.111	0.674	-0.252
GB	P										**1.000**	-0.796**	0.067
	G											-0.081	0.063
L/B	P											**1.000**	-0.138
	G												-0.183
SPY	P												**1.000**
	G												

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

PH: Plant height, EBT/H: Ear bearing tiller/hill, PL: Panicle length, PW: Panicle weight, G/P: Grains/panicle, SS/P: Sterile spikelets/panicle, 1000-GW: 1000-Grain weight, DFF: Days to fifty per cent flowering, GL: Grain length, GB: Grain breadth, L/B: Grain length/grain breadth, SPY: Single plant yield.

Table 4. Mean value of yield and yield attributes in 42 lowland rices

S. No.	Varieties	Parentage	PH	EBT/H	PL	PW	G/P	SS/P	DFF	1000-GW	GL	GB	L/B	SPY
1	Gayatri	Pankaj x Jagannath	93	11.3	23.1	3.5	113.3	16.3	136.3	22.6	6.8	3	2.2	23.7
2	Utkalprava	Waikyaku x CR1014	140.3	11.6	25	2.6	156	19	138.3	18	7.9	2.2	3.5	21.3
3	Varshadhan	IR31432-8-3-2	162.6	10.8	25.2	4.8	178.3	10.3	142	28.6	9.5	2.6	3.5	14.5
4	Durga	Pankaj x CR1014	121	12	23.6	3.4	137.6	18	150.6	22	7.9	2.3	3.4	16
5	Ketekijoha	Savitri x Badsabhog	136.3	13.3	26.6	2.2	80	16.6	129	17.6	8.1	2.1	3.8	9.9
6	Mahalaxmi	Pankaj x Mahsuri	155.4	13.2	23	4.1	186	16	130.3	20.3	8.3	2.7	3	12.2
7	Padmini	Mutant of CR1014	144.1	11.4	28	2.7	123.3	29	126.3	14	7.6	1.9	3.8	14.2
8	Purnendu	Patnei23 x Jaldhi2	163.6	14	26.6	4.1	178.3	17.3	142.6	21.6	8	2.5	3.1	13.6
9	Tulsi	CR151-79 x CR1014	132.7	14.7	26	3.4	193	18	151.6	22.6	8.6	2.4	3.5	14.7
10	Moti	CR151-79x CR 1014	114.3	10.3	26.1	3.6	152.6	16.3	125.3	24	9.1	2.3	3.9	14.9
11	Surendra	OR158-5 x Rasi	147.2	10.2	26	2.8	136.3	20.3	131	30.6	8	2.5	3.2	13.8
12	Dharitri	Pankaj x Jagannath	102.3	11	25.6	3.7	132	18.6	132.6	22.6	7	2.7	2.5	16.5
13	Mandyavijay	Sona x Mahsuri	139.6	11.1	26.2	2.8	160.3	18	123	16.6	7.8	2.2	3.5	12.8
14	Dubraj	Land race	143.5	9.5	22	2.7	150.6	16.6	126.6	17	8.1	2.3	3.4	12.7
15	Sarala	CR151 x CR1014	99	13	24.5	2.4	170.6	14.3	144	20.6	8.1	2.2	3.5	15.9
16	Kanchan	Jajati x Mahsuri	161.5	12.2	25.3	4.2	175.3	17	136.6	22	8.2	2.5	3.2	12.5

Table 4. Contd.

Table 4. Contd...

S.No.	Varieties	Parentage	PH	EBT/H	PL	PW	G/P	SS/P	DFF	1000-GW	GL	GB	L/B	SPY
17	Sashi	IR 50 xPatnei-23	130.1	10.1	27.1	3	111.3	18	134.6	21.5	9.3	2.3	4	16
18	Sabita	Pure line of Boyan	148.5	11.7	23.8	3.8	137	16.3	130.6	31	10.9	2.5	4.3	16.9
19	Rajshree	Pure line sel	132.8	13.6	26.1	3	169.6	16	129	24.3	9.6	2.3	4.1	16
20	BPT5204	GEB 24 x TN-1 x Mahsuri	81.8	12.9	21.3	3.3	119.3	22.6	122.3	14.5	7.8	2.1	3.7	14.2
21	Salivanana	RP5-32 x Pankaj	109.5	9.9	24.2	3.4	142.6	17.3	134.3	22.3	7.9	2.9	2.7	15.2
22	FR 13A	Pure line sel.	153.5	13.1	24.3	2.4	41.6	27.6	131.6	25.6	8.5	3	2.7	11.6
23	Nalini	Pur line sel.	164.5	10	24.1	3.6	163	21	137.6	21	8	2.4	3.2	17.2
24	Dinesh	Laladhi-2 x Pankaj	159.7	9.4	24.1	3.8	143.3	16	136	23.3	7.9	3.3	2.3	17.8
25	Bhagirathi	Jingasali x Patnei-23	164.2	12.3	22.7	4.3	153	17	126.3	25.6	7.7	3.2	2.3	16.1
26	Panidhan	CR151-79 x CR 1014	135.8	12.8	25.9	4	159.6	16	143.3	19.3	8.9	2.4	3.7	17.2
27	Jogen	IR-20xSML 40-10-4	91.6	9.2	23	2.6	100.6	27.6	122.3	28.3	9.9	2.5	3.9	13.7
28	Swarna	Vasishtha x Mahsuri	96.1	20.2	24.2	3.3	157	15.3	123.6	19	7.7	2.5	3	18.9
29	Matangini	Pure line sel.	173.7	10.2	24.3	3.6	129.6	22.6	125.6	25.3	7.9	3	2.5	15.9
30	Hanseswari	Pure line sel.	175.5	11	23.6	4.3	139	16.3	125.3	24.3	8.1	3.2	2.5	10.3
31	Savitri	Pankaj x Jagannath	105.3	8.1	26.2	4	145	19.3	137.6	24.6	7	2.8	2.5	17.8
32	Sonamani	Velki x Mahsuri	160.6	13.3	31.3	3.9	155	17	131.3	27	8.3	3	2.7	18.6
33	Neerja	Pure line sel.	137.5	11	23	3.8	170.6	18.6	140	25.3	9.5	2.8	3.3	10.4
34	Golak	Jhingasali x CN544	158	8.3	24	3.4	162	18.3	134.3	25.6	7.7	3.2	2.3	14.8
35	Lunishree	Nonasali mutant	140.8	8.2	25.5	3.4	80.6	17.3	132.3	30.3	10.7	2.5	4.3	13.4
36	CR1014	T-90 x Uranga urangan	134.3	10.1	27.5	2.7	146.6	16	138	14	7.9	1.9	4.1	14.5
37	Mahasuri	Taichung 65 x Mayanga Ebos 60802	144.1	13.5	24.1	2.2	155	15	128	15.6	7.6	2.3	3.2	15.7
38	Dhusura	Land race	158.1	10.3	28.4	2.1	138.3	16	128.3	13.7	6.7	2.2	3	13.4
39	Saraswati	Pankaj x Patnei-23	176.3	12	23.2	3.9	176.6	15.6	136.6	26.3	7.9	3.2	2.4	13.8
40	Ranjeet	Pankaj xMahsuri	105.9	10.8	26.1	2.8	156.3	21.6	124.3	13.9	7.8	2.3	3.3	17.9
41	Sudhir	FR13A x CNM539	152.1	7.8	29.1	4.2	186.8	23.3	132	28.3	10.2	2.4	4.1	17.2
42	Pooja(Check)	Vijay x T-141	91.9	10.1	27.2	2.7	145.3	16	130.3	19.3	7.9	2.3	3.3	18.8
	Mean		136.6	11.4	25.1	3.3	145.4	18.1	132.9	22.1	8.3	2.5	3.3	15.3
	CV(%)		2.1	13.6	4.6	9.5	10.1	16.6	0.3	2.2	3.1	3.9	4.8	16.2
	SEM±		1.6	0.9	0.6	0.1	8.5	1.7	0.2	0.2	0.1	0.05	0.09	1.4
	CD(5%)		4.7	2.5	1.8	0.5	24	4.9	0.7	0.8	0.4	0.1	0.2	4

PH: Plant height, EBT/H: Ear bearing tiller/hill, PL: Panicle length, PW: Panicle weight, G/P: Grain/panicle, SS/P: Sterile spikelet/panicle, DFF: Days to fifty per cent flowering, GL: Grain length, GB: Grain breadth, L/B: Grain length/grain breadth, SPY: Single plant yield.

values for different characters are given in Table 3. In all these cases, genotypic correlation coefficients were higher in magnitude than phenotypic correlations. This indicated that there was strong inherent association among the traits and therefore, the selection based on phenotypic traits could be effective in achieving the genotypic gain for different attributes. Plant height was significantly positively correlated with panicle weight, grains/panicle, 1000-grain weight, and grain breadth. Panicle weight showed positive correlation with grains/panicle, days to fifty per cent flowering, 1000-grain weight, grain length and grain breadth. This indicates that panicle weight will increase with the increase of above-said characters. 1000-grain weight was positively correlated with grain length and grain breadth suggested that increase of 1000-grain weight depended on the increase of grain breadth and grain length. L/B ratio was positively correlated with panicle length and grain length. Days to fifty per cent flowering showed positive correlation with grains/panicle. Grains/panicle will increase with increase of days to fifty per cent flowering. Plant height showed negative correlation with L/B ratio and yield. L/B ratio was negatively correlated with panicle weight and grain breadth and this may be due to the decrease of panicle weight and grain breadth. EBT/H and panicle length showed negative correlation with 1000-grain weight, grain breadth respectively. Yield expressed positive association with EBT/H, panicle length, panicle weight, grains/panicle and days to fifty per cent flowering but negatively correlated with sterile spikelets/panicle, 1000-grain weight and grain length. Hence, these characters should be given due consideration during formulation of selection criteria in the crop improvement programme. Similar studies were reported by Reddy *et al.* (1997) in lowland rice and Chauhan *et al.* (1993) in upland rice.

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Inheritance of Mature Fruit Colour in Capsicum

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An experiment was conducted at Indian Agricultural Research Institute, Regional Station, Katrain (HP), India during 2001-2008 to study the inheritance of mature fruit colour in capsicum (*Capsicum annuum* var. *grossum*). Two inbreds each of 4 different mature fruit colours (red, yellow, orange and yellow orange) were crossed in complete diallele fashion to determine the dominance relationship. Red colour was found dominant over others whereas yellow-orange was recessive to all others. From analysis of a series of F_2 generations and test cross of all possible F_1 progeny it was established that when the *c* locus is silent (*i.e*., homozygous recessive) the *y* locus controls the appearance of orange colour (*Y_cc*) vs. yellow orange (*yycc*). On the other hand when the *y* locus is homozygous recessive, the *c* locus controls the expression of yellow (*yyC_*) vs. yellow-orange (*yycc*) colour. Dominant genes at both the loci resulted in red colour while recessive *yycc* led to appearance of yellow-orange colour in the mature fruit of capsicum. No linkage between the loci was found and cytoplasmic inheritance of this trait was absent.

Key Words: Capsicum, Fruit colour, Carotenoids

Introduction

Fruit colour of sweet pepper has attained commercial importance. Of late there has been increasing demand of coloured capsicum resulting in a pressure on vegetable breeding institutions and seed companies to launch such products in market. At vegetable stage varied colours, *viz.*, green, yellow, cream, white, chocolate, purple etc. are known whereas at mature stage a great assortment of shades of red, orange, yellow and yellow-orange have been observed. The colour of ripe sweet pepper fruit is due to presence of various pigments. In the light of above facts, it has become imperative for breeders to obtain insight into the genetics and inheritance of colour. Lang *et al.* (2004) found on TLC (thin layer chromatography) of red and orange fruits that capsanthin-one of the major carotenoids was absent in orange fruits. Further observation through PCR (polymerase chain reaction) polymorphism of *CCS* (capsanthin-capsorubin synthase) gene and TLC pattern of carotenoid composition co-segregated completely in the F_2 population suggesting that the *CCS* gene, responsible for capsanthin synthesis, controls the orange and red colour of capsicum by changing the carotenoid composition. The orange colour is caused by lack of expression of *CCS* gene. There have been many reports which throw only limited light on the matter. Lefebvre *et al.* (1998), Popovsky and Paran (2000) reported the *CCS* gene to control the segregation of yellow and red colour. Thorup *et al.* (2000) have localized the structural genes from carotenoid pathway on F_2 genetic map of capsicum.

Materials and Methods

Studies were carried out at Indian Agricultural Research Institute, Regional Station, Katrain during 2001 to 2008 with a view to develop superior hybrids of capsicum with different mature fruit colours. Lines with different fruit colours were obtained from various sources and selfed and selected for desired colours repeatedly for five years. Only single plant progenies were brought forward each year. The homozygosity of these lines for character under study was confirmed before effecting crossing by growing large populations of their selfed single-plant progenies to observe any variation. In order to work out the inheritance of mature fruit colour, the purelines used are presented in Table 1.

These lines were crossed in complete diallel fashion and the first filial generation (F_1) was grown out to observe the dominance relationship of colours. A few plants of each F_1 were selfed to produce the F_2 seeds. The F_2 generations were analyzed for segregation of colour in the mature fruit. The F_1 of each cross was also test crossed for confirming the outcomes of the F_2 analysis. In the test crosses, the homozygous recessive line, *i.e*., light orange D-20 was taken as test cross parent. For avoiding confusion leading to wrong conclusions the experiments were conducted in parts and progenies of different crosses were grown over many years so that there was enough population size of each progeny to make observations. The goodness of fit to Mendelian ratios was calculated by the chi-square method.

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Table 1. Material used in the experiment

Line/inbred	Mature fruit colour	Source
Yolo Wonder	Red	IARI, RS, Katrain
HC-201	Red	DRDO, Pithoragarh, Uttarakhand
Golden Pepper-3	Orange	A line purified from a collection obtained from Indo-Israel project, IARI, New Delhi in 2000
Goldmine (AC-49)	Orange	A line obtained from GBPUAT, Pantnagar in 1999, maintained since then at IARI, RS, Katrain
Yellow Capsicum	Yellow	EC113372
DP-2	Yellow	Pure-breeding, yellow, non-pungent Paprika line obtained from segregation of selfed progeny of DARL-204 developed from DRDO, Pithoragarh, Uttarakhand, maintained at IARI, RS, Katrain
Golden Lion	Light orange (yellow-orange)	EC203600, maintained as a germplasm line at IARI, RS, Katrain
D-20	Light orange (yellow-orange)	EC203602

This investigation aims to provide answers to following questions: (i) Whether the carotenoid pigmentation in mature fruit in capsicum is controlled by a gene with 2 alleles, a gene with more than two alleles or more than one genes? (ii) What is the dominance relationship between the colours? (iii) Does any linkage exist between the genes governing this trait? (iv) Is this character controlled by cytoplasmic genes? (v) What are the contrasting colours produced by first locus in case the 2nd locus is homozygous recessive and *vice-versa*?

Table 2. F_1 progenies of crosses between purelines with different fruit colours

	Red	Orange	Yellow	Yellow-Orange
Red	Red	Red	Red	Red
Orange	Red	Orange	Red	Orange
Yellow	Red	Red	Yellow	Yellow
Yellow-Orange	Red	Orange	Yellow	Yellow-Orange

Results

The observations were recorded on plants grown in field at fruit maturity stage. From Table 3 it is clear that red is dominant over all other colours and yellow-orange is recessive to all others. The complete diallele among the four colour types did not show any difference in reciprocal crosses, thus ruling out any possibility of maternal (or cytoplasmic) control of this character. A cross between red and yellow-orange segregates in a dihybrid ratio of 9:3:3:1 in the F_2 generation (Table 3). The red phenotype appeared in a proportion of 9/16 and the yellow-orange phenotype appeared in a proportion of 1/16. Therefore, it can be inferred that a pure breeding line with red mature fruit colour contain the homozygous dominant alleles on both the loci and the yellow-orange phenotype has homozygous recessive alleles on both the loci. The F_2 progeny of the cross between the purelines with red and yellow orange fruit colours segregated in dihybrid ratio of 9:3:3:1 which is possible when there are at least two loci

Table 3. Segregation pattern of progeny of different crosses in second filial generation (F_2)

	Genotype of F_1 hybrid	Total plants	F_2 dihybrid ratio				Ratio	χ^2
			Red	Orange	Yellow	Yellow-Orange		
Red x Orange (*YYCC* x *YYcc*)	*YYCc*	37	28	9			3:1	0.009
Red x Yellow (*YYCC* x *yyCC*)	*YyCC*	42	32		10		3:1	0.03
Red x Yellow-Orange (*YYCC* x *yycc*)	*YyCc*	62	33	12	13	4	9:3:3:1	0.28
Orange x Yellow (*YYcc* x *yyCC*)	*YyCc*	66	35	14	12	5	9:3:3:1	0.53
Orange x Yellow-Orange (*YYcc* x *yycc*)	*Yycc*	26		19		7	3:1	0.05
Yellow x Yellow-Orange (*yyCC* x *yycc*)	*yyCc*	31			22	9	3:1	0.27

controlling the carotenoid differences. This was proved by the observations presented in Table 3. As may be expected, the F_2 progeny of the two intermediate phenotypes (*i.e.*, yellow and orange) also exhibited segregation in the same ratio. From Table 2, it clearly appears that the F_1 progeny of the cross between yellow and orange purelines are red and the F_2 generation shows segregation as stated above (Table 3) suggesting that these two colours are controlled by dominant genes on either of the loci concerned and exhibit a complementary action for producing red phenotype. The second filial generation (F_2) of the cross between red and orange segregates in a ratio of 3 red: 1 orange, similarly the F_2 of the cross between red and yellow segregates in 3:1. This indicates that these two colours (orange and yellow) behave as monogenic recessive to red. In the same manner, when yellow is crossed with yellow-orange the F_2 generation of this cross shows a ratio of 3 yellow:1 yellow-orange. A similar segregation is observed when orange pureline is crossed with yellow-orange.

The test cross progenies, *i.e.*, between the F_1 generation and the recessive parental pureline (yellow-orange fruit colour) were grown and fruit colours were recorded. The test cross progeny of the cross red X orange and red X yellow segregated in a ratio of 1:1 (Table 4, cross serial nos. 1 and 2). Similarly, the test cross of the F_1s of yellow X yellow-orange and orange X yellow-orange showed a segregation of 1:1 (Table 4, cross serial nos. 5 and 6). In case of red X yellow-orange and yellow X orange, the segregation of the test cross progeny was found to fit satisfactorily in the ratio of 1:1:1:1 (Table 4, cross serial nos. 3 and 4).

Discussion

Colours, besides appealing the consumer preference, have effect on other characters. In onion, coloured bulbs have been reported to be highly resistant to onion smudge organism, *Colletotrichum circinans* where as white bulbs were susceptible (Clarke *et al.*, 1944). In case of capsicum also, carotenoid differences have been shown to be affecting nutritional properties.

Lang *et al.* (2004) observed a Mendelian ratio of 3:1 (red:orange) suggesting dominance of red over orange. Since there are four alternate colours, it suggests that the character is not controlled by one locus. The F_2 progeny of the cross between the lines with red (homozygous recessive at both loci) and yellow-orange (homozygous recessive at both loci) fruit colours segregated in dihybrid ratio of 9:3:3:1 which can be accounted for by assuming that there are at least two loci.

Since in many studies the locus or the gene has been referred to as capsanthin-capsorubin synthase gene (Lang *et al.*, 2004), this gene is being designated *C-c*. The other locus controlling the expression of yellow colour in mature fruits has been repeatedly named as *Y-y* locus, therefore, for the purpose of analysis we term this locus *y*. Thus the pureline with red fruit colour has *YYCC* constitution and the one with yellow orange has *yycc* constitution. The progeny of cross between red and yellow-orange phenotypes was test crossed with the parent homozygous recessive at both the loci, *i.e.*, yellow-orange.

