

Full Length Research Paper

## Selection strategy for seed yield and maturity in field pea (*Pisum sativum* L. arvense)

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The experimental material consisting of 19 genotypes of field pea were grown during *Rabi* 2009-2010 to study genetic variation, character association and direct effects of component characters on yield and maturity. Analysis of variance was highly significant for all the characters studied, indicating ample scope of selection. High magnitude of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for seed yield per plant followed by number of pods per plant and 100 seed weight, whereas low estimates were observed for number of seeds per pod, plant height, days to 50% flowering, pod length and days to maturity. High heritability coupled with high genetic advance as percent of mean was recorded for seed yield per plant followed by number of pods per plant and 100 seed weight. However, high heritability associated with moderate genetic advance was observed for number of seeds per pod, plant height, days to 50% flowering and pod length. Seed yield per plant had significant and positive association with pods per plant but it had significant negative association with days to maturity. Path coefficient analysis revealed that pods per plant had greatest positive effect on seed yield per plant followed by pod length, 100 seed weight, days to 50% flowering and seed yield per plant while, the direct negative effect on seed yield per plant were exhibited by plant height and days to maturity. The study revealed that greater emphasis should be given to these characters for yield improvement.

**Key words:** Field pea, genetic variation, heritability, correlation, path coefficient, yield.

### INTRODUCTION

Pulses have been given the status of wonder crop, a unique gift bestowed by nature to mankind for number of reasons. They are important and excellent crop for natural resource management, environment security, crop diversification and consequently for viable agriculture. This is inexpensive source of protein for millions of people. Despite being the largest producer in the world, the country is short in supply of pulses. Production and productivity of most of the pulse crops

have either declined or at best stagnated resulting in a sharp reduction in the per capita availability of pulses.

Field pea (*Pisum sativum* L. arvense) is the most important legume crops of India, belongs to leguminosae family, largely confined to cooler temperate zone between the tropic of cancer and mediterranean region. Inception of the genetic improvement programme for seed yield and its component traits in any crop requires identification of suitable and adaptable genotypes for a

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**Table 1.** Analysis of variance for quantitative characters in field pea.

S/N	Characters	Mean sum of squares		
		Replications df = 2	Treatments df = 18	Error df = 36
1	Days to 50% flowering	6.81	91.94**	4.46
2	Plant height	0.03	75.00**	13.70
3	Number of pods/plant	53.74	47.11**	8.50
4	Pod length	0.09	0.54	0.08
5	Number of seeds/pod	0.05	0.19	0.16
6	Days to maturity	0.21	32.31**	5.10
7	100 seed weight	1.51	18.82**	0.32
8	Seed yield/plant	1.33	19.40**	1.27

\*\*Significant at 1% level of significance.

particular agro climatic zone for using directly and also as base material for further improvement in order to break the existing yield plateau. The efficiency of selection based on estimates of character association can further be enhanced by as curtaining direct and indirect effect of component traits towards expression of seed yield. Present investigation was undertaken to estimate positive and negative correlation of yield component traits with seed yield per plant, direct and indirect effects on various component characters on seed yield in order to do selection of desirable genotypes for various quantitative characters.

## MATERIALS AND METHODS

The experimental material consisting of 19 genotypes of field pea, received from Indian Institute of Pulse Research, Kanpur (U.P.) under All India Coordinated Research Project on Improvement of MULLaRP Crops. Genotypes were grown in randomized block design with three replications at Department of Genetics and Plant Breeding, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Allahabad, India during *Rabi* 2009-2010. Recommended cultural practices were followed to raise a healthy crop. The observations were recorded on 10 randomly selected plants were *viz.*, days to 50% flowering, plant height, number of pods per plant, days to maturity, pod length, number of seeds per pod, 100 seed weight and seed yield per plant. Data obtained were subjected to analysis of variance to test the significance according to the procedure given by Fisher and Yates (1938). Genetic variability calculated by the procedure given by Burton (1952), heritability by Lush (1949) and Burton and Dewane (1953) and genetic advance by the formula given by Johnson et al. (1955). Correlation coefficients were computed at genotypic and phenotypic levels between pair of characters adopting the method given by Al-Jibouri et al. (1958) and path analysis by the procedure of Dewey and Lu (1959).

