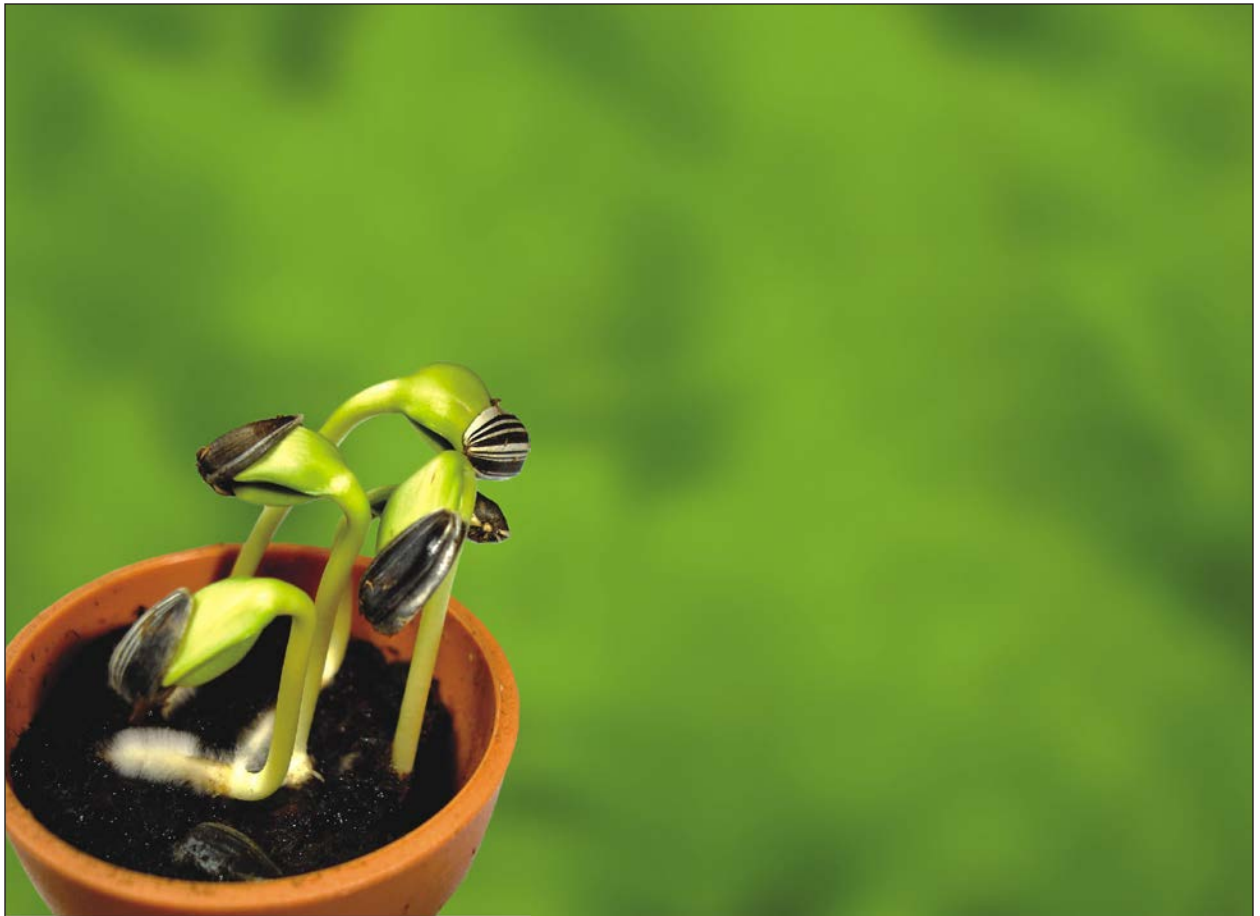




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Heritability, Character Association and Path Analysis Studies in Early Segregating Population of Field Pea (*Pisum sativum* L. var. *arvense*)

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ABSTRACT

The present study was aimed at finding out the nature and magnitude of genetic variability and association studies in segregating population of the field pea for grain yield and other yield component traits to select the transgressive segregants for further breeding programme. Twenty F_2 field pea plant population were grown in Randomized Block Design (RBD) with 3 replications to assess the variability and association patterns for the characters under study. Significant differences were observed among all the F_2 plants for all the characters studied, except for days to emergence. Moderate to high heritability (broad sense) coupled with moderate genetic advance as percent of mean was recorded for the characters plant height, pod length and 100 seed weight indicating role of additive gene action in the expression of these traits. Numbers of pods per plant, plant height, number of primary branches per plant, 100 seed weight and number of clusters per plant were the major characters contributing to grain yield as these traits were significantly and positively associated with grain yield per plant. Number of pods per plant recorded highest positive direct effect on grain yield per plant via positive indirect effects of plant height and number of primary branches per plant.