Since there is no distortion in the normal Mendelian dihybrid ratio of 9:3:3:1, it is clear that the genes controlling the carotenoid differences are not linked. Yellow and orange

Table 4. Segregation pattern of progeny of different crosses in second filial generation (F_2)

S.No.	Cross	F_1	Total plants	Test cross progeny				Ratio	χ^2
				Red	Orange	Yellow	Yellow-Orange		
1.	Red x Orange (*YYCC* x *YYcc*)	Red *YYCc*	81	42	39			1:1	0.11
2.	Red x Yellow (*YYCC* x *yyCC*)	Red *YyCC*	47	22		25		1:1	0.19
3.	Red x Yellow-Orange (*YYCC* x *yycc*)	Red *YyCc*	37	9	8	10	10	1:1:1:1	0.3
4.	Orange x Yellow (*YYcc* x *yyCC*)	Red *YyCc*	47	12	11	11	13	1:1:1:1	0.23
5.	Orange x Yellow-Orange (*YYcc* x *yycc*)	Yellow *Yycc*	43		23		20	1:1	0.21
6.	Yellow x Yellow-Orange (*yyCC* x *yycc*)	Orange *yyCc*	41			19	22	1:1	0.22

genotypes are the intermediate ones with *yyC_*and *Y_cc* constitution, respectively. The pure breeding yellow and orange genotypes would be *yyCC* and *YYcc*. The red colour of mature fruit appears when the dominant allele is present on both the loci (*Y_C_*). Orange and yellow colours are recessive to red. From the results presented in Table 3 is apparent that the F_1s of red x orange and red x yellow are red while the selfed progeny of these F_1s produced a ratio of 3 red: 1 orange and 3 red: 1 yellow, respectively. Consequently it can be hypothesized that in these crosses, orange and yellow behave as simple monogenic recessive characters with respect to red. The relation between orange and yellow colour can be easily understood from the observations. When purebred orange and yellow lines were crossed, the progeny was red (Table 2). This F_1 progeny when selfed resulted in a population segregating in a ratio of 9:3:3:1 (red: orange: yellow: yellow-orange) (Table 4). Therefore, it can be postulated that these two loci are complementary and red colour appears when dominant alleles are present on both the loci (*C_Y_*). The cross between orange and yellow orange resulted in an orange hybrid which on selfing showed a segregation fitting well into the ratio of 3:1 (orange: yellow-orange). Similarly, the cross between yellow and yellow-orange gave a yellow hybrid in F_1 which segregated almost clearly in a ratio of 3:1 (yellow: yellow-orange). It follows from here that yellow-orange appears when both the loci are homozygous recessive and when the *c* locus is silent (*i.e.*, homozygous recessive) the *y* locus controls the appearance of orange colour (*Y_cc*) vs. yellow orange (*yycc*). On the other hand, when the *y* locus is homozygous recessive, the c locus controls the expression of yellow (*yyC_*) vs. yellow-orange (*yycc*) colour. The segregation pattern of the test cross progenies (Table 4) confirmed that there are two loci involved; there is no linkage between the genes and their two alternative alleles on both the loci.

A similar two gene system (*CCRR*) has been reported by Clarke *et al.* (1994) controlling the 3 colour scheme in onions. They also hypothesized an additional 3rd locus I responsible for appearance of intermediate red colour between red and white which modifies the appearance of red, white and yellow in clear classes. Tomes *et al.* (1953), too, has demonstrated two genes (*RRTT*) controlling the carotenoid pigment system in tomato. This system bears more resemblance to the results obtained from the present investigations. According to their report, the red colour is controlled by *R_T_*, yellow by *rrT_* and tangerine, *i.e.*, orange by *R_tt*. They also found a third gene *b* responsible for appearance of beta-orange colour due to synthesis of beta-carotene. Taking this study further Jenkins and McKinney (1953) on crossing yellow (*rrTT*) and tangerine (*RRtt*) tomatoes found that the F_1 hybrid was red and the F_2 segregated 9 red: 3 yellow: 3 tangerine: 1 yellow-tangerine.

In some cases the yellow-orange (light orange) may be enough deep coloured to be mistakenly classified as orange due to environmental effects or various loci affecting the intensity of colour expression or variously the amount of pigments. This may modify the observed ratio to 9 red: 3 yellow: 4 orange. MacArthur has reported this ratio in tomato first in 1934.

Although brown (or chocolate coloured) pepper fruits are also found, it is not due to any separate pigment but is a result of the combination of the normal red pigments and undecomposed chlorophyll. The retention of chlorophyll is governed by *cl* gene (Smith, 1950). While observing the effect on phenotypes of red, yellow, orange and light orange types may be of some interest, the *cl* gene has nothing to do with carotenoid pigment system of capsicum.

Kormos and Kormos (1960) reported that there were three independent genes, *viz.*, *y*, *c*-1 and *c*-2. According to their analysis *c*-1 and *c*-2 in recessive expression reduced the pigmentation of *y*. However, this report has been questioned severely by Hernandez and Smith (1985) on account of reporting only 6 phenotypes instead of normal 8 that are expected from interaction of 3 pairs of genes and use of only 2 gene symbols to identify each of the 6 phenotypes. Moreover, Kormos (1954) has reported yellow colour as recessive to orange which has neither been found anywhere else in literature nor been reported by any of the subsequent workers. In the present study, the two traits were found complementary. Report of Hernandez and Smith (1985) describes 3 pairs of genes corresponding with 8 phenotypic classes in the F_2 generation of a cross between white and red. A careful perusal of their findings indicates that they have found *y* locus governing the expression of red vs. yellow colour and *c*-2 locus determining the segregation of red and orange fruit colour (corresponding to the *y* locus and *c* locus of the present investigation, respectively). This report is in close conformity with the findings of the present investigation. A third locus mentioned by Hernandez and Smith (1985), *viz.*, *c*-1 is a modifier of expression of *y* and *c*-2 loci. The *c*-1 locus in recessive configuration reduces the pigmentation of *y* and *c*-2 loci. Similar observation about the *c*-1 locus was made by Thorup *et al.* (2000).

According to a report by Lefebvre *et al.* (1998), the candidate gene *y* for yellow pigmentation is present on chromosome 6 whereas according to a study by Romer *et al*. (1993) *c*-locus is located on chromosome 4. Huh *et al.* (2001) found that the polymorphism of *Psy* (phytoene synthase) gene co-segregated with the yellow and red fruit colour where as Lang *et al.* (2004) reported similar co-segregation of *CCS* gene with red and orange fruit colour. It corroborates the suggestion of Lang *et al.* (2004) that there are a series of genes responsible for synthesis of different pigments which finally determine the colour of mature fruit. The vast range found among the paprika genotypes by several investigations (Anu *et al.,* 2002) stand testimony to the fact that there must be several other factors including QTLs, modifier genes and environment which affect the intensity of colour development in ripened fruits of capsicum.

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Evaluation of Hot Pepper (*Capsicum annuum* L.) Germplasm of Diverse Origin for Various Horticultural Characters

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A set of thirty three genotypes of hot pepper collected from Punjab, Rajasthan and AVRDC (Asian Vegetable Research and Development Centre), Taiwan were evaluated for various horticultural characters. The material was sown in a complete Randomized Block Design with three replications during 2002-03. Analysis of variance indicated significant genotypic differences for all the characters which showed presence of wide variability in the material. Genotypes Punjab Lal, S-99-3, S-5, Punjab Guchhedar, S-12-1 and S-103 provided higher yield per plant (563.75 g, 555.57 g, 553.10 g, 540.23 g, 521.33 g, 516.13 g) respectively. Punjab Lal and S-12-1 were resistant to fruit rot and virus complex while Punjab Guchhedar, S-99-3 and S-103 were resistant to fruit rot and moderately resistant to virus complex. Genotypes S-2530, S-2, S-5, S-99-3 and S-30 were significantly superior to check varieties for colouring matter. Similarly, S-99-3 and S-5 were also identified for high capsaicin coupled with high yield and could be utilized for the genetic improvement of hot pepper for yield and quality characters.

Key Words: Hot pepper, Chilli, Yield, Quality

Introduction

Hot pepper (*Capsicum annuum* L.) belongs to family Solanaceae and is one of the most valuable commercial spice crop of India. It is grown for export as well as for domestic market. It is widely used in preparing different dishes, pharmaceuticals and in beverage industries throughout the world. It is mainly grown for red fruits, used as spice in powdered form, as medicine and also in pickles of many kinds. Dry chilli powder, soup, sauces, ketchup and oleoresin are its important processed products. Its fresh green fruits, used as salad, are a rich source of vitamin C and A. The important quality characters in chilli are pungency and red colour in fruits. India is the largest producer of chilli in world but productivity is very low as compared to other countries, namely, Japan and Korea due to diseases particularly, viral diseases (virus complex).The important viruses which attack chilli and cause significant losses are cucumber mosaic virus (CMV), leaf curl virus (LCV) and tobacco mosaic virus (TMV) (Horvath, 1986). The improvement in any character through selection depends upon the extent of genetic variability present in the germplasm. Improvement in fruit yield which is an important character may be achieved through selection of one or more direct or indirect components. Therefore, the present study was undertaken to evaluate the chilli genotypes for yield, quality character and tolerance to various diseases, *viz.*, fruit rot and viruses.

Materials and Methods

The present investigation was conducted at Vegetable Research Farm and Biochemistry Laboratory, Department of Vegetable Crops, Punjab Agricultural University, Ludhiana during 2002-03. Ludhiana is situated at a latitude of 30°-54´N and longitude of 75°-48´E and at a mean height of 247 meters above sea level. This place is characterized by very hot and dry summer (April to June) followed by hot and humid period and cold winters during December to January. The average rainfall of the area is 600 mm, most of which is received during the monsoon season. A composite soil sample from 0-15 cm depth was taken from the experimental field before transplanting whose physico-chemical properties were as follows: soil texture-loamy sand; soil pH-8.5; organic carbon-0.18%; electrical conductivity (mmhos/cm)-0.20.The experiment comprising thirty-three genotypes of chilli, collected from Punjab and Rajasthan states of India and Asian Vegetable Research and Development Centre (AVRDC), Taiwan including three check varieties (Punjab Guchhedar, Punjab Lal and Punjab Surkh), were grown in a Randomized Complete Block Design. The genotypes and their sources are given in Table 1. The seeds of these genotypes were grown in nursery in first week of November and transplanted in the field during the second week of March. A distance of 60 cm and 30 cm was maintained between rows and plants, respectively. Recommended agronomic and plant protection practices were followed to raise healthy crop. Eight plants per plot in each replication were planted and data were recorded on five randomly taken plants per plot in each replication. The observation were recorded on plant height (cm), fruit length (cm), number of seeds per fruit, fruit weight (g), number of branches per plant, number of fruits per plant, days to first fruit harvest, fruit yield per plant (g), fruit rot (%), virus complex (%), colouring matter (ASTA units by Rosebrook *et al.*, 1968), ascorbic acid content (mg/100 g) by AOAC (1975), chlorophyll content of green fruits (mg/g) by Anderson and Bourdman (1964) and capsaicin content (%) by Bajaj and Kaur (1979). The analysis of variance for Randomized Complete Block Design was calculated by the formula given by Allard (1960).

Results and Discussion

The analysis of variance carried out for different characters revealed highly significant differences among genotypes for all the characters. Mean value and range for each character studied are presented in Table 2. The varietal means for different characters are given in Tables 3 (a) and (b). Fruit length varied from 3.83–9.90 cm and genotype S-5 possessed the maximum fruit length. Plant height varied from 60.37 to 117.57 cm. The maximum plant height was recorded in genotype S-86-1. Number of seed was found maximum in S-59. Fruit weight varied from 1.07 to 6.15 g with general mean of 3.74 g. Maximum fruit weight was recorded in S-3-1 which was followed by S-24 (6.0 g), S-1-1 (5.97 g), S-86-1 (5.90 g) and S-8-1-2 (5.33 g). Mean number of branches per plant were 6.01 with range of 4.00-8.67 and maximum number of branches per plant found in Punjab Guchhedar.

Mean value for number of fruits per plant was 135.65 while this character varied from 28.63 to

Table 1. List of genotypes of diverse origin evaluated in the study

S. No.	Genotype	Characters	Origin
1	S-1	Medium ht; medium sized, less pungent fruit	Kapurthala, Punjab
2	S-2	Tall plant; medium sized, less seeded, dark green fruit	Bathinda, Punjab
3	S-3	Medium ht; small sized, less pungent fruit	Bathinda, Punjab
4	S-4	Medium ht; small sized, heavily seeded, less pungent fruit	Kapurthala, Punjab
5	S-5	Small ht; long sized, highly pungent, dark red fruit at maturity	Kapurthala, Punjab
6	S-6	Tall plant; small, less seeded fruit	Bathinda, Punjab
7	S-8	Small ht; small, less pungent fruit	Kapurthala, Punjab
8	S-13	Small ht; long, less pungent fruit	Kapurthala, Punjab
9	S-23	Small ht; medium sized, highly pungent fruit	Kapurthala, Punjab
10	S-24	Medium ht; long, less pungent fruit	Bathinda, Punjab
11	S-30	Small ht; long, dark red fruit at maturity	Bathinda, Punjab
12	S-35	Tall and highly branched plant; less pungent fruit	Kapurthala, Punjab
13	S-59	Small ht; medium sized, heavily seeded fruit	Bathinda, Punjab
14	S-86	Medium ht; medium sized, less pungent, light green fruit	Bathinda, Punjab
15	S-103	Small ht; medium sized, moderately pungent fruit	AVRDC, Taiwan
16	S-1-1	Tall plant; long, dark green fruit	Jaipur, Rajasthan
17	S-3-1	Medium ht; long, less pungent fruit	Bathinda, Punjab
18	S-5-1	Medium ht; small, highly pungent fruit	Bathinda, Punjab
19	S-8-1-2	Small ht; small, heavily seeded fruit	AVRDC, Taiwan
20	S-12-1	Small, highly branched plant; less pungent fruit	Bathinda, Punjab
21	S-30-1	Medium ht; medium sized, dark green fruit	AVRDC, Taiwan
22	S-33-1	Medium, highly branched plant; small, less pungent fruit	Kapurthala, Punjab
23	S-86-1	Tall plant; long, less pungent fruit	Bathinda, Punjab
24	S-99-3	Small ht; highly pungent & dark red fruit at maturity	Bathinda, Punjab
25	S-99-4	Tall, highly branched plant; dark green fruit	Kapurthala, Punjab
26	S-106-1	Small ht; medium sized, highly seeded fruit	AVRDC, Taiwan
27	S-108-2	Small ht; small, light green fruit	AVRDC, Taiwan
28	S-370-2-1	Tall; medium sized, dark green fruit	AVRDC, Taiwan
29	MS 12	Medium ht; small sized, pungent fruit	Kapurthala, Punjab
30	S-2530	Medium ht; medium sized, dark red fruit at maturity	Kapurthala, Punjab
31	Punjab Guchhedar	Medium ht; medium sized fruits borne in cluster picked without stalk	Kapurthala, Punjab
32	Punjab Lal	Small ht; small, erect, more pungent fruit	Kapurthala, Punjab
33	Punjab Surkh	Small ht; long, dark red fruit at maturity	Kapurthala, Punjab

AVRDC: Asian Vegetable Research and Development Centre

Table 2. Mean and range of different characters in hot chilli

Character	Range	**Mean**
Plant height (cm)	60.37–117.57	81.75
Fruit length (cm)	3.83–9.90	6.58
Number of seeds/ fruit	17.27–71.33	37.62
Fruit weight (g)	1.07–6.13	3.74
Number of branches/plant	4.00–8.67	6.01
Number of fruits/plant	28.63–514.37	135.65
Fruit yield/plant (g)	166.07–563.73	378.63
Chlorophyll content (mg/g)	0.11–0.70	0.35
Days to first fruit harvest	70.00–95.00	90.65
Capsaicin (%)	0.30–0.91	0.57
Ascorbic acid (mg/100g)	99.90–140.50	123.39
Colouring matter (ASTA units)	83.36–216.36	145.52
Virus complex (%)	6.06–52.76	17.64

514.37. The maximum number of fruits per plant was found in Punjab Lal followed by Punjab Guchhedar and S-5-1. Fruit yield varied from 166.07-563.73 g with mean value 378.63 g. Maximum fruit yield was found in Punjab Lal (563.73 g) followed by S-99-3 (555.56 g), S-5 (553.10 g), Punjab Guchhedar (540.23 g), S-12-1 (521.33 g) and S-103 (516.13 g). Similar type of variability was recorded in fruit yield, fruit length, number of fruit per plant by Khurana *et al.* (2003) and Kumar *et al.* (1999). Mean value for chlorophyll content was 0.35 mg/g with range from 0.11-0.70 mg/g. Maximum chlorophyll content was recorded in S-99-4. There was no incidence of fruit rot in any genotype under field conditions. There were ten genotypes, *viz.,* Punjab Lal, Punjab Surkh, S-2530, S-1, S-12-1, S-23, S-30-1, S-59, S-106-1, S-370-2-1 which were having less than 10% virus complex.

