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Short Communication

GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN DIVERSE COLLECTION OF INDIAN AND EXOTIC GERMPLASM LINES OF PEA (*PISUM SATIVUM* L.)

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Pulses have been given the status of 'wonder crop', a unique gift bestowed by nature to mankind as pulses are relatively high in protein content, which makes the diet more balanced in its nutritive value, and their ability to develop a symbiotic relationship in their root nodules with the nitrogen fixing bacteria of *Rhizobium species* to enhance the soil fertility. Pea (*Pisum sativum* L.) a temperate crop, is one of the sixth major pulse crops cultivated globally and is second highest yielding grain legume next to broad bean (*Vicia faba*). The area of pea cultivation in India is 0.59 million ha, the production is 0.80 million tons of dry peas and the average yield being 13.56 q/ha. However, the present level of productivity of peas is still far below than world's average productivity of 15.70 q/ha (FAO, 2006). Keeping the aforesaid view in mind, the present investigation was based on evaluation of 54 genotypes of pea to study the extent of genetic variability, nature and magnitude of correlation coefficient as well as direct and indirect effects of the eight yield contributing traits on seed yield.

The present experiment was carried out at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi during the winter season (2006-07). For the experiment, 54 diverse genotypes of pea (*Pisum sativum* L.) were provided by the All India Coordinated Research Project on MULLaRP.

Material consisting of fifty four genotypes of pea was sown in single rows plot of 13 m length with three replications. Row-to-row and plant-to-plant distance was maintained at 60 cm and 15 cm respectively. Recommended agronomic practices and plant protection measures were followed to raise a good crop. After eliminating the border plants, observations were recorded on ten randomly selected plants from each plot on nine quantitative characters *viz.* days to flowering, days to maturity, plant height, number of primary branches, number of pods per plant, pod length, number of seeds per pod, 100-seed weight and seed yield per plant.

The genotypic and phenotypic variance and heritability in broad sense were estimated by Lush (1940). Genetic advance was expressed as percentage of mean was estimated by Govindasamy et al. (1973). The association between yield and component traits was based on genotypic and phenotypic correlation coefficients (Goulden, 1952). Path coefficient analysis as applied by Dewey and Lu (1959) was used to partition the genotypic correlation coefficient into components of direct and indirect effects.

The mean sum of squares showed significant difference for all the characters under study, except for the number of primary branches per plant and pod length, indicating presence of considerable genetic variability.

The variability in terms of range was highest in 100-seed weight (3.75-24.05) and lowest in pod length (4.21-7.07). The GCV was found to be less than PCV for all traits studied which indicated that these characters were having interaction with environment to some extent (Ram and Singh, 1993). Heritability estimate is a useful tool in terms of selection concept. Heritability (h^2) value was maximum for plant height (96.70) followed by seed yield per plant (96.20), 100-seed weight (95.90) and seeds per pod (90.60).High heritability estimates for these characters were also reported by Sureja *et al.* (2000), Chaudhary *et al.* (2003), and Singh *et al.* (2006). The genetic advance (GA) expressed as percentage of mean, was maximum for seed yield per plant (72.00) followed by pods per plant (55.39) and 100-seed weight (47.96). The minimum GA value was recorded for days to maturity (10.41).The results are in harmony with Tyagi and Srivastava (2002), Vikas *et al.* (1999). Heritability in conjugation with genetic advance would be more beneficial for getting better response in selection from elite population (Johnson *et al.*, 1955). In the present study, seed yield per plant, 100-seed weight, plant height and pods per plant exhibited high heritability along with high genetic advance. According to Panse (1957), variability of these characters was predominantly due to additive gene effects and phenotypic selection would be effective.

Phenotypic and genotypic correlation coefficients were worked out among all nine characters under study and the results have been presented in Table 1. The seed yield per plant showed significant and positive correlation with pods per plant, 100-seed weight and plant height. Therefore, seed yield can be increased by selecting taller plant that bear higher pod and have high seed weight. 100-seed weight had significant and positive correlation with pod length and plant height. Number of seeds per pod was strongly associated with plant length. Pods per plant were positively and significantly associated with number of primary branches. This suggests that higher pods per plant are possible in varieties which bear more number of primary branches.

In general, the magnitude of genotypic correlation coefficient was higher than the respective phenotypic correlation coefficient, indicating strong association between the characters. This may be due to the effect of environment in modifying the total expression of the genotypes, thus altering the phenotypic expression (Nandpuri et al., 1973). The trend of correlation coefficients revealed positive and highly significant association of yield per plant with plant height, pods per plant and 100 seed weight. Srivastava and Singh (1989), Vikas *et al.* (1999), Kumar *et al.* (2003), Singh *et al.* (2006) reported a similar trend in pea. The correlation analysis made in this study revealed positive and highly significant association of the traits viz., days to flowering and days to maturity, pod length and seeds per pod, pods per plant, seed yield per plant and 100 seed weight with pod length and seed yield per plant . Hence it may be concluded that these traits may be considered as the most important yield contributing attributes in pea.