## RESULTS AND DISCUSSION

The analysis of variance for different characters showed that the mean sum of squares due to genotypes showed significant differences for most of the characters under study except for pod length and number of seeds per pod

at 1% level of significance, indicating the presence of substantial amount of genetic variability among the field pea genotypes (Table 1). Highly significant differences observed for days to 50% flowering (91.94\*\*), plant height (75.00\*\*) and number of pods per plant (47.11\*\*). In other words, the performance of the genotypes with respect to these characters was statistically different, suggesting scope for yield improvement in field pea. High genetic variability for different quantitative traits in field pea was also reported by Kumar et al. (2003) and Jitendra et al. (2010).

High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for seed yield per plant (32.08, 35.28) and number of pods per plant (25.82, 33.27) and 100 seed weight (16.29, 16.70), indicating the presence of high amount of variation and role of environment on the expression of these traits, whereas low estimates were observed for plant height (8.73, 10.98), days to 50% flowering (7.07, 7.60), pod length (6.05, 7.46) and days to maturity (2.67, 3.34), suggesting the little role of environment in the expression of these characters. These findings are in agreement with the reports of Sonali et al. (2009) and Jitendra et al. (2010) with respect to number of pods per plant and seed yield per plant. Heritability estimates were found high (> 60%) for 100 seed weight (95.10%) followed by days to 50% flowering (86.70%), seed yield per plant (82.70%), number of seeds per pod (69.0%), pod length (65.9%), days to maturity (64%) and number of pods per plant (60.2%) (Table 2). Johnson et al. (1955) suggested that heritability and genetic advance when calculated together would prove more useful result predicting the resultant effect of selection on phenotypic expression. Expected genetic advance as percent of mean indicates the mode of gene action in the expression of traits, which helps in choosing an appropriate breeding method.

Genetic advance as percent of mean for various characters noticed that high (>20%) genetic advance as percent of mean was recorded for seed yield per plant (60.09%) followed by number of pods per plant (41.29%)

**Table 2.** Genetic parameters for eight characters in field pea.

S/N	Character	Genotypic coefficient of variation (GCV)	Phenotypic coefficient of variation( PCV)	Heritability (%) (bs)	Genetic advance (GA)	GA as % of mean
1	Days to 50% flowering	7.07	7.60	86.70	10.36	13.57
2	Plant height	8.73	11.28	59.90	7.21	13.92
3	Number of pods/plant	25.82	33.27	60.20	5.74	41.29
4	Days to maturity	2.67	3.34	64.00	4.96	4.40
5	Pod length	6.05	7.46	65.90	0.66	10.12
6	Number of seeds/pod	9.15	10.98	69.00	0.59	15.67
7	100 seed weight	16.29	16.70	95.10	4.99	32.73
8	Seed yield/plant	32.08	35.28	82.70	4.61	60.09

and 100 seed weight (32.73) and moderate (10-20%) estimate of genetic advance were noticed for number of seeds per pod (15.67), plant height (13.92%) and days to 50% flowering (13.57%), while low (<10%) genetic advance was recorded for days to maturity (4.40%) (Table 2).

High heritability coupled with high genetic advance as percent of mean were observed for 100 seed weight, seed yield per plant and number of pods per plant. Estimate of GCV was also high for these traits indicating presence of additive gene effects suggesting more scope of selection for these traits, whereas days to maturity showed high heritability coupled with low genetic advance as percent of mean, which revealed that selection could be delay for further generation. Plant height showed moderate heritability along with moderate genetic advance as percent of mean, indicating that these characters showed intermediate expression for both additive and dominance gene effect. Similar findings have been reported by Jitendra et al. (2010). Traits like days to maturity showed lower GCV and low genetic advance indicating limited scope of improvement of these traits by selection.