Table 3(a). Mean values of different genotypes for various traits

Genotypes	Plant height (cm)	Fruit length (cm)	No. of seeds /fruit	Fruit weight (g)	No. of branches/plant	No. of fruits/ plant	Fruit yield/ plant (g)	Total Chlorophyll content (mg/g)
S-1	82.83	6.00	27.33	2.63	7.00	134.40	357.63	0.28
S-2	98.17	6.50	19.33	2.47	8.33	188.43	423.80	0.64
S-3	78.40	4.07	48.47	3.97	6.33	47.17	191.50	0.39
S-4	86.43	5.30	63.33	3.23	6.33	104.30	313.03	0.15
S-5	68.27	9.90	43.67	4.70	7.33	122.90	553.10	0.19
S-6	98.97	3.83	17.27	4.33	5.00	121.43	485.87	0.25
S-8	76.90	5.97	51.03	4.00	6.00	82.87	305.53	0.53
S-13	65.73	8.57	22.53	3.13	7.33	66.67	200.10	0.28
S-23	62.77	7.30	34.00	3.17	5.00	124.53	392.63	0.30
S-24	84.40	8.47	34.00	6.00	5.33	48.73	238.87	0.49
S-30	76.97	9.07	58.80	4.47	7.00	95.23	381.20	0.15
S-35	100.27	6.47	41.90	3.23	8.33	113.40	340.23	0.35
S-59	74.03	7.00	71.33	4.00	5.00	110.77	443.23	0.55
S-86	82.10	7.54	28.03	4.47	5.00	80.23	346.00	0.23
S-103	74.00	7.27	26.93	3.20	6.33	172.00	516.13	0.25
S-1-1	107.73	8.33	28.03	5.97	4.00	35.27	172.33	0.57
S-3-1	87.03	8.07	39.80	6.13	5.33	28.63	166.07	0.45
S-5-1	93.20	5.33	29.01	1.63	6.00	306.40	459.63	0.11
S-8-1-2	76.83	5.73	61.47	5.33	5.00	69.77	347.30	0.44
S-12-1	76.13	7.50	52.37	4.00	7.33	130.33	521.33	0.43
S-30-1	82.67	6.43	21.10	4.00	6.33	128.67	490.47	0.63
S-33-1	82.07	5.60	45.00	2.47	8.33	91.27	228.23	0.22
S-86-1	117.50	8.30	25.07	5.90	5.00	53.60	321.80	0.16
S-99-3	62.47	5.13	50.50	4.07	6.00	148.10	555.57	0.25
S-99-4	110.47	5.17	21.53	2.47	7.67	158.40	316.83	0.70
S-106-1	60.37	6.70	59.93	3.97	5.00	85.60	331.83	0.53
S-108-2	66.00	5.43	27.07	2.30	4.33	139.30	348.97	0.13
S-370-2-1	103.07	6.63	34.80	4.17	4.33	118.67	474.73	0.57
MS 12	82.67	4.77	65.93	3.33	5.00	94.37	282.23	0.23
S-2530	82.40	6.57	21.00	3.87	6.33	105.17	394.50	0.13
Punjab Guchhedar	65.27	5.30	20.27	1.93	8.67	477.30	540.23	0.13
Punjab Lal	65.93	4.57	23.63	1.07	4.00	514.37	563.73	0.15
Punjab Surkh	62.73	8.40	26.23	3.83	4.00	178.27	490.23	0.53
CD (p = 0.05)	4.59	0.87	9.82	0.48	1.84	16.71	40.10	0.01

Table 3(b). Mean values of different genotypes for various traits

Genotypes	Days to first fruit harvest	Capsaicin (%)	Ascorbic acid (mg/100g)	Colouring matter (ASTA units)	Virus complex (%)
S-1	95.00	0.33	130.77	145.43	6.06
S-2	95.00	0.50	130.60	215.47	16.06
S-3	85.00	0.48	121.17	96.50	17.76
S-4	95.00	0.46	128.63	152.37	36.40
S-5	95.00	0.90	108.20	210.53	26.93
S-6	95.00	0.68	127.83	175.50	18.63
S-8	95.00	0.45	120.47	151.17	24.36
S-13	94.67	0.59	140.40	164.20	26.93
S-23	95.00	0.80	136.43	145.27	8.70
S-24	95.00	0.30	140.50	100.70	52.76
S-30	94.67	0.46	101.50	210.27	17.63
S-35	95.00	0.50	135.93	145.30	17.50
S-59	80.00	0.75	116.80	151.13	6.76
S-86	80.00	0.47	104.87	97.17	19.03
S-103	88.00	0.58	125.40	86.10	18.13
S-1-1	95.00	0.45	138.97	164.33	16.53
S-3-1	95.00	0.40	115.90	150.23	18.43
S-5-1	95.00	0.85	141.17	151.10	26.93
S-12-1	86.00	0.35	136.07	85.50	8.00
S-30-1	95.00	0.48	131.13	151.87	9.33
S-33-1	95.00	0.45	108.97	149.33	17.73
S-86-1	91.67	0.43	131.37	101.80	25.46
S-99-3	85.00	0.92	114.90	210.43	16.63
S-99-4	95.00	0.48	125.00	163.87	18.63
S-106-1	87.00	0.54	115.43	101.73	8.40
S-108-2	95.00	0.48	120.07	99.30	17.36
S-8-1-2	88.00	0.48	124.47	206.17	15.33
S-370-2-1	95.00	0.47	115.57	153.40	8.59
MS 12	95.00	0.90	135.90	96.87	18.46
S-2530	88.00	0.61	104.77	216.37	7.80
Punjab Lal	83.33	0.91	99.90	92.43	8.50
Punjab Guchhedar	80.00	0.86	116.50	83.37	18.53
Punjab Surkh	70.00	0.65	126.33	177.17	7.80
CD (p = 0.05)	1.83	0.02	1.89	17.02	1.74

Note: There was no incidence of fruit rot on any of the genotypes. It did not appear under natural epiphytotic condition

Punjab Surkh was found early yielding than other genotypes. Capsaicin content varied from 0.30-0.91% with mean value of 0.57%. The genotypes S-99-3 and Punjab Lal were statistically at par for capsaicin content. Ascorbic acid varied from 99.90–140.50 mg/100 g. Maximum ascorbic acid content was found in S-24 (140.50 mg/100 g) and S-13 (140.40 mg/100 g). Kumar *et al.* (2003) also found wide variability in ascorbic acid content in 30 chilli genotypes. The range of colouring matter was 83.36–216.36 ASTA units with a mean value of 145.52. Maximum colouring matter was found in S-2530 (216.37 ASTA units) followed by S-2 (215.46 ASTA units), S-5 (210.53 ASTA units), S-99-3 (210.43 ASTA units) and S-30 (210.26 ASTA units).

Genotypes Punjab Lal, S-99-3, S-5, Punjab Guchhedar, S-12-1 and S-103 provided higher yield per plant. Punjab Lal and S-12-1 were resistant to fruit rot, virus complex while Punjab Guchhedar, S-99-3 and S-103 were resistant to fruit rot and moderately resistant to virus complex. Genotypes S-2530, S-2, S-5, S-99-3 and S-30 were significantly superior to check varieties for colouring matter. Similarly, genotypes S-99-3 and S-5 were also identified for high capsaicin content, yield and quality characters. The results identified the genotypes possessing the desirable horticultural characteristics, which the breeder can make use of in production of new improved cultivars.

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Genetic Variability for Seedling Traits in Indian Mustard under Moisture Stress Conditions

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Eighty advanced progenies of Indian mustard derived from interspecific hybridization along with four check varieties were evaluated in an Augmented Randomized Complete Block Design with five blocks during *rabi* 2008-09. The data were subjected to obtain estimates of variability, heritability and genetic advance and correlations for different seed and seedling characteristics. Adequate variability was present for seed yield per plant, oil content, germination percentage, shoot length, root length, seedling elongation, fresh seedling weight and vigour index. Broad sense heritability was high (>50%) for all these characters. The seed yield per plant had positive and significant correlation with test weight, root length, seedling elongation and vigour index. On the basis of this study, it is suggested that test weight, root length, seedling elongation and vigour index should be considered in selection programme for yield improvement in the segregating material generated by using selected advance lines.

Key Words: Indian mustard, Vigour index, Heritability, Correlations

Introduction

Indian mustard [*Brassica juncea* (L.) Czern and Coss] is cultivated in a wide range of agro -climatic conditions. The productivity of this crop is low as it is normally grown on marginal and light texture soil using conserved moisture received from monsoon rains in about 37% of the total area under the crop. Depending on planting time and winter rain, the crop is exposed to water stress at one or more phenological stages when stored water becomes depleted (Kumar, 2001). This calls for screening and development of genotypes having good plant stand and vigour under prevailing environmental conditions because farmers with no or limited irrigation facilities opt for rapeseed-mustard as a crop, however, many times poor plant stand owing to poor germination due to limited moisture and/or mortality of seedling due to high temperature causes heavy losses in terms of yield (Kumar *et al.*, 1995). Ensuring good plant stand under prevailing condition is the biggest challenge to the *Brassica* researchers. The seed size, seed weight and vigour index influences the crop stand by ensuring germination and survival of seedling through supply of nutrients to the growing seedlings under field conditions (Gontia and Awasthi, 1999). Seedling vigour determines the ability of nutrient uptake from soil; thereby enhances the vegetative growth under adverse environmental conditions (Kant and Tomar, 1995). Deep root and long shoot are important survival traits under moisture stress. Therefore, it is important to design genotypes having deep root, and high vigour index. The information on genetic variability for seed and seedling traits and character association between these traits is scanty in Indian mustard. Therefore, the present investigation was planned to get information on these aspects.

Materials and Methods

The material for present investigation consisted of 80 advanced progenies of Indian mustard derived from inter-specific crosses between *Brassica juncea* x *B. carinata.* These progenies were evaluated during *rabi* 2008-09 in an Augmented Randomized Complete Block Design (Fedrer, 1956). The material was divided into five blocks, each block consisted of 16 progenies and 4 check varieties, namely, RH–819, PBR–97, Varuna and Rohini which were common to each block. In each block progenies and check varieties were sown in two row plots of 5 m length, spaced 30 cm apart with plant to plant distance of 10 cm achieved by thinning at 15-20 days after sowing. The experiment was conducted under rainfed condition and no presowing irrigation was given even for germination. Observations were recorded on ten randomly selected plants for seed characters. Oil and protein content were estimated by using Near Infrared Reflectance Spectroscopy apparatus. The laboratory experiment for study of seedling traits, *viz.* seed germination percentage, shoot length, root length, seedling elongation (cm), fresh seedling weight (mg) and vigour index was carried out in Petri dishes (9 cm diameter) by using the same seed lot as used for seed traits. 50 seeds of each genotype were placed in Petri dish with four replications, lined with two layers of Whatman filter paper (ISTA, 1985). Distilled water was applied to each petri dish for germination and recording of other seedling observations. The whole set

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*Author for Correspondence: Email: vvs_71@yahoo.co.in of Petri dishes were kept in BOD incubator at 25°C and 75 % RH for germination. Seeds with radical emergence of 2 mm length were counted for germination (Lang, 1965). Daily germination was recorded up to 7 days. Observations for seedling traits were recorded on ten randomly selected seedlings from each replication after 7 days. Vigour index was calculated by using the formula: VI = Germination (%) x (Root + Shoot length). Genotypic and phenotypic coefficient of variations, heritability in broad sense and genetic advance were calculated as per standard procedure. The simple correlation studies were carried out among the seed and seedling traits to know the relationship among the traits.

Results and Discussion

The varieties released so far, though have shown marked superiority over local types under irrigated conditions, could not make a desired impact under rainfed condition particularly in the arid and semi-arid zones and this perhaps is one of the major factor for poor adoption of the newly released varieties by resource poor farmers with limited irrigation facilities. Genotypes are generally developed and tested under the best agronomic conditions, the conditions which hardly prevail at farmers field (Meena *et al*., 2008). The varieties developed and recommended for cultivation should, therefore, possess besides high yield, the traits which ensure stability under diverse set of conditions. Assessment of genetic variability for quantitative traits is the first step in any breeding programme and presence of adequate genetic variability indicates about the possibility of the genetic improvement in crop species, as genetic variability is directly related to advancement that can be made by selection.

Analysis of variance revealed significant differences among progenies for most of the characters except protein content and test weight. This indicated that material had sufficient variability for these traits and response to selection may be expected in the breeding programme for seed yield and seedling traits, which may be used for further improvement. The block effects were non significant for all seedling traits except germination percentage indicating non-sensitivity of the material to the environment for these characters (Table not presented).

Estimates of genotypic and phenotypic variances indicated that in general, magnitude of the PCV was higher as compared to GCV for all the characters in the present investigation indicating a positive effect of environment on the character expression. The variances of various characters were compared on the basis of coefficient of variation. Seed yield per plant followed by root length exhibited comparatively higher estimates of genotypic as well as phenotypic coefficient of variation (Table 1). It indicated that simple selection for root length might be advantageous. These results were in agreement with earlier reports of Das *et al.* (2001) and Singh *et al.* (2007). In an augmented design, it is assumed that the estimate of error variance is inflated and thus may not check the variation among genotypes with precision. With the help of GCV and PCV alone, it is not possible to determine the amount of variation, which is heritable. Thus, the heritability estimate along with genetic advance is more meaningful.

Since, in augmented design only the error variance of check varieties could be subtracted from the variance of genotypes a portion of it may be confounded with the genotypic variance used for calculating the heritability, therefore, caution should be exercised in interpreting the estimates of heritability values as they represent only the upper limit of heritability. The estimates of heritability in present investigation were of higher magnitude (>50%) for all the characters studied. Similar reports were made by Swarnker *et al.* (2002) and Meena *et al.* (2008).

The genetic advance was highest for seed yield per plant followed by root length, seedling elongation and fresh seedling weight. These findings indicate that there is good scope for development of genotypes having deep root system, high seed yield per plant and high shoot length, which would perform better in water stress conditions. High heritability values accompanied with high genetic advance were observed for root length and fresh seedling weight. Similar reports of high heritability with high genetic advance for these characters were made by Meena *et al.* (2008). This indicates that selection will be more effective for these characters in comparison to other.

The correlation coefficients based on mean values of seed and seedling characters are presented in Table 2. Seed yield per plant showed positive and significant correlation with root length, test weight, seedling elongation and vigor index. Therefore, high yielding genotypes can be developed with deep root and fast growing seedling traits for efficient use of scarce water resource. The result of present investigation is in accordance with the report of Sikarwar *et al.* (1997) and Meena *et al.* (2008). 1000-seed weight was found to be positively and significantly associated with shoot length and fresh seedling weight while negatively associated with oil content; this indicated that bolder seeds had thicker seed coat (Sharma and

Table1. Overall mean value of progenies, their range, genotypic and phenotypic coefficients of variation, heritability in broad sense and genetic advance as percentage of mean for seed and seedling traits in Indian mustard

Character	Mean	Range	Genotypic coefficient of variation (GCV)	Phenotypic coefficient of variation (PCV)	Heritability in broad sense (%)	Genetic advance as percentage of mean
Seed yield per plant (g)	8.10	4.14-16.12	18.43	22.52	66.96	31.07
*Test weight (g)	3.81	2.23-4.42	–	–	–	–
*Protein content (%)	19.61	17.61-21.03	–	–	–	–
Oil content (%)	42.93	40.75-44.89	1.31	1.74	57.14	2.05
Germination percentage	93.47	86.25-99.25	2.72	3.32	57.43	3.93
Shoot length (cm)	4.63	3.66-5.94	8.08	9.41	73.68	14.28
Root length (cm)	8.74	5.28-13.39	12.10	14.65	68.29	20.61
Seedling elongation	13.37	10.17-18.77	9.22	10.73	73.78	16.31
Fresh seedling weight (mg)	52.22	38.82-68.01	9.12	9.79	86.82	17.52
Vigour index	12.49	8.68-16.29	8.28	10.37	63.69	13.61

*As mean sum of squares were non significant for this characters, genetic parameters could not be estimated

Table 2. Correlation coefficient on the basis of unadjusted values (phenotypic level) between different characters of Indian mustard

Characters	Seed yield per plant (g)	Test weight (g)	Protein content (%)	Oil content (%)	Germination percentage	Shoot length (cm)	Root length (cm)	Seedling elongation	Fresh seedling weight (mg)
Test weight (g)	0.234*								
Protein content (%)	0.032	-0.068							
Oil contents (%)	-0.077	-0.044	-0.301**						
Germination Percentage	-0.057	0.148	-0.231*	0.261*					
Shoot length (cm)	-0.006	0.228*	-0.188	0.100	0.089				
Root length (cm)	0.286**	0.014	-0.259*	-0.111	-0.299**	0.264*			
Seedling elongation	0.273*	0.082	-0.283**	-0.067	-0.233*	0.540**	0.954**		
Fresh seedling weight (mg)	0.050	0.223*	-0.048	0.053	-0.190	0.262*	0.301**	0.343**	
Vigour index	0.256*	0.130	-0.360**	0.011	0.062	0.577**	0.890**	0.956**	0.296**

*Significant at p= 0.05, ** Significant at p= 0.01

Singh, 1994). Thicker seed coat reduces the oil percent and increases the fibre content of seed meal. Therefore, genotypes with medium seed size have to be selected for maximizing the oil production/unit. Oil content revealed significant positive correlation with germination percent. Similar result was earlier obtained by Swami and Bajaj (1988) and Ozer and Dogru (1999). Shoot length had positive and significant correlation with seed yield, root length, seedling elongation, and fresh seedling weight and vigour index as earlier reported by Sharma and Singh (1994). Seedling elongation revealed significant and positive correlation with seed yield, shoot length, fresh seedling weight and vigour index (Kant and Tomar, 1995).

Protein content showed negative correlation with all the characters under study except seed yield per plant. Similarly, oil content exhibited negative correlation with seed yield per plant, protein content, root length, and seedling elongation. Germination percentage also showed negative correlation with seed yield per plant, protein content, root length, seedling elongation and fresh seedling weight. Adams (1967) had shown that component compensation and negative correlation arise in response to competition between developmentally flexible components.

Association between some characters was non significant which implies that the two variables are not linearly related on these two may be related but in a non linear fashion (Gomez and Gomez, 1980). It was also noted that characters which exhibited positive association with seed yield per plant also exhibited positive association among themselves thus these characters could be simultaneously improved to increase the seed yield.

The conclusion from present study indicated that root

Table 3. Selected advance breeding lines with desirable seed and seedling characteristics

Progeny	Seed yield per plant (g)	Test weight (g)	Protein content (%)	Oil content (%)	Germination percentage	Shoot length (cm)	Root length (cm)	Seedling elongation	Fresh seedling weight (mg)	Vigour index
08-537-40	16.12	3.91	19.65	41.66	92.25	4.97	9.76	14.73	56.40	13.57
08-541-44	14.47	3.32	19.70	42.45	90.00	5.04	10.01	15.05	53.93	13.60
08-538-41	14.12	4.06	20.15	42.38	96.25	5.10	10.69	15.79	52.28	15.14
08-553-57	12.57	4.42	19.92	42.00	92.00	4.75	9.11	13.86	66.08	12.77
08-548-52	10.77	3.68	19.92	42.82	92.00	4.20	7.77	11.97	43.39	11.00

length, seedling elongation and vigour index are most important characters that should be considered in selection procedure because all these characters had high heritability, moderate genetic advance and also exhibited positive association with seed yield ultimately these characters would result in enhancement of yield in moisture stress conditions having variable moisture regimes. On the basis of present experimentation, the advanced breeding lines with the characters necessary for developing stable high oil yielding lines for variable moisture regimes are presented in Table 3. These lines may be used in crossing programme to select desirable segregants.

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Combining Ability Analysis in Chilli (*Capsicum annuum* L.)

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Genetic analysis was carried out through diallele method for estimation of combining ability using nine parents. The analysis revealed that parents and crosses differed significantly for general and specific combining ability effects. The relative magnitude of *gca* variances was higher than the *sca* variance, indicates the role of additive component in the expression of all the traits except green fruit yield which was found to be under the control of non-additive gene action. The parents HC-7 for green fruit yield, fruit weight, fruit length, and earliness, HC-51 for green fruit yield, number of fruit per plant and earliness were found to be the best general combiner. The crosses HC-7 x HC-51, HC-8 x HC-37 and HC-51 x HC-34 were the best specific crosses for green fruit yield and its contributing traits. These combinations may be further tested for promotion of F_1 hybrids in Chilli.

Key Words: Chilli, Combining ability, Gene action

Introduction

The chilli (also chili or chile) is a member of the nightshade family, Solanaceae. It is an important spice, condiment, vegetable crop, being cultivated since prehistoric times in Peru and Mexico. The pungency of chilli is due to capsaicin, which has medicinal value also. When chilli is eaten it makes the brain to release endorphins, a natural pain killer present in the body. The endorphin lowers blood pressure and helps to fight against cancer. Being an often cross-pollinated crop, it exhibits wide variability for different quantitative and qualitative traits. Thus, there is a wide scope of improvement through heterosis breeding among genetically diverse genotypes. Information on combining ability facilitates the choice of suitable parents for hybridization programme to develop promising F_1 hybrids. The diallele mating design helps in determining both general and specific combining ability of parents and hybrids combination, respectively. Further it helps in formulating the suitable breeding strategy for improvement. Therefore, the present study was undertaken to identify suitable potential combination in order to have superior F_1 hybrids.

Materials and Methods

The present investigation was conducted during 2007-2008 at experimental farm of Indian Council of Agricultural Research (ICAR)-Research Complex for Eastern Region (RCER), Research Centre, Ranchi. Nine diverse lines of chilli, namely, HC-7, HC-8, HC-51, HC-33, HC-23, HC-5, HC-62, HC-37 and HC-34 were crossed in all possible combinations excluding reciprocals using half-diallele mating design. The seedling of nine parents along with their 36 F_1s were transplanted on 07.05.07 in randomized block design at a spacing of 60 x 50 cm with three replications. The observations were recorded on 10 random selected plants in each treatment over replication for six characters, *viz*., green fruit yield (q/ha), fruit weight (g), fruit length (cm), fruit breadth (cm), days to 50 per cent flowering and number of fruits per plant. The genetic analysis for combining ability estimates were calculated according to method 2 and model 1 of Griffing (1956).