Key words: Field pea, segregating population, variability, heritability, genetic advance, correlation and path analysis

INTRODUCTION

Field pea (*Pisum sativum* L. var. *arvense*) is amongst the most important legume crop of India, belongs to family Leguminosae, largely confined to cooler temperate zone between the tropic of Cancer and Mediterranean region (Anonymous, 2001). Cultivation of pea has lead to a gradual separation of types: for vegetable use, for seed and fodder (field pea) (Duke, 1981; Santalla *et al.*, 2001), In India, pea is grown in an area of 0.59 million hectares (ha) with production of 0.80 million tons and productivity of only 1355.9 kg ha⁻¹ (Food and Agriculture Organization, 2008). It is mostly grown in Uttar Pradesh, Madhya Pradesh, Bihar, Assam and Orissa which together account for about 95% of the total area and production of pea in India. Productivity of this crop has remained stagnant and area is shrinking due to lack of high yielding varieties, competition from irrigated wheat and more remunerative pulses. To increase the production of this crop there is need to operate field pea breeding programme in efficient manner.

In breeding programmes for self-fertilizing crops, a large number of crosses are made every year. To manage large number of recombinant lines in later generation, it would be highly desirable to start selection among crosses as early as possible. Developments in biometrical genetics have led to the suggestion that early generation trials may be used to predict the ranking of the crosses according to their likelihood of producing superior recombinant lines. Such cross prediction methods have been applied to a wide range of crop species such as barley, rice, potato, ryegrass, onion, sunflower and oilseed rape. The F_2 or F_3 derived lines are far from being homozygous and early generation selection relies on the assumption that the performance of a line at an early generation of selfing is predictive of its performance at homozygosity (Chahota *et al.*, 2007). Empirical studies in different self-pollinated crops have indicated that early generation selection is sometimes effective and sometimes ineffective (Bernardo, 2003). In order to improve the yield through selection, it is essential to have a thorough knowledge on genetic variability available in the germplasm and the extent to which the desirable traits are heritable, which requires a better insight of the ancillary characters for better selection. Therefore, the present study was aimed at finding out the nature and magnitude of genetic variability and association studies in segregating population of the field pea for grain yield and other yield component traits to select the transgressive segregants for further breeding programme.

MATERIALS AND METHODS

Twenty F_2 field pea plant population were grown in Randomized Block Design (RBD) with 3 replications during *rabi* 2006-07 at the field experimentation center of the Department of Genetics and Plant Breeding, Allahabad Agricultural Institute-Deemed University, Allahabad. Each plant was represented by single row plot of 3 m with a row to row spacing of 60 cm. Observations were recorded on 10 randomly selected plants from each progeny in each replication for 10 quantitative traits viz., days to emergence, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, pod length, number of clusters per plant, 100 Seed weight and grain yield per plant. Mean values were subjected to statistical analysis and the analysis of variance was worked out to test the significance of F and t-test according to the procedure of RBD analysis of Panse and Sukhatme (1967). The Genotypic Coefficient of Variance (GCV), Phenotypic Coefficient of Variance (PCV) and heritability in broad sense was estimated as per the formula given by Burton and de Vane (1953). Expected genetic gain was worked out as per the method given by Lush (1949). Correlation coefficients were computed at genotypic and phenotypic levels between pairs of characters adopting the formula given by Al-Jibouri *et al.* (1958) and path coefficient analysis of Dewey and Lu (1959) was used to estimate the actual contribution of an attribute and its influence through other characters considering seed yield as a dependent variable.

RESULTS

The analysis of variance (Table 1) showed significant differences for most of the characters under study except for days to emergence, which indicates the presence of variation for all the characters among the population. Maximum variability was recorded for plant height, followed by number of pods per plant, number of clusters per plant and grain yield per plant.