Path coefficient was calculated taking seed yield per plant as dependent variable and rest of eight characters as independent variables (Table 2). The direct and indirect effect of yield contributing traits on yield revealed that the maximum positive direct effect was exhibited by pods per plant followed by 100-seed weight, days to maturity and pod length, while days to flowering, number of primary branches and plant height had negative direct effect on yield. High direct effects for above traits were also reported by Kumar *et al.* (2003), Arya *et al.* (2004), and Singh *et al.* (2006). The high positive direct effect of number of pods per plant on yield per plant resulted from strong and positive correlation between them.

Table 1. Correlation coefficient among nine character of pea.

Characters	Correlation coefficients	Days to maturity	Plant height	Number of Primary branches	Pods per plant	Pod length	Seeds per pod	100-Seed weight	Seed Yield per Plant
Days to flowering	r_p	0.814**	-0.057	-0.095	0.031	0.101	0.110	-0.056	-0.018
	r_g	0.902**	-0.072	-0.102	0.013	0.094	0.115	-0.078	-0.024
Days to Maturity	r_p		-0.057	-0.106	-0.003	0.046	0.109	-0.075	-0.008
	r_g		-0.061	-0.135	-0.006	0.030	0.111	-0.084	-0.016
Plant height	r_p			0.067	0.227	0.134	0.235	0.332*	0.384**
	r_g			0.065	0.219	0.150	0.244	0.341*	0.358**
Number of primary branches	r_p				0.455**	0.012	-0.042	-0.048	0.226
	r_g				0.502**	0.008	-0.078	-0.040	0.241
Pods per plant	r_p					-0.217	-0.004	-0.239	0.462**
	r_g					-0.230	-0.024	-0.270	0.505**
Pod length	r_p						0.577**	0.422**	0.078
	r_g						0.620**	0.458**	0.089
Seeds per pod	r_p							0.066	0.041
	r_g							0.073	0.044
100-seed weight	r_p								0.393**
	r_g								0.378**

*, ** Significant at $P = 0.05$ and $P = 0.01$ level of significance respectively.

r_p = Phenotypic correlation coefficient, r_g = Genotypic correlation coefficient

Table 2. Direct and Indirect effects of eight component traits on seed yield in pea.

Characters	Days to flowering	Days to maturity	Plant height	Number of Primary branches	Pods per plant	Pod length	Seeds per pod	100-seed weight	Correlation
Days to flowering	-0.133	0.117	0.004	0.009	0.009	0.005	0.000	-0.036	-0.025
Days to Maturity	-0.120	0.130	0.004	0.012	-0.004	0.002	0.000	-0.039	-0.015
Plant height	0.010	-0.008	-0.062	-0.006	0.154	0.009	0.000	0.156	0.253
Number of primary branches	0.014	-0.018	-0.004	-0.085	0.352	0.000	0.000	-0.018	0.241
Pods per plant	-0.002	0.001	-0.014	-0.043	0.702	-0.013	0.000	-0.124	0.507
Pod length	-0.013	0.004	-0.009	-0.001	-0161	0.058	0.001	0.211	0.090
Seeds per pod	-0.015	0.014	-0.015	0.007	-0.017	0.036	0.001	0.033	0.044
100-seed weight	0.010	-0.011	-0.021	0.003	-0.190	0.026	0.000	0.459	0.276

Residual effect = 0.5481

The pod length had positive direct effect on seed yield (0.058) but it had relatively low correlation with yield per plant. There was very low positive direct effect for seeds per pod (0.001). However, the correlation between this character and seed yield was positive (0.044) due to positive indirect effect via pod length, 100-seed weight, days to maturity and number of primary branches. Finding of path analysis indicated that pods per plant, seed weight and days to maturity had high direct effect towards seed yield accompanied with moderate to high correlation with yield per plant. The path coefficient analysis thus showed that number of pods per plant, 100-seed weight, days to maturity and pod length would exert a high direct influence on increasing yield per plant. Breeder should therefore, concentrate on these characters during selection of elite genotypes.

A significant difference among genotypes for all characters indicates that there is ample scope for selection of promising lines from present gene pool for yield improvement. High broad sense heritability along with high GCV for plant height, yield per plant, 100-seed weight, seeds per pod and pods per plant revealed that, these traits can be exploited during selection. Correlation study showed that, grain yield per plant may be improved by selecting tall genotypes having more number of pods per plant and high seed weight. Path coefficient analysis suggests that pods per plant, seed weight and plant height may serve as effective selection attributes yield improvement in pea. On the basis of per se performance the lines viz., EC-507770, IC-218989, EC-341724, EC-208390, IC-395309, DMR-11 and IC-208365 were found to be best genotypes for multiple traits, so these can be used as parents for future breeding programmes.

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