Results and Discussion

Highly significant variances (Table 1) were observed for general and specific combining ability effects for all the traits. However, the relative magnitude of *gca* variances was higher than the *sca* variances indicating thereby, that the additive component was of major importance in the expression of all the traits, except green fruit yield, which was found to be under the control of both additive and non-additive genetic effect, simultaneously. These findings are in close conformity of Gopalkrishnan *et al.* (1987) and Pandey *et al.* (1981).

General combining ability study had successfully led to making choice of suitable parent. This valuable information on green fruit yield and its component would

Table 1. Analysis of variance for combining ability

Source	df	Green fruit yield	Fruit weight	Fruit length	Fruit breadth	Days to first flowering	No. of fruits/ plant
gca	8	2581.28**	0.42**	2.84**	0.028**	41.37**	5284.84**
sca	27	2652.22**	0.19**	0.95**	0.019**	17.05**	2887.47**
Error	70	557.39	0.003	0.007	0.006	3.50	377.04

Table 2. Estimates of general combining ability effects of parents

Parents	Name	*Source	Green fruit yield	Fruit weight	Fruit length	Fruit breadth	Days to first flowering	No. of fruits/ plant
HC-7	Pusa Jwala	IARI	20.41**	0.28**	1.00**	-0.02**	-3.08**	-12.35**
HC-8	LC-333	Lam	3.34	-0.06**	0.04*	-0.06**	-0.65	22.01**
HC-51	HC-1-1	HARP, Ranchi	20.11**	0.01	-0.32**	-0.04**	-1.98**	19.51**
HC-33	Local Collection	HARP, Ranchi	-12.40*	0.26**	-0.10**	0.06**	0.86	12.21*
HC-23	B. Dabbi	Dharwar	3.17	-0.04**	-0.05*	0.02**	2.11**	15.16**
HC-5	KA-2	IIVR, Varanasi	-10.29	0.19**	0.38**	-0.01**	0.95*	7.54
HC-62	HC-2-1	HARP, Ranchi	-15.10*	0.06**	-0.36**	0.05**	-0.65	-31.67**
HC-37	Local Collection	HARP, Ranchi	-11.76*	-0.25**	-0.13**	-0.06**	1.60**	-11.86*
HC-34	Local Collection	HARP, Ranchi	2.52	-0.21**	-0.46**	-0.02**	0.84	-20.56**
SE (gi)			5.95	0.013	0.02	0.006	0.47	4.49

* National identity number (IC No.) of the lines utilized shall be taken in due course of time except KA-2 and Pusa Jwala

Table 3. Estimates of specific combining ability effects of crosses

Crosses	Green fruit yield	Fruit weight	Fruit length	Fruit breadth	Days to first flowering	No. of fruits/ plant
HC-7 x HC-8	-50.86**	0.39**	0.37**	0.07**	0.97	-46.25**
HC-7 x HC-51	53.99**	0.02	0.24**	-0.03**	2.31*	-28.75*
HC-7 x HC-33	34.82*	0.11**	0.36**	-0.02*	-1.79	-17.45
HC-7 x HC-23	2.59	0.20**	0.03	0.01	1.21	34.84**
HC-7 x HC-5	3.55	0.06*	0.24**	-0.01	0.61	42.22**
HC-7 x HC-62	22.12	-0.25**	-0.33**	-0.001	-1.78	27.18*
HC-7 x HC-37	20.03	-0.18**	-0.07	0.05**	-1.53	15.62
HC-7 x HC-34	-86.24**	-0.35**	-0.85**	-0.07**	-0.01	-27.42*
HC-8 x HC-51	-29.77*	0.16**	-0.85**	0.20**	-0.12	-24.85*
HC-8 x HC-33	-10.18	0.46**	0.87**	-0.03**	3.03**	-26.81*
HC-8 x HC-23	35.08*	-0.28**	0.09*	-0.05**	1.03	28.74*
HC-8 x HC-5	-2.29	-0.30**	-0.19**	-0.02*	-1.56	33.61**
HC-8 x HC-62	-12.47	-0.31**	0.06	-0.11**	-0.45	-23.67*
HC-8 x HC-37	41.68**	-0.09**	-0.29**	-0.01	-2.70**	13.51
HC-8 x HC-34	28.82*	-0.03	-0.66**	-0.05**	-0.19	45.72**
HC-51 x HC-33	-67.77**	-0.60**	-0.42**	-0.14**	2.37**	61.94**
HC-51 x HC-23	-37.52**	-0.04	-1.22**	0.18**	-0.13	-36.26**
HC-51 x HC-5	19.69	0.25**	0.89**	-0.08**	-1.73	-27.64*
HC-51 x HC-62	1.59	-0.16**	0.70**	-0.11**	0.88	12.57
HC-51 x HC-37	20.75	0.18**	0.38**	0.02*	-0.87	19.26
HC-51 x HC-34	39.05**	0.08**	0.28**	-0.05**	-2.69*	23.72*
HC-33 x HC-23	38.75**	0.23**	-0.17**	0.05**	-6.39**	30.95**
HC-33 x HC-5	14.70	-0.13**	-1.01**	0.09**	-4.07**	-23.59*
HC-33 x HC-62	9.10	-0.11**	-1.09**	0.18**	-0.71	-8.88
HC-33 x HC-37	-6.32	-0.02	0.63**	-0.06**	3.53**	26.81*

greatly help in proper classification of parental lines. On the basis of *gca* effect, parent HC-7 for green fruit yield, fruit weight, fruit length and earliness, HC-51 for green fruit yield, earliness and number of fruits per plant, HC-33 for fruit weight, fruit breadth and number of fruits per plant, HC-23 for number of fruits per plant, HC-5 and HC-62 for fruit weight were found best general combiner (Table 2). General combining ability effects include both additive and additive x additive type of gene action, which represent fixable genetic variance.

The specific combining ability effects (Table 3) exhibited that, the number of crosses that had desirable significant effect were 7 for green fruit yield, 13 for fruit weight, 16 for fruit length, 12 for fruit breadth, 2 for earliness and 11 for number of fruits per plant. The three best performing crosses showing highest specific combining ability effect in order of merit were HC-7 x HC-51, HC-8 x HC-37, HC-51 x HC-34 for green fruit yield; HC-5 x HC-62, HC-8 x HC-33, HC-7 x HC-8 for fruit weight; HC-23 x HC-34, HC-51 x HC-5, HC-8 x HC-33 for fruit length; HC-8 x HC-51, HC-51 x HC-231, HC-33 x HC-62 for fruit breadth; HC-33 x HC-23, HC-37 x HC-34, HC-33 x HC-5 for earliness and HC-62 x HC-34, HC-51 x HC-33, HC-8 x HC-34 for number of fruits per plant. The result obtained indicated that in most of the crosses, which exhibited the best *sca* effects was having at least one of the out standing parental lines for that particular trait. More or less similar observation has also been made by Srivastava *et al.* (2004). From the present study, it was also evident that the best cross combination for most of the characters generally involved one good and one poor general combiner with high *sca* effects, may be due to a complimentary type of gene action which can be fixed in the segregating generation. Contrary to this crosses with high *sca* effects involving poor x poor combiners, may be utilized for exploring of hybrid as the non-additive, non-fixable genes seems to play a major role. Among combinations based on the *sca* values the crosses, namely, HC-7 x HC-51, HC-8 x HC-37, HC-51 x HC-34 were found superior and these combinations can be further tested for promotion of F_1 hybrids in chilli.

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Important Crop Germplasm Introduced in India during 2008

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Exchange of plant material on a world wide basis had been mostly carried out without regard to well defined procedures. NBPGR is the nodal institute which facilitates import of germplasm as per the existing procedure for research or experimental purposes. In the present scenario, where the access to germplasm is restricted due to many national and international Treaties/Acts, it is important to search for and introduce on priority trait-specific germplasm for use in various crop breeding programmes. NBPGR continues to work towards identifying promising trait-specific germplasm through literature search and personal contacts and introduce the same for utilization by Indian plant breeders in various crop improvement programmes enhancing yield parameters, incorporating resistance/ tolerance to various biotic and abiotic stresses and value addition.

Key Words: Germplasm, Traits, Exotic, Introduction

Plant Genetic Resources (PGR) are the genetic material of plants which are of value for present and future generations of human kind. Often used as a synonym to plant germplasm it can be defined as seed, a plant or plant part including cell cultures, genes and DNA sequences that are held in a repository or collected from wild as the case may be and that is useful in crop breeding, research or conservation because of genetic attributes. Term 'germplasm' is used to describe a collection of genetic resource for an organism or genetic material which forms the physical basis of inherited qualities.

Exchange of plant genetic resources plays a vital role in crop improvement programmes world wide. They are the heritage to be conserved for current and future generations and to be utilised for the food and nutritional security of the ever increasing world population. Germplasm introduction has played a pivotal role in the establishment of large number of crops and development of improved varieties in India. Apprehensions on restricted exchange were raised with the inclusion of Intellectual Property Rights in Trade Related aspects of Intellectual Property Rights (TRIPS) section of World Trade Organization (WTO) and other International agreements and conventions which entered into force. To regulate access to the germplasm and to ensure that it is used legally, exchange is done under Material Transfer Agreements (MTAs). The MTA defines the terms and conditions which are binding on the parties signatory to it.

As per the existing procedure for import of germplasm for research or experimental purposes, the Government of India by enacting the New Seed Development Policy (1989) and Plant Quarantine (Regulation of Import into India) Order 2003, has made it obligatory for all plant breeders and researchers intending to import seed/planting materials, to fulfill the two mandatory requirements, first, the import permit (IP) before import of any material and second, the phytosanitary certificate from the country of origin. These two documents must accompany every consignment of seed/planting material imported from abroad for research purposes.

The applicant desirous of importing seed/planting material for research/experimental purposes has to apply to the Director, National Bureau of Plant Genetic Resources, New Delhi on a prescribed application form (PQ 08), can be downloaded from NBPGR website *www.nbpgr.ernet.in*. Along with the application form a demand draft of Rs. 150/- (for Govt./public organizations) or Rs 300/- (for private organization/seed companies) as service charges, as the case may be, in favour of Director, NBPGR, New Delhi, as processing fee for the issuance of IP should be sent.

Phytosanitary certificate is a document regarding the health status of consignment being imported, is issued by the official agency of the donor country. It is also issued by the NBPGR for all germplasm material meant for export to foreign countries. It should also be ensured that the consignment must be addressed to the Director, NBPGR. For all imported material, the port of entry is New Delhi. The material so introduced shall after quarantine clearance is assigned an Exotic Collection (EC) number which remains unchanged and then material is forwarded to the recipient.

A part of such sample (~10%) is deposited to National Genebank as voucher sample which is subsequently sent to appropriate NAGS for multiplication. The multiplied seed in sufficient quantity is returned back for long-term storage to serve as base collection. 90% of the material introduced through literature search is sent to NAGS. In the year 2008, a total of 666 import permits were issued to public and private organisations for import of germplasm for research purposes. Of the total import permits issued, 36% belonged to private seed companies/sector and 64% to public organizations/institutes. Of the public sector, 53% were issued to applicants from NBPGR, 23% to other ICAR institutes, 15% to SAUs, 4% to ICRISAT and 5% to other Govt. organizations.

In the present scenario, it is more important to search for trait-specific germplasm and access them from various sources. During 2008, the Bureau introduced 25,450 accessions from 43 countries which included trait-specific germplasm in crops, namely, wheat, barley, rice, maize, sunflower, tomato, chilli, strawberry and avocado. However, the major per cent of germplasm (56%) was imported from IARC's and 8% from USDA. National gene banks/ other institutes accounted for 36% of the total import. The trait-specific germplasm and wild species introduced during 2008 are given in Table 1 and 2, respectively. A total of 286 accessions of transgenic seed material were also introduced (Table 3).

Table 1. Trait-specific germplasm introduced during 2008

Crop/EC No./Country	Specific Traits	Distribution
Triticum aestivum EC633778-784, ICARDA, Syria	PBW343 new version lines carrying genes resistant to Ug 99 and yellow rust	DWR, Karnal, Haryana
T. aestivum EC634055, USA	Variety Guymon resistant to wheat *Soil borne mosaic virus* and *Spindle streak mosaic virus*	DWR, Karnal, Haryana
T. aestivum EC631734, USA	Translocation line carrying a segment of chromosome 5, including softness genes *Pin a & Pin b*	DWR, Karnal, Haryana
T. aestivum EC631987-002, USA	Isogenic hard wheat lines differing for the presence of high grain protein gene GPC-B1	DWR, Karnal, Haryana
T. aestivum EC632017, USA	Germplasm resistant to biotypes 1 & 2 of Russian wheat aphid, semi dwarf, early maturing	DWR, Karnal, Haryana
T. turgidum EC631967-986, USA	Near isogenic hard spring lines differing in puroindoline alleles, controlling grain hardiness, useful to study the basis for texture & quality differences in hard wheat	DWR, Karnal, Haryana
T. turgidum EC631987-632002 USA	Isogenic lines differing for presence of high grain protein gene Gpc B 1. May serve as a source of increased grain protein for hard red, white spring wheat breeding program and provide material to investigate the effect of Gpc B1 in high protein background	DWR, Karnal, Haryana
T. turgidum ssp *turgidum* EC633777, Canada	Adapted to drier regions, source of resistance to races of loose smut	DWR, Karnal, Haryana
H. vulgare EC631731, USA	Variety Lentah-superior yield & test weight, most widely used as green feed	IGFRI, Jhansi, UP
H. vulgare EC631732, USA	Variety Clearwater-hull less, low phytate and high available (CV 335) phosphorus concentrations in the grain, superior feed quality	IGFRI, Jhansi, UP
H. vulgare EC631946, USA	Variety Tetonia-high yielding, resistance to spot blotch & net blotch	DWR, Karnal, Haryana
H. vulgare EC634221-27, USA	Lines resistance to Russian wheat aphid, each line has a different source of resistance in malting barley cultivar backgrounds	DWR, Karnal, Haryana
Oryza sativa EC634219-20, USA	Mutant germplasm lines having improved resistance to sheath blight, bacterial panicle blight & narrow brown leaf spot	DRR, Hyderabad, AP
Zea mays EC633803, USA	Resistance to western corn rootworm	DMR, New Delhi
Helianthus annuus EC634078-80, USA	Source of resistance to races of loose smut	DOR, Hyderabad, AP
Lens culinaris EC631332, Turkey	High yielding and high level of winter hardiness	IIPR, Kanpur, UP
Capsicum annuum EC611331-611364, Taiwan	Tolerant to aphids	IIHR, Bangalore, Karnataka
Capsicum annuum EC612322, Vietnam	Very hot, 55-60 days maturity, extremely prolific, tolerant to *Phytophthora*, TMV & bacterial wilt	IIVR, Varanasi, UP

Table 1. Contd.

Table 1. Contd.

Crop/EC No./Country	Specific Traits	Distribution
Capsicum annuum EC628891-920 EC631683-687, Taiwan	Lines resistant to *Chili veinal mottled virus*, *Poty virus* Y and bacterial wilt	BCKV, Kalyani, WB
Cucumis melo EC612132, Vietnam	Arkanga hybrid melon variety, fruits have a netted skin, light green crispy flesh, strong tolerance to *Fusarium* blight strains 0 & 1	IARI, New Delhi; IIVR, Varanasi, UP
C. melo EC612133, Vietnam	Very vigorous hybrid variety Alien tolerant to both powdery and downy mildew, prolific, medium early, can be harvested within 40-45 days weighing about 1.2-1.3 kg/fruit, green flesh, juicy and sweet	IARI, New Delhi; IIVR, Varanasi, UP
C. melo EC612134, Vietnam	Yellow skinned with oblong shape and cream coloured flesh, weight approximately 2.5 kg/fruit	IARI, New Delhi; IIVR, Varanasi, UP
L. sativa EC612126, Vietnam	Variety Minetto–crisp headed, iceberg type medium small size, black seeded variety, resistant to heat and humidity, tolerant to tip burn	IARI, New Delhi; IIVR, Varanasi, UP
L. sativa EC612127, Vietnam	Fast fall amid early variety, black seeded, loose leaf type	IARI, New Delhi; IIVR, Varanasi, UP
L. sativa EC612128, Vietnam	Butter head type major variety for heavy lettuce production, recommended for winter and autumn production in temperate areas and tolerant to *Bremia*	IARI, New Delhi; IIVR, Varanasi, UP
L. esculentum EC631955-963, Taiwan	Resistant to root knot nematode	PAU, Ludhiana, Punjab
L. esculentum EC632003-21, Taiwan	Lines tolerant to bacterial wilt, *Tomato mosaic virus, Fusarium* wilt and gray leaf spot	College of Agriculture, Dharwad, Karnataka
L. esculentum EC635523-27, Taiwan	Resistance to *Tomato leaf curl virus*	College of Horticulture, KAU Kerala
L. esculentum EC635528-33, Taiwan	Resistant to bacterial wilt	College of Horticulture, KAU, Kerala
L. esculentum EC612858-869, Taiwan	Lines resistant to bacterial wilt, *Tomato mosaic virus, Fusarium* wilt and gray leaf spot	M/S Metahelix Life Sciences, Bangalore, Karnataka
L. esculentum EC614997-615029, Taiwan	Resistant to whitefly transmitted geminivirus, bacterial wilt, *Tomato mosaic virus*	M/S Krishi Dhan, Vegetable seeds, Pune, MS
L. esculentum EC611883-891, Taiwan	Heat tolerant lines	TNAU, Periyakulam, TN
Fragaria vesca EC619154-56, USA	Varieties Lamour, Clancy, Seneca–excellent fruit quality and flavour, firm flesh and good texture	M/s MAHYCO, N Delhi
Malus domestica EC612824-25, USA	Resistant to fire blight	NBPGR, RS Shimla, HP
M. sieversii EC612822-23, USA	Resistant to apple scab	NBPGR, RS Shimla, HP
Persea americana EC632072, USA	Variety Pollock with low oil, early type, very large fruits weighing 750 g	CHES, Chettalli
P. americana EC632073, USA	Variety Pinkerton with long pear shaped fruits, excellent peeling characteristics	CHES, Chettalli
Deschampsia antarctica EC631954, Chile	Antarctic hair grass–new crop, native to Antarctica	M/S Avesthagen Limited, Bangalore, Karnataka
Chicorium intybus EC612129, Vietnam	Variety Scarole–giant voluminous heads with white compact heart, slow bolting and good tolerance to tip burn & bolting	IARI, New Delhi; IIVR, Varanasi, UP
C. intybus EC612130, Vietnam	Variety Frisee–green suitable for spring production, performs well both in open fields and protected cropping and tolerant to bolting	IARI, New Delhi; IIVR, Varanasi, UP
C. intybus EC612131, Vietnam	Variety Grosse bouclee–large broad leaves, escarole endive tight and very well filled with curled heart, suitable for spring and summer production in temperate areas, used for both fresh markets and salad packs, good resistance to bolting	IARI, New Delhi; IIVR, Varanasi, UP

Germplasm Exchange Unit at NBPGR is continuously making all efforts for introducing diverse plant genetic resources by way of bibliography screening of various journals/ periodicals, reports, catalogues, index seminums and online databases. The widely searched websites are detailed at the end for reference.