Grain yield per plant exhibited maximum value of phenotypic coefficient of variation (45.32) followed by number of pods per plant (33.16) and number of clusters per plant (33.05), where as low estimates were observed for days to maturity (4.14) followed by days to emergence (6.78) and

Table 1: Analysis of variance for 10 quantitative traits in 20 F₂ field pea segregants

SoV	d.f	Days to emergence	Days to flowering	Days to maturity	Plant height	No. of primary branches per plant	No. of pods per plant	Pod length	No. of clusters per plant	100 seed weight	Grain yield/plant
Replication	2	0.15	16.62	75.62	4735.13	2.90	3309.3	0.12	232.21	49.6	2450.7
Treatment	19	0.61	42.69**	66.26**	2851.43**	1.096*	832.76*	1.3523**	425.32*	23.75**	452.63*
Error	38	0.41	12.06	2.318	230.98	0.59	447.72	0.19	177.67	4.0348	242.05
SEM		0.36	1.95	085	8.55	0.43	11.90	0.25	7.50	1.130	8.75
CD		1.0624	5.74	2.52	25.121	1.27	34.97	0.72	22.03	3.32	25.71

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

Table 2: Estimates of genetic parameters for 10 quantitative characters in 20 F₂ field pea segregants

Characters	VG	VP	GCV	PCV	h ² (broad sense)	GA	GA as percent of mean
Days to emergence	0.06	0.48	2.51	6.79	13.74	0.19	1.92
Days to flowering	10.21	22.26	4.67	6.89	45.87	4.46	6.52
Days to maturity	21.31	23.63	3.93	4.141	90.19	9.03	7.69
Plant height	873.48	1104.46	21.22	23.87	79.09	54.14	38.88
No. of primary branches per plant	0.17	0.76	10.18	21.69	22.06	0.39	9.85
No. of pods per plant	107.26	554.98	14.58	33.17	19.33	9.38	13.21
No. of clusters per plant	82.55	260.22	18.61	33.05	31.72	10.54	21.59
Pod length	0.39	0.578	12.06	14.75	66.83	1.05	20.32
100 seed weight	6.57	10.60	12.82	16.29	61.96	4.16	20.79
Grain yield/plant	46.01	288.06	18.11	45.32	15.97	5.58	14.91

days to 50% flowering (6.89). Maximum value of genotypic coefficient of variation was recorded for plant height (21.22) followed by number of clusters per plant (18.61) and grain yield per plant (18.11). Lowest genotypic coefficient of variation was observed for days to emergence (2.5) followed by days to maturity (3.93) and days to 50% flowering (4.67). The studies on genotypic and phenotypic coefficient of variation indicated that the magnitude of GCV and PCV was highest in case of grain yield per plant, plant height, number of clusters per plant, number of pods per plant, indicating the presence of high amount of variation and role of environment on the expression of these traits.

The estimates of heritability were varied from 90.19 to 13.73% (Table 2). Plant height exhibited high heritability (79%) coupled with moderately high genetic advance as percent of mean (38.88). Pod length, 100 seed weight and number of clusters per plant exhibited moderately high heritability with moderate genetic advance as percent of mean. The highest genetic advance was recorded for the character plant height (59.14), whereas grain yield per plant (5.58), 100 seed weight (4.15), days to flowering (4.45), pod length (1.04), number of primary branches per plant (0.39) and days to emergence (0.19) had low estimates of genetic advance.

From the correlation studies (Table 3) it is evident that the traits, plant height, number of primary branches per plant, number of pods per plant, number of clusters per plant and 100 seed weight exhibited significant and positive association with seed yield per plant. Further, character days to maturity exhibited significant and negative association with grain yield per plant.

Path analysis studies (Table 4) revealed that trait number of pods per plant (1.2286) depicted maximum direct effect on seed yield followed by plant height (0.6536) and 100 seed weight

Table 3: Estimates of genotypic (g) and phenotypic (p) correlation coefficient for ten quantitative characters in 20 F₂ field pea segregants