Character association studies could be highly useful to know the suitability of various characters for selection, because selection of any particular character may effects desirable or undesirable changes in other related characters. Further, direct selection for seed yield may not be effective, because yield is not controlled by a single gene but all the genes controlling the yield component characters are responsible for seed yield. High genotypic and environmental interactions are likely to restrict the improvement, if selection is based mainly on yield alone by considering it as a simple character. Therefore, the character association between yield and yield components are of considerable importance in selection programmes.

Correlation analysis revealed that seed yield per plant recorded high significant and positive association with number of pods per plant (0.697\*\*) and significant negative association with days to maturity (-0.413\*\*) (Table 3). Ghobary (2010) and Jitendra et al. (2010)

earlier reported that number of pods per plant exhibited significant and positive association with seed yield per plant. Pods per plant recorded significant and negative association with days to maturity (-0.427\*\*) and pod length had significant and positive association with 100 seed weight (0.379\*\*). Days to maturity have significant and positive association with 100 seed weight (0.285\*) and days to 50% flowering (0.377\*\*). Hundred seed weight showed significant and positive association with pod length (0.379\*\*).

In plant breeding, it is very difficult to have complete knowledge of all component characters on seed yield. Residual effects measure the role of other possible independent variables. The residual effects observed in present study were 1.3307 for genotypic path and 0.6523 for phenotypic path coefficient analyses. Number of pods per plant showed the highest direct effect on seed yield per plant at both phenotypic and genotypic levels (Tables 4 and 5). Similar results are earlier reported by Kumar et al. (2003), Kumar and Sharma (2006), and Ghobary (2010).

Direct effect of any character on seed yield per plant gives an idea about effective selection that can be made to bring improvement. The indirect effect indicates the interrelation of component characters towards contribution to yield. Thus, selection for number of pods per plant, days to maturity, number of seeds per pod and pod length would give good response in yield improvement. It may therefore, be argued that if other factor are held constant, an increase in these characters individually would be reflected in an increased in seed yield. Other important characters which had negative direct effects on seed yield per plant are days to 50% flowering, plant height, number of seeds per pod. Similar results were earlier reported by Kumar et al. (2003). The present experiment concluded that field pea genotypes used in this experiment showed significant genetic variability. High heritability coupled with high genetic advance were observed for seed field per plant followed by number of pods per plant and 100 seed weight. Number of pods per plant recorded highly significant positive correlation and positive direct effect on seed yield per plant. It is apparent that seed yield in field pea

**Table 3.** Estimation of correlation for eight component characters *inter-se* and with seed yield in field pea.

Characters	Coefficient	Plant height	Number of Pods/ plant	Days to maturity	Pod length	Number of Seeds/ pod	100 seed weight	Seed yield/ plant
Days to 50% flowering	rg	-0.380	0.091	0.483	0.100	-0.352	0.146	-0.015
	rp	-0.243	0.030	0.377**	0.025	0.008	0.132	0.034
Plant height	rg		0.230	0.062	0.042	-0.569	0.093	0.033
	rp		0.122	-0.003	-0.033	0.166	0.086	0.012
Number of pods/plant	rg			-0.550	0.191	-0.296	0.207	0.999
	rp			-0.427**	0.068	0.071	0.137	0.697**
Days to maturity	rg				0.161	-0.640	0.356	-0.619
	rp				0.108	0.229	0.285*	-0.413**
Pod length	rg					-0.413	0.494	0.384
	rp					0.029	0.379**	0.237
Number of seeds/pod	rg						0.181	-0.218
	rp						0.006	0.048
100 seed weight	rg							0.235
	rp							0.210

rg = Genotypic correlation; rp = phenotypic correlation.

**Table 4.** Phenotypic path analysis for seed yield per plant in field pea

Characters	Days to 50% flowering	Plant height	Number of pods/ plant	Days to maturity	Pod length	Number of seeds/ pod	100 Seed weight	Seed yield/ plant
Days to 50% flowering	<b>0.093</b>	-0.023	0.003	0.035	0.002	0.001	0.012	0.034
Plant height	0.013	<b>-0.052</b>	-0.006	0.001	0.002	-0.009	-0.004	0.012
Number of Pods/ plant	0.016	0.065	<b>0.535</b>	-0.229	0.037	0.038	0.073	0.697
Days to maturity	-0.113	0.001	0.128	<b>-0.299</b>	-0.032	-0.069	-0.085	-0.413
Pod length	0.004	-0.006	0.012	0.018	<b>0.170</b>	0.005	0.065	0.237
Number of Seeds/ pod	0.001	0.013	0.006	0.018	0.002	<b>0.080</b>	0.001	0.048
100 Seed weight	0.020	0.013	0.021	0.043	0.057	0.001	<b>0.149</b>	0.210

\*\*Significant at 1% level of significance; Residual effect = 1.3307.