Access to germplasm and information under the new regime in India has to take into account the established

Table 2. Wild species introduced (47 species; 15 genera)

Genus (Country)	Species	Distribution
Acacia (Australia)	*A. ampliceps, A. salicina, A. sternophylla*	CSSRI, Karnal
Aegilops (USA)	*A. geniculata, A. kotschyii, A. longissima, A. pergegrina, A. speltoides, A. tauschii*	DWR, Karnal
Arachis (USA)	*A. paraguirenies*	ICRISAT, Patancheru
Capsicum (Taiwan)	*C. pubescens, C. praetocox, C. chacoense, C. chinensis*	IIHR, Bangalore
Fragaria (USA)	*F. vesca*	Mahyco, New Delhi
Geranium (Denmark)	*G. cinereum, G. platopetalum*	HPAU, Palampur
Helianthus (USA)	*H. anomalus, H. bolanderi, H. deserticola, H. giganteus, H. debilis-silvestris, H. debilis, H. cucumeri, H. neglectus, H.resinous, H. strumosum*	DOR, Hyderabad
Lens (Syria)	*L. lamottei, L. nigricans*	HPAU, Palampur
Malus (USA)	*M. sieversii*	NBPGR RS, Shimla
Nicotiana (USA)	*N. africana, N. alata, N. suavensis*	CTRI, Rajahmundry
Oryza (Philippines)	*O. glaberrima, O. latifolia, O. minuta, O. nivara, O. punctata, O. rufipogon*	ADAC &RI, Navalurkuttapu, Trichy
Solanum (Spain)	*S. berthauii, S. quitoense, S. vernei*	NBPGR RS, Shimla; CPRI, Shimla
Triticum (USA)	*T. shaerococcum, T. turgidum*	DWR, Karnal
Vicia (Syria)	*V. dasycarpa, V. narbonensis*	AVRDC-RCSA, Patancheru
Vitis (USA)	*V. mustangensis*	NRC Grapes, Pune

Table 3. Details of transgenic seed material introduced

Crop/EC No./Country	Specific traits	Distribution
Oryza sativa EC611943-612003, Belgium	Transgenic rice containing *Cry Ab, Cry 1c* and BAR genes	M/s Bayer Biosciences Pvt. Ltd., New Delhi
O. sativa EC626367-398, Belgium	Containing *Cry 1 Ab, Cry 1Ac* and BAR genes	M/s Bayer Biosciences Pvt. Ltd., New Delhi
O. sativa EC630492-494, China	Expressing *Cry 2A, Cry 1c* & *Cry 1Ac* genes for imparting resistance against rice stem borer & rice leaf folder	Pioneer Overseas Corp., Hyderabad
O. sativa EC630495-96, Philippines	Containing *ferritin* gene, insect and pest tolerance	RRS, Chinsurah, West Bengal
Zea mays EC613093-97, USA	Inbred lines with Bt corn (MON 89034) namely LT2001-LT2005	M/s Monsanto India Ltd, New Delhi
Z. mays EC618165, Philippines	Modified *MEPSPS* gene from corn imparting tolerance to Glyphosate (GAZI)	M/s Syngenta India Ltd., Pune
Z. mays EC626511-515, USA	Transformed with 6 plasmid vectors containing *GUS* reporter gene & different promoters from corn	Dupont India Pvt. Ltd., Hyderabad
Z. mays EC628300, USA	Transgenic stalk corn Hybrids Hishell (MON 89034X NK603)	M/s Monsanto India Ltd., New Delhi
Z. mays EC633153-157, USA	Containing *Cry 1F* and *PAT* gene conferring resistance to lepidopteran pest & tolerant to herbicide Glufosinate ammonium	Dow Agro Sciences, Mumbai
Z. mays EC633163-66, USA	Containing *Cry 1F* & *Cry 1Ab* gene	UAS, Bangalore
Gossypium hirsutum EC617735-84, USA	Containing Roundup Ready (RR) Flex Glyphosate resistant trait (RPF CPUEPSPS) event 88913	M/s Emergent Genetics India Pvt. Ltd. C/o Monsanto India Ltd,, Hyderabad
G. hirsutum EC617785-834, USA	Bollgard II, insect resistant (*Cry 1Ac* & *Cry 2Ab* gene)	M/s Emergent Genetics India Pvt. Ltd. C/o Monsanto India Ltd,, Hyderabad
G. hirsutum EC618167, USA	Containing *2 MEPSPS* gene	M/s Bayer Biosciences Pvt Ltd., Hyderabad
G. hirsutum EC618168-70, USA	Lines H1318, H1010 and H1352 containing combination bar gene, *Cry 1Ab* & *Cry 2Ac* gene	M/s Bayer Bio Sciences Pvt. Ltd., New Delhi

institutional mechanism and various Acts in force relating to agro-biodiversity. The requests of indentor are to be dealt depending on the status of requesting party and the conditions for access under different categories. The NBPGR is continuing its efforts to identify promising trait-specific germplasm through literature search and personal contacts and introduce the same for utilization by Indian plant breeders.

Recipients of the imported germplasm are requested to provide feedback information on the germplasm supplied to help keep up continued reciprocal exchange of germplasm with foreign sources. Such feed back information would help in effective introductions and further help in studies relating to the performance of imported material under Indian agro-climatic conditions.

Online Databases used for Search

- http://www.ars-grin.gov/npgs/searchgrin.html
- http://www.bioversityinternational.org/nc/scientific_information/information_sources/germplasm_databases/list_of_germplasm_databases.html
- http://eurisco.ecpgr.org
- http://www.ngb.se/Material/
- http://www.ngb.se/sadc/Material/accsadc.html
- http://www.singer.cgiar.org/

Estimation of Genetic Divergence in the Seedling Trees of Pecan Nut (*Carya illinoensis* Koch.)

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Genetic variability, heritability, genetic gain, GCV, PCV and correlation studies were carried out in 18 genotypes of pecan (*Carya illinoensis* Koch.). The maximum range was observed in traits kernel percentage (40.20-63.46 %) and minimum range was recorded in traits shell thickness (0.53-1.26 mm). The coefficient of variance for different traits varied from minimum (6.74) in nut width to maximum (34.97) in shell thickness. High heritability was found for traits nut length (98.7), nut weight (97.68), nut width (95.51), nut height (95.00) and kernel percentage (92.41). High GCV (44.49) was exhibited by kernel weight, nut weight (43.84) and moderate for nut length (29.23) and kernel percentage (24.21), PCV was estimated highest for kernel weight (52.74), nut weight (44.36) and moderate for nut length (29.45) and kernel percentage (25.18). The traits shell thickness and nut width exhibited low GCV (0.73) and PCV (12.97) respectively. The nut weight was positively correlated with the nut length, nut width, kernel weight, shell thickness and shell weight, whereas it had negative correlation with the kernel percentage.

Key Words: ***Carya illinoensis*, Genetic variability, Heritability, Seedling trees, Correlation coefficient, Pecan nut**

Introduction

Nature has endowed Kashmir valley with many temperate fruit crops. Much work has been done on leading fruit crops but scanty information is available in minor fruits. Among these minor fruits, Pecan nut (*Carya illinoensis* Koch.) is one which belongs to hickories group and is the cultivated species in Juglandacae family. These are grown successfully in areas receiving moderate to high snowfall in winter with moderate hot summers. Jammu and Kashmir, Himachal Pradesh and hills of Uttaranchal are the states where pecan is under sporadic cultivation. In India, almost all the pecan trees are of seedling origin and exhibit considerable variability for various nut, shell and kennel characters. Pecan is monoecious and wind pollinated, which also lead to extreme variation in trees raised through seeds. As such, each seedling tree represent itself as an individual selection. Determination of nature and magnitude of genetic diversity and variability in nut and kennel character is pre-requisite for any breeding programme for bringing further improvement by means of selection. Therefore, selection from wild population has proved to be a useful tool for fruit breeders to estimate the genetic variability. Therefore, an attempt was made to evaluate the seedling origin pecan tree in the Kashmir valley and gather necessary information on the nature and degree of genetic divergence present in seedling tree, which could help to select elite type for direct use as clones for mass multiplication by standardized vegetative techniques or for further improvement through selection and hybridization.

Materials and Methods

The present investigation on genetic variability in pecan nut (*Carya illinoensis* Koch.) was carried out on 18 seedling selections growing at Shalimar Campus of SKUAST-K, Srinagar, Jammu and Kashmir during the year 2007-08, situated at an altitude of 1588 m above mean sea level lying between latitude 35º5´-34º7´ North and longitude 74º5´-74º9´ East. The area falls under typical temperate zone environment conditions. To know the magnitude of variability, mature nuts were collected in the months of October and November. The collected samples were properly dehulled and dried at room temperature and then stored for 20 days. Dried nuts were used to record various nut, shell and kernel metric traits. The data were recorded on the nut length (mm), nut width (mm), nut height (mm) and shell thickness (mm) by using digital Vernier Caliper. Nut weight (g), kernel weight (g) and shell weight (g) were estimated by using highly sophisticated digital balance and kernel percentage was calculated by the method described by Westwood (1993). The data were recorded thrice and pooled data were analyzed statistically for estimation of variability as suggested by Panes and Sukhatme (1985) and genetic divergence was determined by statistical formula given by Johnson *et al.* (1956). Genotypic and phenotypic coefficient of variance was calculated as per the formula suggested by Burton and Devane (1953).

Results and Discussion

The genotypes under the study showed significant difference for all traits indicating wide variability among them (Table 1). The maximum range was observed in traits kernel percentage (40.20-63.46 %) followed by nut length (28.14-53.34 mm), however minimum range was recorded in traits shell thickness (0.53-1.26 mm). The coefficient of variance for different traits varied from minimum (6.74) in nut width to maximum (34.97) in shell thickness. The analysis of variance for all eight traits showed that mean square was highly significant for all parameters. Analysis of variance revealed significant difference among all the traits studied indicating the existence of genetic variability among them. However, absolute variability in different traits did not permit in deciding as to which trait was showing the highest degree of variability. Similar trend of result was reported by Sundouri and Sharma (2005). The traits which had highest per cent contribution in the variability was kernel percentage (37.03%), followed by nut length (27.22%) and least was also contributed by trait shell thickness (0.57%). The traits contributing maximum variability were important for the purpose of fixing priority of parent for hybridization programme. These findings are in confirmation with the finding of Srivastava and Sharma (2006) in apricot and Chaturvedi *et al.* (1980) in grapes.

The magnitude of GCV, PCV, ECV and heritability involved in the expression of various traits are presented in Table 2, which can precisely be used for making comparison between traits of different metric parameters. Maximum magnitude of GCV, PCV and ECV were recorded for trait shell weight. High GCV (44.49) was exhibited by kernel weight, nut weight (43.84) and moderate for nut length (29.23) and kernel percentage (24.21), PCV was estimated highest for kernel weight (52.74), nut weight (44.36) and moderate for nut length (29.45) and kernel percentage (25.18). The traits shell thickness and nut width exhibited low GCV (0.73) and PCV (12.97), respectively. ECV was observed high in kernel weight (28.09) and moderate in kernel percentage (6.94) and nut weight (6.60) whereas low in other traits. From the present study, it is quite apparent that all the traits except kernel weight and shell weight had less pronounced difference between GCV, PCV and ECV and the parameters employing that variability was due to genetic constitution. In general, the magnitude of PCV was greater than GCV denoting that environmental factors influenced their expression. Further the wide difference between GCV and PCV for kernel weight and shell weight depicted that they were prone to environmental fluctuations, whereas, narrow difference between GCV and PCV for rest of the traits revealed that they were relatively stable to environmental variations. GCV, PCV and ECV estimates for various traits and characters in various fruits have also been estimated by authors Panday and Bisht (1998) and Attri *et al.* (1999) in pomegranate and mango, respectively.

High heritability was found for traits nut length (98.7), nut weight (97.68), nut width (95.51), nut height (95.00) and kernel percentage (92.41). High heritability for different traits indicate that large proportion of phenotypic variance has been attributed to genotypic variance and therefore, reliable selection could be made from these traits on the basics of their phenotypic expression rather than genetically constitution. High heritability alone with genetic advance and genetic gain was observed for nut length, nut weight and kernel percentage indicating that the traits were controlled by additive gene effect (Panes, 1957) and it would respond very well to continuous selection, so that considerable improvement of these traits might be possible. Moderate to low heritability, genetic advance and genetic gain for the rest of the traits suggested that these were controlled by non-additive gene effect having low genetically gene action. Panes (1957) suggested that high genetic advance, genetic gain and heritability provides good scope for improvement as

Table 1. Range, mean, coefficient of variance and per cent contribution of different traits in seedling trees of pecan nut

Traits	Range	Mean	S.D.	Coefficient of variance	Per cent contribution
Nut length (mm)	28.14-53.34	37.23	0.73	13.40	27.22
Nut width (mm)	16.43-21.76	18.56	0.29	16.74	13.60
Nut height (mm)	15.51-21.98	18.36	0.38	19.58	13.41
Nut weight (g)	3.09-8.74	5.54	0.21	26.58	4.07
Shell weight (g)	1.64-4.97	2.76	0.14	19.15	2.03
Shell thickness (mm)	0.53-1.26	0.78	0.67	34.97	0.57
Kernel weight (g)	1.33-4.73	2.78	0.14	28.87	2.04
Kernel percentage (%)	40.26-63.46	50.37	2.01	16.93	37.03

Table 2. Estimation of various genetic constrains for different nut traits in pecan

Traits	Nut length	Nut width	Nut height	Nut weight	Kernel weight	Shell thickness	Shell weight	Kernel percentage
GCV	29.23	12.68	15.83	43.84	44.49	0.73	51.69	24.21
PCV	29.45	12.97	16.24	44.36	52.74	21.39	59.21	25.18
ECV	3.41	2.69	3.58	6.60	28.09	22.12	28.89	6.94
Heritability	98.70	95.51	95.00	97.68	71.16	30.03	76.21	92.41
G. Advance	22.27	4.73	5.84	24.98	2.15	0.08	2.58	24.15
G. Gain	59.86	25.48	31.78	89.26	77.31	1.88	92.95	47.94

Table 3. Genotypic and phenotypic correlation coefficient in pecan

Traits		Nut width (mm)	Nut height (mm)	Nut weight (g)	Kernel weight (g)	Shell thickness (mm)	Shell weight (g)	Kernel percentage (%)
Nut length (mm)	G	0.330	0.328	0.845	0.744	0.384	0.380	- 0.059
	P	0.223	0.222	0.769	0.696	0.340	0.365	-0.065
Nut width (mm)	G		0.691	0.545	0.229	0.616	0.682	-0.447
	P		0.611	0.480	0.181	0.579	0.656	-0.509
Nut height (mm)	G			0.608	0.313	0.605	0.711	-0.412
	P			0.529	0.288	0.577	0.661	-0.472
Nut weight (g)	G				0.842	0.457	0.881	-0.81
	P				0.810	0.433	0.839	-0.90
Kernel weight (g)	G					0.147	0.487	0.456
	P					0.123	0.429	0.431
Shell thickness (mm)	G						0.611	-0.497
	P						0.561	-0.508
Shell weight (g)	G							0.528
	P							0.496

such characters are grown by additive gene action. Low genetic gain indicates that the involvement of non-additive gene action and improvement through selection for these characters could be rather ineffective.

Correlation studies are essential in evaluating and brining the improvement for many characters and also to access the impact of selection for one trait on other related one. The extent of variation in the studied traits of pecan was mostly by the inherent genetically constitution which appeared in the phenological form while studying the traits. The genotypic and phenotypic correlation coefficients among all the characters are presented in Table 3. The magnitude of correlation coefficient revealed that the genotypic correlation was higher than those of the corresponding phenotypic correlation coefficient indicating the inherent association among the various traits. The nut weight was positively correlated with the nut length, nut width, kernel weight, shell thickness and shell weight, whereas it had negative correlation with the kernel percentage. Shelling percentage had positive correlation only with kernel weight and shell weight. Kernel weight also had positive correlation with nut length, nut weight but negative correlation with shelling percentage. The weight of nut showed a direct correlation with nut length, nut width and kernel weight, which is the important selection criterion for nut crops. The correlation coefficient exerted by kernel percentage with nut weight has low magnitude. Nut length and nut width showed very high correlation and also with other parameters studied and are in accordance with those obtained by Sharma and Sharma (2001) in walnut and Kaushal and Sharma (2003) in pecan.

From the above study on mean performance and other genetic parameters of different nut traits, it is revealed that nut character, *viz*., nut weight, kernel weight, nut length and nut width were most important traits for selection of genotypes from the wild seedling population of the pecan nut fruit. The other traits such as shell thickness and shell weight are considered as second most important characters for selection in pecan nut. Considerable importance has been attached to correlation study in the crop improvement because it plays key role in the simultaneous selection process of a group of characters for breeders, who are always concerned with the selection of superior genotypes.

The phenotypic characters do not lead to excepted genetic advance mainly due to genotypic × environmental (G×E) interaction as well as due to undesirable association between the component characters at genotypic level. The knowledge of nut weight and its attributing characters are of considerable use towards the selection of superior genotypes.

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Genetic Variability, Heritability and Genetic Advance Studies in Cabbage (*Brassica oleracea* var. *capitata* L.)

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Genetic variability, heritability and genetic advance were estimated for marketable and its component yield traits in 29 lines of cabbage (*Brassica oleracea* var. *capitata* L.). The study showed high ranges for marketable yield (122.00-363.00), marketable head (75.00-99.00) and days to marketable maturity (69.67-112.00). The highest estimates of PCV and GCV were for marketable yield (PCV= 32.08, GCV= 29.95) followed by net weight of head (PCV= 30.42, GCV= 27.05) and gross weight per plant (PCV= 28.79, GCV= 26.17) and low for harvest index (PCV= 12.53, GCV= 10.73) followed days to marketable maturity (PCV= 11.99, GCV= 9.20) and marketable head (PCV= 9.37, GCV= 3.41). Narrow differences between PCV and GCV, gave evidence to the lines that the variability existing in them was mainly due to their genetic make up. High heritability was noticed for shape of head (93.1%) followed by compactness of head (92.00%), marketable yield (87.2%), and gross weight per plant (82.5). Number of non-wrapper leaves, harvest index, marketable head and length of stalk showed moderate heritability estimates. Days to marketable maturity showed low heritability estimates (49.2%). High heritability in broad sense indicated that large proportion of phenotypic variance was attributable to the genotypic variance and were less influenced by the environment. High genetic advance was observed for marketable yield (58.00), whereas it was low for days to marketable maturity (14.53), marketable head (2.56), length of stalk (15.00) and harvest index (19.00) and indicates that these traits are likely to respond better to selection.

Key Words: Cabbage, Genetic variability, Heritability, Genetic advance

Introduction

Cabbage (*Brassica oleracea* var. *capitata* L.), a member of Brassicaceae, is one of the most important vegetables in the world. It occupies the pride place among the cole crops due to its delicious taste, flavour and nutritive value. Modern compact head cabbage cultivars are descended from wild, non-heading types originating in east Mediterranean and Asia minor. Cabbage is being grown throughout the world and the leading countries are China, India, Russia, Korea, Japan and the USA. In India, it is next only to cauliflower with acreage and production statistics of 240 thousand ha and 43,000 thousand metric tonnes, respectively. Inspite of its economic importance only a limited research on varietal development has been carried out in India on account of crossing work and seed production possible in the high hills only. Of late, breeding and seed production have also been possible in the mid hills and north Indian plains due to the availability of tropical germplasm. There is a wide scope to develop high yielding varieties for seed production in mid and high hills. Estimation of genetic variability in the germplasm of a particular crop is prerequisite for making any effective breeding programme. Selection of parents to be included in the hybridization programme should be based on genetic distance. Most of the important characters including marketable yield are highly influenced by environment, since they are polygenically controlled. This makes the selection process difficult. Therefore, knowledge of heritability for different component traits were essential for any crop improvement programme, because the heritable component is the consequence of genotype and is inherited from generation to generation (Wright, 1921). Estimation of genetic advance together with heritability would be helpful in assessing the nature of gene action. Genetic coefficient of variation together with heritability estimates gives reliable indication of the amounts of the extent of improvement accepted from selection and further remarked that accepted genetic gain under particular system, which provides a true practical information needed by a breeder. Hence, an investigation was carried out for estimating genetic variability, heritability and genetic advance among marketable and its component yield traits in 29 lines of cabbage.

Materials and Methods

The present investigations were carried out at the Experimental Farm of Hill Agricultural Research and Extension Centre, Bajaura, Kullu, Himachal Pradesh with 29 diverse lines of cabbage obtained from different sources. The details of genetic stocks studied are given in Table1. The seeds of all diverse lines were sown on 15 cm raised seedbeds in nursery and the seedlings were transplanted in the main plot after one month. Plot size was 1.8 m x

Table 1. Diverse lines of cabbage and their sources under study

Lines	Sources
EC481002	Horticultural Research International, Wellsborne, UK
EC481006	-do-
EC481007	-do-
EC481015	-do-
EC481016	-do-
EC481019	-do-
EC481022	-do-
EC481030	-do-
EC481031	-do-
EC481035	-do-
EC481039	-do-
EC481040	-do-
EC481045	-do-
EC481055	-do-
EC481056	-do-
EC481058	-do-
EC481060	-do-
EC481067	-do-
Glory	IARI, Katrain
KGAT-l	CSK HPKV, Palampur
KGAT-ll	-do-
KGAT-lll	-do-
First of June	IARI, Katrain
Early Ball Head	-do-
Avon Crest	-do-
Pusa Mukta	-do-
AC-208	-do-
India Market	-do-
Golden Acre	-do-

2.25 m having 20 plants spaced at 45 cm x 45 cm. Gap filling was restored, wherever needed to ensure uniformity. The experiment was laid out in a randomized block design with three replications. Uniform cultural operations were followed as per the recommended package of practices. Observations on the characters, namely, marketable yield (q/ha), marketable head (%), net weight of head (kg), gross weight per plant (kg), compactness of head, shape of head, number of non-wrapper leaves, length of stalk (cm), days to marketable maturity and harvest index in each replication were recorded. Except days to marketable maturity, marketable head (%) and marketable yield, the observations were recorded on 10 randomly selected plants in each plot. In the process of random labeling the border plants were avoided. Phenotypic and genotypic coefficients of variations were estimated according to Burton and Devane (1953). Heritability in broad sense was calculated as per formula given by Burton and Devane (1953) and Allard (1960). The expected genetic advance resulting from the selection of 5% superior individuals were worked out as suggested by Burton and Devane (1953) and Johnson *et al.* (1955). Genetic gain expressed as per cent of population mean was calculated by the method given by Johnson *et al.* (1955).

Results and Discussion

The estimates of genetic parameters of variability, *viz.,* phenotypic and genotypic coefficient of variation (PCV and GCV) along with heritability in broad sense (h^2) and genetic advance (GA) as percentage of mean for different characters are given in Table 2. The data revealed that there were significant differences among lines for various component traits. High ranges for marketable yield (122.00-363.00), marketable head (75.00-99.00) and days to marketable maturity (69.67-112.00) were observed. The higher phenotypic coefficient of variation than those of genotypic coefficient of variation indicated the predominant role of environment in the expression of the traits, which is in consonance with the result obtained by Yadav (1998).

The estimates of PCV and GCV were high for marketable yield (PCV=32.08, GCV=29.95) followed by net weight of head (PCV=30.42, GCV=27.05) and gross weight per plant (PCV= 28.79, GCV= 26.17), whereas low for harvest index (PCV=12.53, GCV=10.73) followed days to marketable maturity (PCV= 11.99, GCV=9.20) and marketable head (PCV=9.37, GCV=3.41). These results were in broad conformity to those of earlier researchers (Swarup and Sharma, 1965; and More and Wallace, 1987) although moderate to high estimates of means, PCV and GCV for marketable yield, gross weight per plant, net weight of head, number of non-wrapper leaves and days to marketable maturity have been reported by them. The low estimates of marketable head, net weight head, gross weight per plant, compactness head harvest index and number of non-wrapper leaves indicated that the cultivars of cabbage included in the present study possessed less genetic variability for these characters. Narrow differences between PCV and GCV, gave evidence to the lines that the variability existing in them was mainly due to their genetic make up.

Heritability is useful in predicting the expected progress to be achieved through selection (Burton and Devane, 1953; Johnson *et al.,* 1955). In the present study, the highest heritability was noticed for the shape of head (93.1%) followed by compactness of head (92.00 %), marketable yield (87.2 %), and gross weight per plant (82.5). All these traits exhibited more than 80% heritability (Table 2). Number of non-wrapper leaves, harvest index, marketable head and length of stalk showed moderate

Table 2. Mean, range, coefficient of variation, heritability and genetic advance for various marketable and yield components in cabbage

Traits	Mean	Range	PCV	GCV	h^2	GA
Marketable yield	203.59	122.00-363.00	32.08	29.95	87.2	58.00
Marketable head (%)	90.43	75.00-99.00	9.37	3.41	13.2	2.56
Net weight of head	0.46	0.27-0.77	30.42	27.05	78.8	50.00
Gross weight per plant	0.77	0.52-1.36	28.79	26.17	82.5	50.00
Compactness of head	38.65	19.13-60.43	27.13	26.03	92.00	51.43
Shape of head	1.01	0.75-1.32	14.52	14.10	94.2	28.00
Number of non-wrapper leaves	13.94	10.27-19.50	16.02	14.28	79.4	26.25
Length of stalk	11.80	10.40-17.60	13.78	9.95	52.2	15.00
Harvest index	55.92	45.24-66.74	12.53	10.73	73.3	19.00

heritability estimates. Days to marketable maturity showed low heritability estimates (49.2%). High heritability in broad sense indicated that large proportion of phenotypic variance was attributable to the genotypic variance and that these character differences among the genotypes were real and showed that the above mentioned traits with high heritability values were less influenced by the environment. High heritability for marketable yield and gross weight of head have been estimated earlier by Lal and Solanki (1975) and More and Wallace (1987), shape of head by Swarup and Sharma (1965) and compactness of head Flory and Walker (1940) and More and Wallace (1987).

Johnson *et al.* (1955) stressed that for estimating the real effects of selection, heritability alone is not sufficient and genetic advance along with heritability is more useful. High genetic advance was observed for marketable yield (58.00), whereas it was low for days to marketable maturity (14.53), marketable head (2.56), length of stalk (15.00) and harvest index (19.00) which is in broad conformity to the findings of earlier researchers (Swarup and Sharma, 1965; Lal and Solanki, 1975; Flory and Walker 1940). Moderate to high genetic advance for net weight of head (Bhagchandani *et al.,* 1977; More and Wallace, 1987), gross weight per plant; compactness of head, number of non-wrapper leaves and shape of head reported by (Swarup and Sharma, 1965; Lal and Solanki, 1975), which was slightly variance with the present findings. High heritability along with moderate genetic advance was observed for shape of head (28.00), compactness of head (51.43), net weight of head (50.00), gross weight per plant (50.00) and number of non-wrapper leaves (26.25), these findings were at variance with those of Swarup and Sharma (1965) and Lal and Solanki (1975), who reported high heritability associated with low genetic advance. High heritability along with moderate genetic advance for these traits may be attributed to the additive gene action linked with non-additive effects and these may be improved through selection followed by hybridization.

However, high heritability associated with high genetic advance was observed for marketable yield in conformity with the findings of (Swarup and Sharma, 1965). High heritability coupled with high genetic advances in marketable yield indicates that this trait is likely to respond better to selection. Length of stalk along with harvest index had moderate heritability associated with low genetic advance and these findings were variance with those of More and Wallace (1987), who reported high heritability associated with moderate genetic advance.

Moderate heritability with low genetic advance was observed for marketable head (2.56) which is in contrast to the findings of Swarup and Sharma (1965) who reported low heritability coupled with low genetic advance for this trait. Low heritability in combination with low genetic advance was observed for days to marketable maturity (14.53), which varies with the findings of Swarup and Sharma (1965), who reported high heritability with high genetic advance for this trait. Characters with low heritability coupled with low genetic advance are more under the influence of non-additive gene action and environment and do not respond to selection.

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Correlation and Path Coefficient Analysis in Wheat

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To understand the association of yield and yield attributes and their contribution to each other, 179 genotypes including four check varieties were evaluated in an Augmented Block Design with 18 blocks. Each block (excepting one block) contained 10 test genotypes and 4 check genotypes. The data on five random selected plants of each genotype were recorded on 14 quantitative characters, including grain yield and its component characters. The phenotypic coefficient of variation was high for most of the characters, especially, the biological yield per plant, tillers per plant, plant height and grain yield. Correlation coefficient analysis revealed that nine characters namely, biological yield per plant, tiller number per plant, grain weight per ear, grains per ear, harvest index, spikelets per spike, plant height, flag leaf area and flag leaf sheath length showed significant and positive correlation with grain yield. Path coefficient analyses revealed that biological yield followed by harvest index and grains per ear were the only traits that showed highest positive direct effects towards grain yield.

Key Words: Character association, Path coefficient analysis, Grain yield, Wheat

Introduction

Among the cereals which have played a significant role in the evolution of human civilization, wheat (*Triticum aestivum*) is an important food crop and a source of almost 20 per cent of total calories of the world population. Grain yield in wheat is a complex character affected directly or indirectly by every gene present in plant (Waqas *et al*., 2005). Genotypic and phenotypic correlations indicate the degree to which various morpho-physiological characters are associated with economic productivity (Alam *et al*., 1992). Expression of complex trait yield is dependent upon the inter-relationship of its component traits. The selection programme for high yield requires not only the understanding and knowledge of the variability present in the germplasm of the crop, but also the association and contribution of various plant attributes towards grain yield. Therefore, in the present investigation we have shortlisted important traits which have strong association with grain yield. Grafius (1969) and Singh *et al*. (1997) emphasized the need to base the selection for yield on principal components which have a very strong association. Most of the traits of economic importance were quantitative characters whose expression is conditioned by the polygenes. Such traits are analyzed and studied using the biometrical approaches. In view of this, correlation and path coefficient analyses on a large number of wheat genotypes representing considerable genetic variability was done.

Materials and Methods

One-hundred-seventy-nine wheat genotypes of Indian and exotic origin including four check varieties namely, UP 2425, PBW343, HD 2687 and PBW435 were evaluated in an Augmented Block Design at Ch. Charan Singh University, Meerut during rabi season. Each genotype was planted in a row plot of 3 m each. Recommended cultural practices were followed to raise a good crop of wheat. Five randomly selected plants were used to record. The material was evaluated in an Augmented Block Design with 18 blocks, each block (excepting one block) was assigned 10 test genotypes selected randomly and four check varieties. Each genotype in a block, whether test or check, was assigned at random to a single row plot of 2 m length. Line to line and plant distance was kept at 30 cm and 10 cm, respectively.

Results and Discussion

The analysis of variance for fourteen quantitative characters is presented in Table 1. The mean squares due to checks for all the 14 characters studied were highly significant except biological yield per plant and grain yield per plant. Suggesting the presence of considerable variability for different characters among the wheat accessions under investigation. However, the mean squares due to block were non-significant for most of the traits except the four traits. Nevertheless, the genotype means were adjusted for block effects to remove to effect of soil heterogeneity. The estimates of phenotypic coefficients of correlation among the 14 characters are presented in Table 2. The correlation coefficient were calculated for all possible pairs of 14 characters giving rise to a total 91 pairs of characters. Of the total 91 pairs of characters,

Table 1. Analysis of variance for 14 quantitative characters of four check varieties evaluated in eighteen blocks in an Augmented Block Design

		Characters													
Source	d.f.	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Checks	3	429.74**	35.32**	470.15**	279.69	24.74**	29.74**	10.12**	14.64**	119.14	3.07	157.52*	0.37	3.06**	356.63
Block	17	16.92	0.73	61.03	7.47	1.14	1.78	4.23*	3.59	70.54	13.81	93.95**	0.21	0.43*	252.64*
Error	51	14.58	0.60	90.51	6.49	0.71	1.23	2.11	2.66	49.23	14.34	39.45	0.73	0.23	117.98

*,** : Significant at 5% and 1% levels, respectively.

only 45 combinations of characters, the correlation coefficients were not statistically significant, suggesting that such characters are not associated and selection for one trait will not effect the performance of other traits. Therefore, only the correlation coefficients among 46 paired combinations of characters are important to be interpreted. Out of the significant correlation coefficients, only two combinations biological yield and harvest index, and tiller number and harvest index showed significant negative correlation coefficients. This suggested that there was no corresponding increase in grain yield with increase in biomass and tiller number. All the characters except peduncle length, spike length (excluding and including awns) and 100-grain weight showed significant positive correlation with grain yield. This suggests that increase in the intensity of these characters may bring about increase in grain yield. Similar relationship with grain yield was also reported earlier by Dhonde *et al.* (2000) and Bergale *et al.* (2001). Biological yield per plant, which showed the maximum degree of correlation with grain yield and seems to be the most important trait for improving grain yield, also showed significant positive correlation with tillers per plant, spikelets per spike, plant height, flag leaf sheath length, flag leaf area, grain weight per ear and spike length. This suggested that increase in such characters was responsible for increase in biological yield. Positive association of these characters with biological yield was also reported by Gupta *et al.* (1977), Sharma *et al.* (1998), Singh *et al.* (1998) and Khumkar *et al.* (2001). It may also be important to mention that the phenomenal increase in wheat yield potential during the past few decades is attributed to increase of harvest index (Kulshrestha and Jain, 1982). The general consequence of this progression has been that the modern varieties are high yielding with

Table 2. Estimates of phenotypic correlation coefficient among 14 quantitative characters in wheat

S. No.	Characters	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	Flag leaf area	1.00	0.35**	0.29**	0.16*	0.08	0.20**	0.16*	0.04	0.19*	0.17*	0.10	0.31**	0.30**	0.03
2	Flag leaf sheath length		1.00	0.48**	0.31**	0.21**	0.26**	0.17*	0.05	0.22**	0.15*	0.01	0.10	0.21**	-0.08
3	Plant height			1.00	0.47**	0.29**	0.04	0.16*	0.15*	0.26**	0.20**	0.05	0.03	0.07	-0.06
4	Peduncle length				1.00	0.04	0.13	-0.10	-0.05	-0.06	-0.03	-0.11	0.00	0.30**	0.01
5	Spike length (excluding awns)					1.00	0.18*	0.42**	0.15*	0.16*	0.14	0.25**	0.05	-0.03	-0.09
6	Spike length (including awns)						1.00	0.24**	0.09	0.12	0.12	0.17*	0.14	0.11	-0.04
7	No. of spikelets/ spike							1.00	0.04	0.26**	0.20**	0.43**	0.27**	-0.06	-0.12
8	Effective tillers/plant								1.00	0.67**	0.59**	-0.01	-0.06	-0.11	-0.15*
9	Biological yield/ plant									1.00	0.80**	0.15*	0.17*	0.02	-0.32**
10	Grain yield/plant										1.00	0.24**	0.30**	0.11	0.24**
11	Grains/spike											1.00	0.58**	-0.12	0.04
12	Grain weight /spike												1.00	0.36**	0.23**
13	100-grain weight													1.00	0.12
14	Harvest index														1.00

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

Table 3. Estimates of direct and indirect effects of various quantitative characters on grain yield in wheat. Diagonal (bold) values represent direct effects and the remaining values are indirect effects of the characters

S. No.	characters	1	2	3	4	5	6	7	8	9	10	11	12	13	Correlation with grain yield
1	Flag leaf area	**-0.01**	-0.00	-0.00	0.00	0.00	0.00	-0.00	0.00	0.17	0.01	-0.03	0.02	0.01	0.17*
2	Flag leaf sheath length	-0.00	**-0.02**	-0.02	0.01	0.00	0.00	-0.00	0.00	0.21	0.00	-0.01	0.01	-0.04	0.15*
3	Plant height	-0.00	-0.01	**-0.04**	0.01	0.00	0.00	-0.00	0.00	0.25	0.00	-0.00	0.00	-0.03	0.20**
4	Peduncle length	-0.00	-0.00	-0.02	**0.03**	0.02	0.00	0.00	-0.00	-0.05	-0.01	0.00	0.02	0.00	-0.03
5	Spike length (excluding awns)	-0.00	-0.00	-0.01	0.00	**0.00**	0.00	-0.00	0.00	0.15	0.03	-0.00	-0.00	-0.04	0.14
6	Spike length (including awns)	-0.00	-0.00	-0.00	0.00	0.00	**0.00**	-0.00	0.00	0.11	0.02	-0.01	0.00	-0.02	0.12
7	Spikelets/spike	-0.00	-0.00	-0.00	-0.00	0.01	0.00	**-0.00**	0.00	0.25	0.06	-0.02	-0.00	-0.06	0.20**
8	Effective tillers/plant	-0.00	-0.00	-0.00	-0.00	0.00	0.00	0.00	**0.04**	0.64	-0.00	0.00	-0.00	-0.05	0.59**
9	Biological yield/plant	-0.00	-0.00	-0.01	-0.00	0.00	0.00	-0.00	0.03	**0.96**	0.02	-0.01	0.00	-0.17	0.80**
10	Grains/spike	-0.00	-0.00	-0.00	-0.00	0.00	0.00	-0.00	-0.00	0.14	**0.14**	-0.06	-0.01	0.02	0.24**
11	Grain weight/spike	-0.00	-0.00	-0.00	0.00	0.00	0.00	-0.00	-0.00	0.16	0.08	**-0.10**	0.03	0.13	0.30**
12	100-grain weight	-0.00	-0.00	-0.00	0.01	-0.00	0.00	0.00	-0.00	0.02	-0.01	-0.03	**0.08**	0.06	0.11
13	Harvest index	-0.00	-0.00	0.00	0.00	-0.00	-0.00	0.00	-0.00	-0.30	0.00	-0.02	0.01	**0.55**	0.24**

Residual = 0.0699

shorter straw but have little or no increase in overall biological yield over their fore bearers and further efforts to increase yield potential have not been successful Gill (1979). In wheat, although the physiological limit for harvest index has been set to 60% (Austin *et al.*, 1980) further improvement of present level of 50% harvest index has not been feasible. Therefore, the future improvement in grain yield of wheat can be attained by increasing the dry matter, *i.e.*, biomass or biological yield (Moss and Musgrave, 1971; Narsyrov, 1978) while maintaining the optimum level of harvest index.

The estimates of direct and indirect effects of various characters on grain yield are presented in Table 3. The path coefficient analysis appeared to provide a clue to the contribution of various components of yield to over all grain yield in the genotypes under study. It provides an effective way of finding out direct and indirect sources of correlation. In the present study, nine characters which showed significant and positive correlation with grain yield, only biological yield, harvest index and grains per ear exhibited direct contribution in increasing grain yield. However, the direct effect of biological yield on grain yield was maximum followed by harvest index. The remaining traits such as flag leaf area, flag leaf sheath length, plant height, spikelets per spike, tiller number etc. which had significant positive correlation with grain yield did not show considerable direct effect towards grain yield, instead, they contributed towards, grain yield indirectly via biological yield. In past also, high magnitudes of direct effects of biological yield have been reported by Sidhu *et al.*, 1976 and Sharma *et al.*, 1998.

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Traditional Wheat (*Triticum aestivum* L.) Genetic Resources for Subsistence in District Pauri of Uttarakhand

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Plant genetic resources are the paramount assets for improvement and development of varieties with desirable traits. In order to fulfill the needs of the breeders, the traditional wheat (*Triticum aestivum* L.) genetic resources of district Pauri in Uttarakhand were studied by using random sampling technique during May 2008. Farmer's selections criteria of varieties, seed exchange system and storage methods, which are very important for subsistence needs of the farming communities were also discussed in the light of sustainable development.