**Table 5.** Genotypic path analysis for seed yield per plant in field pea.

Characters	Days to 50% flowering	Plant height	Number of Pods/ plant	Days to maturity	Pod length	Number of Seeds/ pod	100 Seed weight	Seed yield/ plant
Days to 50% flowering	<b>-0.620</b>	0.236	-0.057	-0.300	-0.062	0.218	-0.090	-0.015
Plant height	0.259	<b>-0.682</b>	-0.157	-0.042	-0.029	0.388	-0.063	0.033
Number of Pods/ plant	0.120	0.302	<b>1.235</b>	-0.723	0.252	-0.389	0.273	0.999
Days to maturity	0.118	0.015	-0.134	<b>0.243</b>	0.039	-0.156	0.087	-0.619
Pod length	0.004	0.002	0.008	0.007	<b>0.042</b>	-0.017	0.021	0.0384
Number of Seeds/ pod	0.096	0.155	0.081	0.175	0.113	<b>-0.273</b>	-0.050	-0.218
100 Seed weight	0.009	0.005	0.012	0.021	0.029	0.011	<b>0.058</b>	0.235

Residual effect = 0.6523.

can be improved by selection of such genotype having more number of pods per plant and number of seeds per pod, due consideration should be given to these characters while going for selection.

## REFERENCES

- Al-Jibouri A, Miller PA, Robison HF (1958). Genotypic and environmental variances and co-variances in an upland cotton crops of interspecific origin. *Agron. J.* 50:633-636.
- Burton GW (1952). Quantitative inheritance in grasses. *Proc. 6<sup>th</sup> Int. Grassland Congr.* 1:277-283.
- Burton GW, Devane EH (1953). Estimating heritability in tall Fescue (*Festucaarundian*) from replicated clonal material. *Agron. J.* 45(1):474- 478.
- Dewey DR, Lu KH (1959). Correlation and path coefficient analysis of crested wheatgrass seed production. *Agron. J.* 51:515-518.
- Fisher RA, Yates F (1938). Correlation between relatives on the supposition of Mendalian inheritance. *France Royal Soc., Edinburg.* 52:399-433.
- Ghobary HM (2010). Study of Relationship between yield and some yield components in garden pea (*Pisum sativum* L.) by using correlation and path analysis. *J. Agric. Res. Kafer El- Sheikh Univ.* 36:351-360.
- Jitendra K, Ashraf N, Pal K (2010). Variability and character association in garden pea (*Pisum sativum* L. sub sp. *hortense* Asch. and Graebn). *Progressive Agric.* 10(1):124-131.
- Johnson HW, Robinson HF, Comstock RE (1959). Genotype and phenotype correlation in Soyabean and their implication in selection. *Agron. J.* 74:477-483.
- Kumar B, Lakhi R, Singh JD, Singh B (2003). Correlation and path coefficient analysis in pea (*Pisum sativum* L.). *Progressive Agric.* 3(1/2):141-142.
- Kumar VRA, Sharma RR (2006). Path coefficient analysis for pod yield and its attributes in garden pea (*Pisum sativum* L. sub sp. *hortense* Asch. and Garebn.). *Annals Agric. Res.* 27(1):32-36.
- Lush JL (1949). Intensive correlation and regression of characters. *Proc. American Soc. Animal Prod.* 33:293-301.
- Sonali G, Nirmla C, Saroj D (2009). Genetic variability, correlation and path analysis studies in pea (*Pisum sativum* L.). *Crop Res.* 38(1-3):179-183.