Key Words: Traditional wheat, Traditional knowledge, Pauri, Uttarakhand

Introduction

The district Pauri Garhwal has diverse topography that varies from foot hills of the terai of Kotdwar to the soul lifting meadows of Dudhatoli, sprawling at an altitude of 3,000 msl. which remains snow covered during the winter months. The agro climatic conditions of the region are sub-tropical to temperate. Pauri Garhwal is surrounded by districts Almora, Chamoli, Nainital, Bijnor, Haridwar, Dehradun, Rudraprayag and Tehri. Agriculture and allied activities not only provide livelihood to a large population of the region, but play an important role in their socio-economic and cultural development. The impact of the Green Revolution is hardly visible in the hill region of district Pauri. Agriculture is based on the organic matter (farm yard manure), traditional seed varieties and intensive labour by women folk in the region. More than 85 per cent of the agricultural land is rainfed. Irrigation facilities by and large are confined to valley areas (Maikhuri *et al.,* 2004). District Pauri of Uttarakhand is situated in the Central Himalayan region and the Himalayan region is a well known centre of crop diversity (Jain and Sastry, 1978; Arora, 1990; Khoshoo, 1992). Wheat (*Triticum aestivum* L.) is a major winter crop (*rabi*) of the region; mustard, lentil, pea, khesari etc. are also grown as mixed crops in the wheat crop. Agriculture in the region is based on age-old traditional practices based on traditional knowledge. Traditional farming system not only serves to preserve the diversity of local varieties, but also the human knowledge and behaviour practice that have shaped this diversity (Bellon, 1996). Wheat germplasm from International Wheat and Maize Improvement Center (CIMMYT) has been the core of Indian wheat programme. The local germplasm has also played an important role in the breeding, but its relative importance is minute compared to the exotic germplasm (Rajaram *et al.,* 2006). In the hill agro-climatic region, where agriculture is at the vagaries of rain, traditional local germplasm is the only means to sustain agriculture and livelihood. In order to conserve, utilize and know the present status of the local wheat germplasm in the district Pauri of Uttarakhand, the study was carried out to conserve and subsequently utilise the local diversity.

Materials and Methods

Data on traditional wheat cultivars were collected from primary sources by preparing structured and un-structured questionnaires accompanied with interview schedules at individual farm households *rabi* 2007 and 2008. Sample villages were randomly selected from the entire district. The altitudinal gradients from 450 to 2,100 msl were surveyed. All the development blocks of the district Pauri representing district's agro-ecological niches were covered for the study. In each selected village, 5% households were selected for interview. Thus a total of 75 households were selected as respondent farmers for documentation of wheat varieties in vogue in their villages. During the survey of the district, a non-participant observation method was also employed while recording the information.

Using Participatory Rural Appraised (PRA), information was obtained on the erosion and shift in varietal diversity and changes in farming systems. The information on current status was validated by taking observation in the fields for the primitive cultivars diversity under cultivation. Documentation of wheat cultivars being the major crop is presented in this paper in detail. All possible care was taken to ensure the consistency in farmers naming and describing wheat cultivars by comparing information from farm households and different social groups. Information obtained was authenticated from knowledgeable elderly farmers in the villages.

Results and Discussion

The study revealed that more than 85% cultivated area was rainfed and traditional practices were followed for wheat cultivation. Agriculture was based on organic matter (cowdung and litters) and seed material preserved from the previous harvest as inputs. Primitive cultivars of wheat were named by the farmers on the basis of presence of awns on the spike. Two types of wheat cultivars, awnless and awned were identified by the local farming communities. Awnless cultivars were called as *Mundiya* or *Mundri* and awned cultivars were known as *Jhusia* and *Kishaw* in local dialect in the entire Pauri district. The awned cultivars were further categorized in two local types, *i.e*., *Farmi* or *Deshi.* It was observed in the entire study area that all the improved varieties are awned, none of the awnless variety of improved cultivars was found. The erosion of traditional cultivars of wheat was evident in the region, because of the impact of state driven 'Green Revolution' which pushed the High Yielding Varieties (HYVs), chemical fertilizers, pesticides etc. free of cost initially and at highly subsidized rates later on (Maikhuri *et al.,* 2004). In some valleys of Garhwal, 72 to 95% of traditional landraces have been replaced by HYVs (Maikhuri *et al.,* 1996, 1997, 2001). In the present investigation, in district Pauri 31.12% traditional cultivars of wheat were observed to have been replaced by HYVs. A total of 68.88% of wheat cultivation was still dependent on traditional cultivars *Mundiya* (44.44%) and *Jhusia* (24.44%) due to irregular rain (Table 1). Hence, households were forced to cultivate their age-old traditional cultivars to produce atleast some yield. Local farming communities consider traditional cultivars as drought resistant, as these need less water, whereas HYVs were heavily dependent on irrigation water. Some reduction in traditional crops and varieties had also been reported from several other mountain countries like Nepal, Pakistan, Afghanistan, Bhutan, China (Tibet) etc. (Pratap, 1990; Anwar and Bhatti, 1990; Roder and Gurung, 1990; Sanju, 1990; Regmi, 1990; Houpei *et al.,* 1990).

Another way of naming of varieties was based on seed colour such as red and white called as *Lal gehun* and *Safed gehun* respectively. In *Mundiya* cultivars (awnless), three types of seed colours red, amber and white were observed and collected. It is very interesting to note that in *Jhusia* (awned) cultivars only two types of seed colours red and amber were noticed in the region (Table 2). Drought tolerance is also an important feature for selection of varieties particularly in rainfed areas. Farmers have also classified and selected the local cultivars. *Safed mundri* and *Lal mundri* are considered as drought tolerant by the local farmers. Hence, largely grown in rainfed areas of district Pauri Table 1. Yield of the crop is a major criteria of classification of varieties. *Jhusia, Kishav, Churi* and *Farmi* were some of the landraces with good yield potential. In hills, fodder production is also considered very important to feed the live stocks. Farming communities have classified wheat landraces on the basis of biomass (straw) yield. *Safed mundri, Lal mundri* and *Bhuri mundiya* were identified as having good potential for large biomass locally known as *naluwa* quality. Thus, *Mundiya* landraces were suitable for drought as well as biomass production (Table 4). In view of breeding programme amber colour is most preferred, followed by white. But farmers of the region do not bother for colour. Their first and foremost

Table 1. Wheat cultivars grown by the farmers of district Pauri, Uttarakhand

Cultivars name	Percentage wise grown by the farmers	Desirable traits
Mundiya/Mundri (awnless)	44.44	Awnless, drought tolerant, tasty *chapati,* good biomass (straw) yield
Jhusia/Kishaou (awned)	24.44	Good yield and suitable for animal damage prone areas near by forest land
Farmi/Deshi (HYVs)	31.12	Suitable for irrigated areas need more inputs

Table 2. Seed colour variability in various traditional cultivars of wheat grown area in district Pauri, Uttarakhand

Cultivars name	Seed colour (%)			Total
	Red	Amber	White	
Mundiya/Mundri	30.77	23.08	23.08	76.92
Jhusia	19.23	3.85	0.00	23.92
Total	50.00	26.92	23.08	100.00

Table 3. **Mean value of seed length and width of various landraces with various colours in traditional cultivars of wheat in district Pauri, Uttarakhand**

Cultivars name	Red seeded		Amber seeded		White seeded	
	Length (mm)	Width (mm)	Length (mm)	Width (mm)	Length (mm)	Width (mm)
Mundiya/Mundri	5.91	2.97	6.23	3.07	5.72	2.97
Jhusia	5.87	2.89	6.20	3.27	--	--

Table 4. Ranking of various cultivars on the parameters of desirable traits and area under cultivation

Cultivars name	Ranking on parameters					
	Yield	Drought resistant	Taste/good chapati quality	Good biomass (straw) yield	Animal and bird damage control	Area of under cultivation
Mundiya/Mundri (local)	2	1	1	1	3	1
Jhusia local	1	2	2	2	1	2
Farmi/Deshi (HYVs)	3	3	3	3	2	3

preference is assured yield. Among the traditional cultivars 50% were red, 26.92% amber and 23.08% white seeded. Local farm households prefer red-seeded cultivars because of its better taste in comparison to others and some assured yield. Another study conducted in district Almora of Uttarakhand revealed that the *Khuswao* (awned) wheat, which is promoted by government agencies for better yield, needs more water and has undesirable taste. It is reported to give better yield in the first year and not in subsequent years (Tiwari and Das, 1996).

Seed size as evident in Table 3 indicates an interesting trend that the average seed length and width is bigger in amber colour cultivars. Red and white seeded cultivars were almost similar in length and width. Amber seeded were bold in size in both types *Jhusia* (awned) as well as *Mundiya* (awnless) and produced more yield than others. Among various genotypes collected from the study area on the basis of seed size, colour, plant types etc. it was observed that there were 12-15 different genotypes, namely, *Safed mundri, Lal mundri, Churi, Lal kishav, Safed kishav, Jhusia, Chota mundri, Bada mundri, Bhuri mundri* (brown spikes), *Nan mundri* (plant small in height) etc., which are the major traditional wheat landraces under cultivation in district Pauri of Uttarakhand.

Selection Criteria and Seed Exchange System

For selection of wheat varieties some factors considered were assured yield, drought tolerance, good taste, biomass (straw) yield and damage caused by wild animals and birds. Assured crop yield is of paramount importance as considered by the farmers. *Jhusia* (awned) local varieties were ranked first in view of yield potential, followed by *Mundiya/Mundri* and *Farmi/Deshi.* The area in district Pauri is faced with uncertain rain for cultivation of crops. To cope up with such drought conditions people select the drought resistant cultivars. *Mundiya* (awnless) cultivars have been found suitable for this purpose. *Jhusia/Farmi* (HYVs) cultivars were not drought tolerant in the area. A similar study revealed the same trend in district Almora, Uttarakhand (Tiwari and Das, 1996). Taste of *chapati* is also a major consideration for selection of crop varieties *Mundiya* is the most tasty wheat cultivar followed by *Jhusia.* In Central Himalayan region the traditional agro-biodiversity is complex with strong linkage between crop plants, animals and the forest (Palni *et al.,* 1998), hence biomass (straw) yield is considered very important component of crop husbandry and *Mundiya* has been ranked first followed by *Jhusia* and *Farmi/Deshi* (HYVs) types. In the hill region of Uttarakhand, land holdings are scattered over hill slopes, where crop damage by wild animals and birds is inevitable. For protection of crop from wild animals, awned varieties are found very useful. Farmers select the awned varieties for very far-flung and forest surrounded fields. *Mundiya* (awnless) varieties are very prone to loss by animal and birds. After considering all the above criterion of selection, the *Mundiya* (awnless) varieties are ranked first, *Jhusia* (awned) second and *Farmi/Deshi* (HYVs) third in the entire district Pauri of Uttarakhand (Table 4).

At the time of harvest of crop, elderly women, who possessed good knowledge of crop and seed selection, select the healthy completely matured spikes randomly from the entire field and harvest them separately. These harvested bundles are threshed separately and sun dried very carefully. Before storing, they test the seed moisture by crushing them with teeth. By virtue of their age old knowledge of the viability of grains, healthy grains are selected and stored every season, thereby enhancing the genetic potential of the crop to withstand biotic and abiotic stresses (Ravi Shankar and Selvam, 1998). To protect the seed from insects, cow dung or oak wood ash are mixed with seed material before putting them in the storage bins. Sometimes the leaves of Buch (*Acorus calamus*) or Bakayan (*Melia azadirachta*) are also added in seed material. Traditionally, seeds were stored in hollowed gourdshells (*tumari)* when the quantity to be stored is small, in wooden boxes (*bhakar*) or covered bamboo baskets plastered with cow dung when the quantity is large. Tin containers are now replacing the traditional storage vessels.

Seed exchange system is very informal within the village, the most common being between the farmers of the same village. Women also collect the seeds from the parental villages. Seed are also brought from the neighborhood villages, where there are relatives and friends. In lieu of seed material, farmers return the same amount of grains or another variety of the crop they desire. If the farmer fails to return the seed or grains at that time he returns them after next harvest. Farmers selection and management shape the crop genetic diversity. Several studies have documented the flow of seed of different landraces among small farmers. Seed flow of local landraces takes place as farmers exchange seed among themselves with in the same village, purchase seed from or collect it from other farmers or relatives while visiting or traveling (Sperling and Loevingshon, 1993). Seed exchange and storage systems are all managed by the women folk in the entire Pauri district of Uttarakhand.

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SHORT COMMUNICATION

Genetic Variability and Heritability in Cowpea [*Vigna unguiculata* (L.) Walp.]

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The nature and magnitude of genetic variability was studied for grain yield and its related traits in 72 diverse genotypes of cowpea. Considerable amount of genotypic and phenotypic coefficient of variation was observed for all characters. Moderate to high heritability coupled with high genetic advance as per cent of mean and genetic coefficient of variation was observed in respect of plant height, pod length, 100-seed weight, grain yield per plant, number of branches and number of pods per plant indicated that these characters were under control of additive gene or non-environmental effects and could be dependable for grain improvement in cowpea.

Key Words: Genetic variability, Heritability, Cowpea, Yield components

Cowpea [*Vigna unguiculata* (L.)Walp.] is an important grain legume. Its quick growth has made cowpea essential components of sustainable agriculture in marginal lands and dry regions of the tropics, where rainfall is scanty and soils are sandy with little organic matter. If early maturing varieties are grown as pure crop with required inputs, cowpea has potential of yielding as high as cereals on productivity per day basis. To improve grain yield, information on genetic variability for different characters is necessary. Hence, the present study was undertaken to estimate genetic variability, heritability and genetic advance.

The present study was carried out with 72 diverse genotypes of cowpea obtained from different sources. The experiment was conducted at Research Farm of CCS Haryana Agricultural University, Hisar during *Kharif* 1997 in Randomized Block Design with three replications. Each genotypes was planted in 4 m row plot, keeping inter row spacing of 90 cm and intra row spacing of 20 cm. Observations were recorded on five competitive plants from each plot for nine characters (Table 1). The data were statistically analysed to estimate genotypic and phenotypic coefficient of variation (Burton, 1952), heritability (broad sense) by Hanson *et al.* (1956) and genetic advance.

Analysis of variance showed that the genotypes differed significantly among themselves for all the characters under study. The phenotypic coefficients of variation (PCV) were invariably higher than their corresponding genotypic coefficient of variation (GCV) (Table1). The coefficient of variability (%) at PCV and GCV level were high for plant height, 100-seed weight and grain yield per plant. Low differences between PCV and GCV for all the characters except pods per plant, number of branches and yield per plant indicated that these characters were least influenced by environmental fluctuations. Several earlier workers in cowpea are in support of this view. Bapna and Joshi (1973) reported pod number as the maximum contributing trait to the genetic

Table 1. Mean, range, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability and genetic advance (GA) in cowpea

Characters	Range	Mean	GCV (%)	PCV (%)	Heritability (%)	GA
Days to first flower	35.33-57.00	4015	9.59	10.26	87.33	18.46
Days to maturity	62.66-84.00	73.02	8.43	8.91	89.69	16.46
Plant height (cm)	44.30-263.86	104.90	35.28	35.71	97.60	71.81
Number of branches	2.53-6.86	4.56	20.83	24.91	69.94	35.89
Number of pods per plant	12.80-44.33	23.57	23.88	27.98	72.83	41.98
Pod length (mm)	9.40-28.00	14.91	22.46	22.95	95.76	45.29
Seeds per pod	9.30-17.76	12.20	12.03	13.14	83.79	22.69
100-seed weight (g)	6.23-28.60	12.52	35.01	35.58	96.78	70.95
Grain yield per plant (g)	12.97-56.07	25.15	30.23	34.86	75.22	54.03

**Author for Correspondence: Present Address: PPVFR Authority, NASC Complex, New Delhi–110 012* variability. Similarily, Pandita *et al.* (1982) opined that the seed yield had recorded a high genetic variability. In the present study, the least estimate of GCV was recorded for days to maturity followed by days to first flower. Rewale *et al.* (1995) and Thiyagarajan (1990) reported similar results in cowpea. The heritability estimates in broad sense were very high plant height, 100-seed weight, pod length, for days to maturity, days to flower and seed per pod, whereas these estimates were moderate for number of branches, number of pods per plant and grain yield per plant. Similar results were also recorded by earlier workers, *i.e.*, Thiyagarajan (1990) and Siddique and Gupta (1991). Sharma (1999) and Hazra *et al.* (1999) had also reported high genetic advance coupled with high heritability for different traits in cowpea.

High genetic advance accompanied by moderate to high heritability was recorded for plant height, 100-seed weight, yield per plant, pod length, number of pods per plant and number of branches per plant indicated the additive gene action and reliability of these characters during selection for improving seed yield in cowpea.

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SHORT COMMUNICATION

Role of Traditional Crops and Varieties to Mitigate Emerging Climate Change on Agriculture–A Case Study from Bhor Region, Maharashtra

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The biggest sources of biodiversity in tropical countries, the landraces, are threatened due to over exploitation, changing ecosystems and climatic conditions. India has great variation in climate and topography. In the present study, rural people from Bhor region cultivating traditional crops and varieties and their agricultural diversity for mitigating climatic change are presented.

Key Words: Cropland races, Bhor region, Global warming

Agricultural biodiversity in India consists not only of crops such as wheat, rice, bananas (species diversity) but also of immense variation within each of these crops (varietal diversity). India's rice possesses wide diversity in characters. They vary in crop duration from 60 to over 200 days and can grow in varied elevations, ranging from a meter below sea level to an altitude of 2,000 m. Traditional practice was propagated based on the intimate knowledge of the crop varieties and suitable for climatic conditions was prevalent in ancient India followed by the varietals choice (Sarawgi and Rastogi, 2000). In many parts of the country, varieties were and are still chosen for needs, definitely not for the yields alone. They were chosen for their ability to withstand droughts or floods, resistance to pests, susceptibility to disease, toleration of salinity, time of maturity, size of the grains, colour, aroma, taste, keeping qualities, nutritional values etc.

In recent agricultural practices, use of uniform varieties and hybrids, reduces genetic diversity in crop plants and causes them to be more susceptible to biological stresses such as drought, pest and diseases, water consumption etc. Many of these traditional crop varieties have gone out of cultivation and are lost forever. Genetic loss due to climate change appears to be beginning to have a drastic impact on the world's agriculture (Jackson and Lloyd, 1991).

Maharashtra state has rich diversity of traditional crop plants due to variation in soil, climate and choice of local people. Tribal regions are rich in many crops. Kulkarni *et al*. (1998) collected rice germplasm from Mahadeokoli tribe from western Maharashtra. Present paper deals with traditional agriculture in Bhor region of western Maharashtra and documentation of local traditional crops and their usefulness in changing climatic conditions.

Bhor is covering an area of 892.0 sq km and situated 54 km south of Pune and between 18º.45' N latitude and 73º -15' E longitude. Bhor region has 185 villages and total population is 1,54,903. Bhor area has average rainfall 643.5-800 mm from June to September. The mean daily maximum temperature is 38.10°C in summer. In the month of May, maximum temperature may reach to 41.09°C. December is the coldest month and minimum temperature is 8-9°C. The climate of the area is moist during rainy season and moderate in winter and summer season. The hilly area is of basalt rock formation. The soils of the area are alluvial along the banks of river and black cotton soil in eastern part while red and brown soils on western part. During the field visits, total 182 villages were recorded in Bhor region, out of which 60 villages were visited for data collection of traditional crops during the *kharif* and *rabi* season. A specially prepared questionnaire was used and characters like maturity of the crop, drought resistance, suitability of soils, keeping quality, nutritional value, fodder species, etc. were recorded by interviewing local people.

The main occupation of local people is agriculture. Majority of the people are depended on their farm produce. Agriculture fields are divided into two areas: Flat Land agriculture; and Shifting or *malkush shet* agriculture, collection of forest resources during scarcity of food.

Flat land agriculture: These people prepare agriculture land by operations like plowing, manuring, hoeing,

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Author for Correspondence: *Dr. DK Kulkarni, Email:dilipkkulkarni@gmail.com* sowing, transplanting, weeding, pests and diseases control, harvesting etc. Seedling production of rice is initiated with the onset of the monsoon showers. Cowdung, twigs of forest plants and grasses are arranged in layers over the seedbed and then burned. This practice is called *rabbing* method. It is not uniform in all the regions and changes according to the availability of the plant material. Fields are plowed a number of times in standing water. This *puddling* method is useful for soil facilitates easy transplanting of seedlings. Spacing is generally 22 cm between two spots and at each spot about four seedlings are transplanted. Following local traditional varieties are preferred:

***Oryza sativa* L.** (Rice): Farmers from this area are growing traditional rice varieties. In this region, *Kolamba* has early maturity and less water requirement. *Patani* is drought resistant and suitable in coarse sand or *murmad* soils where water holding capacity of soil is very less. *Kalbhat* is a scented type of rice and generally gown in the middle of the field due to destruction of crop before maturity by wild animals. The yield of rice is very low but has economic value. Some people prefer to grow jowar (barley) crop on coarse soil and drought prone areas.

***Sorghum bicolor* (L.) Moench.** var. *bicolor* (*Jondhla*): There are some local strains like *Dukari* and *Kawali* in Bhor taluka. These strains are cultivated in *kharif* season. In case of *Dukari,* grain colour is yellow. Maturity is in September and cultivated in light soils. White grain is a special character of *Kawali,* cultivated in mixed cropping pattern. It has property of popcorn after proper drying. This popcorn sorghum is conserved for special occasions like marriages or social functions.

Pulses are playing major role in the diet of tribal communities. Tribal people from Bhor region were cultivating pulses on flat land as well as in shifting cultivation, like *Phaseolus vulgaris* L. (rajma)–green pods are boiled and consumed during food shortage, *Castanospermum australe* A. Cumn. (black gram), *Vigna unguiculata* (L.) Walp., subsp. *unguiculata* (Hulga, Kulith), subsp. *cylindrica* (L.) Van. (cowpea) in *kharif* season.

During the *rabi* season *Cicer arietinum* L. (*Harbhara*, pea) is sown as mixed crop in wheat or jowar. The green seeds in unripe stage were used as green vegetables to make curry. After harvesting, pulses are consumed as a supplementary food item. Mostly pulses are grown as mixed crop. This practice resulted into control of diseases and pests likely to be more evenly distributed as each crop has a different tolerance level. Due to mixed cropping pattern total output increases (Mishra *et al*., 2009).

***Malkush shet* or Shifting agriculture:** This practice of *malkush shet* is an old agriculture where forest land is cleared and burned in summer season. In monsoon season, crops are transplanted in heavy rains or thrown into prepared rows of the field. A fixed cropping pattern is followed by the local people. Rotation of cropping pattern is maintained for 3-5 years and later the land is kept fallow for regeneration of forest tree species. This controls soil erosion and helps forest development through coppicing. Finger millet are transplanted on ridges and furrows prepared by a tooth cultivator while other crops like *niger* (*Guizotia abyssinica* Cass) and pulses like pigeonpea (*Cajanus cajan* (L.) Millsp., cowpea (*Vigna unguiculata* (L.) Walp. subsp. *cylindrica* (L.) van Eseltine are broadcast in the field.

***Eleusine coracana* L.** (Nagali, Nachani, ragi): Bhor region is a part of Deccan Plateau or Sahyadri, the families are consuming ragi. Ragi is a very hardy crop as well as a grain of great nutritive value considered more sustaining to people doing hard physical work than any other grain. Generally, people grow this crop in shifting cultivation practices. It is also known as *Malkush sheti*. The tribal farmers grow this crop as traditional variety and it is generally harvested in September-October.

Kitchen garden: Tribal people are sowing seeds of cucurbits for their day to day needs in kitchen garden. Bhor region is rich in diversity of cucurbits like *Benincasia hispida* Cogn. (kohala, ash gourd), *Coccinia grandis* Voigt (ivy gourd, tondali), *Cucumis sativus* L. (Valuk), *Cucurbita maxima* Duch ex Lamk. (dangar, tamda bhopla), *Cucurbita pepo* L. (kashi bhopla), *C. moschata* Duch. ex Poir (kala bhopla), *Lagenaria siceraria* Standley (bottle gourd, dudhi bhopla), *Luffa acuntangula* Roxb. (dodka, shiral), *Luffa cylindrica* (L.) M.J. Roem. (ghosale), *Momordica charantia* L. (bitter gourd, karle), *Trichosanthes anguina* L. (padval). These land races of cucurbits have some medicinal properties, disease resistance, and high keeping quality. Some seeds of cucurbits have commercial values due to its nutritional potential. Some species of *Cucumis* included Valakya, Chivadya, Sendyana, Parosa, Khuhirya, Naringe etc. (Kulkarni and Kumbhojkar, 2004). *Colocasia esculenta* (L.) Schott is a tuber bearing herbaceous plant locally known as *Alu* (taro) and it is grown on waste water in kitchen garden. Leaves, stem and tubers are used as vegetable.

Forest resources: Local communities from Bhor region consume wild tubers, rhizomes and corms either in raw or baked or boiled or roasted form. These are *Dioscorea* *esculanta* Burr. (kanake), *D. pentaphylla* L (chava, shend vel), *D. alata* L. (konphal), *D. sativa* L. (goda karanda), *D. tomentosa* Koen ex Spr. (lavati kand), *D. bulbifera* L. (kadu-kand) and *D. oppositifolia* L. (aniv). Tender shoots, flowering inflorescence, petioles, tubers are cooked before consumption. Similarly, Halunda (*Vigna vexillata* A. Rich) is supposed to stimulate the hunger (Nilegaonkar *et al*., 1985).

The conservation of crop landrace diversity has been hindered in part by the lack of an accepted definition to define the entity universally recognized as landraces. Crop species and the diversity between and within them has significant socio-economic as well as heritage value. Genetic diversity in domesticated species is located in traditional varieties maintained by traditional farming systems exist in tribal pockets. The existence of these traditional crop varieties are severely threatened by genetic extinction primarily due to their replacement by modern crop varieties. Considering importance to landraces it is necessary to prepare an inventory (Brush, 1991). Nene (2004) reported 300 diverse plant species belonging to 90 families utilized as food resources during famine. It includes herbs, flowering stalks, leaves, seeds, kernels, fruits, tubers, etc. Usually these wild species are not in cultivation. Germplasm of traditional crops and horticultural crop plants which are not properly documented. The reason behind this is changing food habits in rural areas. The age old varieties of crop plants and their technologies are not in use since long time. Ultimately our traditional systems got extinct. It is necessary to conserve our heritage of wild plants including wild relatives of crop plants (Kulkarni, 2006).

Local people from Bhor region are cultivating different crops on flat land agriculture, *malkush shet*, kitchen garden and diversity within one crop, mixed cropping ensures security in the event of monsoon failure and increases the returns from the land. Numerous crop combinations are found in small farmers' fields in hilly regions of Maharashtra State. These are frequently grown finger millet *ragi* (*Eleusine coracana* L.) and *niger* (*Guizotia abyssinica* Cass); *jowar* [(*Sorghum bicolor* (L.) Moench)], pigeon pea (*Cajanus cajan* (L.) Millsp., cowpea (*Vigna unguiculata* (L.) Walp. subsp. *cylindrica* (L.) van Eseltine on flat land and shifting cultivation. These crops serve to meet the needs of family consumption and they ensure a fairly balanced diet, the millets being used as a staple food, and the pulses provide proteins. *Ragi* is a very hardy crop as well its grains are of great nutritive value. They are considered more sustaining to people doing hard physical work than any other grain. *Jawar* can withstand considerable drought, and it gives good yields of grain and fodder. Land preparation is delayed due to late onset of monsoon in July, instead of June. It results into late sowing/transplanting of seedlings of rice. Similarly, due to early withdrawn of monsoon the yields of crops are adversely affected due to paucity of water in grain filling state. This is happening due to climatic change. Some insects like stem borer, aphids etc. are severely affecting crops and diseases like mildews, rusts, blights etc. are adversely infecting crops due to these changed climatic conditions. It results into search for alternative source of food material for tribals for their sustenance. They have to depend on forest resources for wild edible plants and tubers. The tribals consume them during the scarcity of food. Efforts were also made to explore the nutritive potential of wild edible tubers and rhizomes which supplement several nutrients (Table 1). Such unconventional wild edible plants are resources of fats, proteins, rich source of micro-nutrients and trace elements (Vartak and Kulkarni, 1987; Kulkarni *et al*., 2003).

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Table1. Proximate analysis of wild edible tubers, rhizomes, corms (g/100 g fresh samples)

Plant species	Edible portion	Moisture %	Protein	Ash %	Fat g%	Reducing sugar
Dioscorea pentaphylla	–	84	3.6	0.95	1.3	7.2
D. esculanta	–	82	1.7	1.3	0.6	12.2
D. oppositifolia	–	86.5	2.5	0.7	1.5	4.4
D. tomentosa	85	79.9	2.1	1.1	2.1	10.3
D. bulbifera	90	76	2.8	1.0	1.2	14.0
Vigna vexillata	82.4	88.3	1.5	1.0	1.2	7.0

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SHORT COMMUNICATION

Relationship Among Seed Yield Attributes in Rice under Temperate Conditions

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Five local cultivars of rice, *viz.*, SKAU-23, SKAU-98, SKAU-105, SKAU-341 and SKAU-382 were evaluated for seed vigour in relation to seed size and boldness. The rice cultivars were graded into four types, *viz.*, (Grade A) partially filled and shriveled seeds, (Grade B) bold coloured seeds, (Grade C) bold discoloured seeds and (Grade D) short bold seeds. The results revealed a positive correlation between seed size and seed vigour during different laboratory conditions under standard techniques. A significant association was also observed between seed boldness and seed vigour. Short sized and bold seeds gave significantly higher values under different vigour tests and hence proved to be more vigourous.

Key Words: Cultivar, Rice, Correlation, Vigour index, Yield, Seed grade

Rice is a most important cereal crop of developing world and a staple food of half of the world's population. About 92 per cent of world's rice is produced and consumed in Asia-Pacific region. Rice being a staple food of Kashmiri people is cultivated on an area of 2.56 lakh hectares in Jammu and Kashmir with a productivity of 32.9 q/ha. The problems of rice cultivation in Kashmir are essentially those of temperate regions associated with long day conditions, short growing season, high altitude and low temperature. During last few years aberrant weather conditions have prevailed in the Kashmir valley resulting in considerable losses in production. High vigourous seeds of superior varieties if available to farmers at convenient time may result in better plant stand in field and lower seed requirement. The principle object of a seed vigour test is to differentiate a wide range of quality levels like high, medium and low vigourous seeds.

As the climatic conditions in Kashmir valley in the early crop season of rice are comparatively cool and the temperature during April-May is not conducive, the germination capacity and the speed of germination are adversely affected. With the result, the plant stand in the field is decreased ultimately reducing the yield. The field response of a particular seed lot may more closely correlate with the vigour test than the ordinary laboratory test depending upon nature of field conditions under which planted. Keeping this in view the present investigations were made to explore the seed vigour using different local cultivars of rice.

The experimental material for the present study consisted of five cultivars of rice, *viz.*, SKAU-23, SKAU-98, SKAU-105, SKAU-341 and SKAU-382 procured from Section of Genetics and Plant Breeding, Rice Research and Regional Station SKUAST-K Khudwani Anantnag (J & K) during June-July 2006. All the cultivars were subjected to physical purity analysis in the laboratory. The pure seed component of all the cultivars was later classified into four categories on the basis of physical appearance and size of seed into following classes:

1. Partially filled and shrivelled seeds-R1 (Grade A)
2. Bold coloured seeds-R2 (Grade B)
3. Bold discoloured seeds-R3 (Grade C)
4. Short bold seeds-R4 (Grade D)

All the grades of each variety were later subjected to various vigour tests in the laboratory, *viz.*, germination on blotter paper (top of paper), germination index (speed of germination),vigour index I, seedling dry weight and seedling dry weight vigour index (vigour index II)

Laboratory Analysis

Hundred seed weight: Hundred seeds from each fraction of all the varities were counted and later weighed on electronic weighing balance.

Rate of germination: Three sets of 25 seeds from all four grades of each variety were placed on a blotter paper inside a 90 cm petridish. After adding 3 ml of distilled water to each petri dish, these were kept inside a germinator (25°C temperature and 97% RH). First count was taken after 48h and final count after 336h. Rate of germination index was calculated according to Seshu *et al*. (1988).

Germination test on top of paper: To calculate seedling root length, seedling shoot length and vigour index, the seeds were allowed to germinate on top of paper. The paper used in this test was free from any type of infection and enough strong to resist any pressure. The seeds were kept at proper distance on germination paper and kept in incubator (25°C and 90% RH).The total number of seeds germinated were counted later.

Seedling root length, seedling shoot length and seedling dry weight: Roll towel method (Seshu *et al.,* 1988) was used to record root and shoot length of seedlings. Measurement of root and shoot length was made on14th day after setting the seeds for germination. After root and shoot measurements, ten seedlings from each set were placed in paper bags and dried in an oven at 80°C for 48h and then weighed on a Mettler balance for obtaining seedling dry weight in mg.

Vigour index I and vigour index II: The germination percentage obtained in the germination test was used to calculate vigour index. The vigour index was calculated adopting the method of Abdul-Baki and Anderson (1973).

Seed weights of different fractions of rice cultivars revealed that 100-seed weight of short bold seeds ranged from 2.30 g–4.90 g in comparison to other fractions which merely touched this level (4.90 g in SKAU-382). Hence, short bold seed component that has higher seed weight in all the cultivars can be considered as more vigourous than other fractions (Grade A, B and C).

The seeds under germination test were examined after 336h. The germination percentage was as low as 44% in SKAU-341 (R1) and as high as 100% in SKAU-382 (R4).The seeds with smaller seed size (short bold seeds) exhibited highest germination percentage in all the rice cultivars: SKAU-23=96%; SKAU-98=88%; SKAU-105=76%; SKAU-341=90% and SKAU-382=100%) (Table 1).

The germination percentage was calculated on 15th day of germination test. The value of germination index (RG) revealed that short bold seed component (R4) in all five rice cultivars had higher values. It means that short bold seeds (R4) got germinated earlier than any other component of seed (SKAU-23, R4=10.11; SKAU-382, R4=17.28) (Table 1).

Table 1. Determination of 100-seed weight, germination percentage and rate of germination index

Name of variety	Fraction of seed (g)	Hundred seed weight (g)	Average weight of seed (g)	Germination percentage (%)	Germination index
* SKAU-23	R1	1.90	0.019	72	6.37
	R2	3.60	0.036	88	7.82
	R3	2.60	0.026	52	6.77
	R4	2.50	0.025	96	10.11
SKAU-98	R1	2.00	0.020	64	5.95
	R2	2.80	0.028	87	11.09
	R3	2.60	0.026	72	11.14
	R4	2.50	0.025	88	13.38
SKAU-105	R1	1.70	0.017	68	5.65
	R2	2.60	0.026	72	6.85
	R3	2.10	0.021	68	6.75
	R4	2.30	0.023	76	7.12
SKAU-341	R1	1.80	0.018	44	7.12
	R2	2.70	0.027	88	13.53
	R3	2.30	0.023	64	12.78
	R4	2.50	0.025	90	15.42
SKAU-382	R1	1.60	0.016	52	6.36
	R2	2.50	0.025	84	17.23
	R3	2.20	0.022	64	15.95
	R4	4.90	0.049	100	17.28

R1=Partially filled and shriveled seed
R3=Bold discoloured seed
* SKAU: Sher-e-Kashmir Agricultural University
R2=Bold coloured seed
R4=Short bold seed
Relative Humidity =70%
Substratum =Paper
Temperature=28°C
Seeds x Replicates =25 x 4

Table 2. Calculation of average seedling length, vigour index I and vigour index II

Name of variety	Fraction of seed	Total seedling length (cm)	Germination percentage (%)	Vigour index I	Seedling dry weight (mg)	Vigour index II
SKAU-23	R1	8.25	72	594.00	42.43	3054.96
	R2	8.16	88	718.08	41.81	3679.28
	R3	8.04	52	418.08	38.58	2006.16
	R4	7.42	96	712.32	43.11	4138.56
SKAU-98	R1	6.47	64	414.08	42.60	2726.40
	R2	8.19	87	712.53	42.56	3702.72
	R3	8.22	72	591.84	42.00	3024.00
	R4	8.31	88	731.28	48.32	4252.16
SKAU-105	R1	7.66	68	520.88	38.64	2627.52
	R2	6.32	72	455.04	31.61	2275.92
	R3	7.00	68	476.00	35.00	2380.00
	R4	7.55	76	573.80	38.96	2960.96
SKAU-341	R1	7.60	44	334.40	38.63	1699.72
	R2	7.73	88	680.24	47.34	4165.92
	R3	7.71	64	493.44	46.52	2977.28
	R4	8.07	90	726.30	42.84	3855.60
SKAU-382	R1	7.26	52	377.52	47.00	2444.00
	R2	7.05	84	592.20	47.32	3974.88
	R3	6.75	64	432.00	46.77	2993.28
	R4	6.89	100	689.00	47.80	4780.00

R1=Partially filled and shriveled seed
R3=Bold discoloured seed
R2=Bold coloured seed
R4=Short bold seed
Seeds x Replicates=25 x 4
Substratum =Paper
Temperature=28°C
Relative Humidity =70%

The highest value of average seedling height was recorded in R4 of SKAU-98 as 8.31 cm and lowest in case of SKAU-105 as 6.32 cm (R2).The highest seedling dry weight was found in R4 of SKAU-98 (48.32 mg) and lowest in R2 of SKAU-105 (31.61 mg). Here the smaller size of seed had a negative correlation with the above mentioned parameters (Table 2). On examining the vigour index I of rice cultivars, the short bold seeds (R4) showed highest values in SKAU-98, SKAU-105, SKAU-341 and SKAU-382 but not in SKAU-23.

Similarly, the vigour index II was found highest in short bold seeds of SKAU-23, SKAU-98, SKAU-105 and SKAU-382, except in SKAU-341, in comparison to other fractions of seed. Hence, the short bold seeds also exhibited a positive correlation with vigour index II.

The present investigation was conducted to study the effect of seed size and in fact the seed boldness (filled or partially filled) on seed vigour. Upon conducting and observing various vigour traits, it was seen that seed vigour was directly associated with seed size and boldness in different rice cultivars. Similar results were obtained by Takeda (1972) while working on correlation of seed weight and seedling length in rice. A positive correlation was found between smaller seed size (short bold seeds) and seed vigour parameters in all rice cultivars except seedling dry weight. Similar observations were also recorded by Sharma *et al.* (1990) while studying 46 local rice cultivars of Himachal Pradesh. The vigour values of partially filled and shrivelled seeds lagged behind in all the rice cultivars brought under study. Amaral (1978) also reported that vigour of rice seeds increased with an increase in seed density.

The short bold seeds were observed to be well filled and showed highest vigour values. This clearly indicates that well filled seeds always give rise to healthy seedlings in comparison to partially filled seeds. The positive correlation of seed weight with seedling length and vigour index II may be because of higher quantity of food reserves in the healthy seeds that may have eventually contributed to the increased shoot length and seedling dry weight. Wu (1975) also got the similar results while working on the seedling growth on rice plants.

The results indicated that larger seed size had nothing to do with the plant stand in the field; and vigour values were found highest in short bold seeds in the present study. So, the farmers need not to worry about the size of the rice seeds as short sized seeds proved to be more vigourous in all the cultivars. The above parameters may also be used in selection of genotypes as parents in improving seed and seedling vigour traits in rice.

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