Characters	r	Days to flowering	Days to maturity	Plant height	No. of primary branches per plant	No. of pods per plant	No. of clusters per plant	Pod length	100 seed weight	Grain yield/ plant
Days to emergence	g	0.75**	0.17	0.59**	-0.2	0.067**	-0.36*	0.05	0.15	0.60**
	p	0.33**	0.06	0.13	0.11	-0.02	0.13	-0.15	-0.18	-0.02
Days to flowering	g	1	0.59**	0.53**	-0.15	0.59**	0.51**	-0.14	0.04	0.04
	p		0.32*	0.26*	0.09	0.19	0.18	-0.22	-0.15	-0.03
Days to maturity	g		1	-0.06	-0.13	-0.11	-0.05	-0.35**	-0.08	-0.73**
	p			-0.06	-0.06	-0.02	-0.01	-0.29*	-0.04	-0.28*
Plant height	g			1	0.67**	0.55**	0.51**	-0.03	-0.002	0.68**
	p				0.19	0.26*	0.25*	0.04	-0.05	0.32*
N o. of primary branches per plant	g				1	0.98**	0.60**	-0.36*	-0.24	0.99**
	p					0.1	0.29*	-0.26*	-0.18	0.0015
No. of pods per plant	g					1	1.00**	-0.83**	-0.44**	0.019
	p						0.68**	-0.24	-0.11	0.68**
No. of clusters per plant	g						1	-0.51**	-0.53**	0.33**
	p							-0.24	-0.13	0.22
Pod length	g							1	0.43**	-0.02
	p								0.39**	0.1
100 seed weight	g								1	0.66**
	p									0.29*

Table 4: Direct (Diagonal) and indirect effects of component traits attributing to seed yield in 20 F₂ field pea segregants at genotypic level

Characters	Days to emergence	Days to flowering	Days to maturity	Plant height	No. of primary branches per plant	No. of pods per plant	No. of clusters per plant	Pod length	100 seed weight
Days to emergence	-0.1076	-0.0813	-0.0188	-0.0643	0.0218	-0.0073	0.0394	-0.0058	-0.0169
Days to flowering	-0.1676	-0.222	-0.1313	-0.1184	0.0330	-0.1329	-0.1138	0.0318	-0.0090
Days to maturity	-0.0623	-0.2112	-0.3572	0.024	0.0465	0.0412	0.0185	0.1279	0.0283
Plant height	0.3903	0.3487	-0.0439	0.6536	0.4371	0.3606	0.3380	-0.0204	-0.0013
No. of primary branches per plant	-0.0144	-0.0106	-0.0093	0.0477	0.0714	0.0699	0.0435	-0.0259	-0.0174
No. of pods per plant	0.0832	0.7355	-0.1416	0.6778	1.2026	1.2286	1.4128	-1.0213	-0.5413
No. of clusters per plant	0.3768	-0.5278	0.0533	-0.5324	-0.6270	-1.1842	-1.0298	0.5261	0.5427
Pod length	0.0049	-0.0129	-0.0323	-0.0028	-0.0327	-0.0751	-0.0461	0.0903	0.0391
100 seed weight	0.1005	0.0258	-0.0506	-0.0013	-0.1559	-0.2818	-0.3371	0.2766	0.6396
r	0.6036	0.0441	-0.7317	0.684	0.9968	0.0189	0.3254	-0.0206	0.6638

(0.6396), while the traits like days to emergence (0.6036), days to flowering (-0.22), days to maturity (-0.3572) and number of clusters per plant (-1.0298) had negative direct effect on grain yield.

DISCUSSION

The analysis of variance reveals significant differences for most of the characters under study except for days to emergence, which indicates the presence of variation for all the characters among the population. High genetic variability for different quantitative traits in field pea was also reported earlier by Tiwari *et al.* (2001), Singh *et al.* (2003), Sharma *et al.* (2003), Ranjan *et al.*

(2006) and Singh and Singh (2006). The studies on genotypic and phenotypic coefficient of variation indicated that the magnitude of GCV and PCV was highest in case of grain yield per plant, plant height, number of clusters per plant, number of pods per plant, indicating the presence of high amount of variation and role of environment on the expression of these traits. The magnitudinal differences were medium to low in GCV and PCV for days to emergence, days to flowering, days to maturity, 100 seed weight and pod length suggesting the little role of environment in the expression of these characters. These findings were in agreement with the findings of Singh and Singh (1999), Mahanta *et al.* (2001), Singh *et al.* (2003) and Sharma *et al.* (2003).

Pod length, 100 seed weight and number of clusters per plant exhibited moderately high heritability with moderate genetic advance as percent of mean. 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 and character number of primary branches per plant showed moderate heritability coupled with low genetic advance as percent of mean, which revealed that selection could be delay for further generation, while traits like days to emergence, days to flowering showed lower GCV, low heritability and low genetic advance indicating limited scope of improvement of these traits by selection.

The correlation coefficient study (Table 3) shows that number of pods per plant serve as most important selection indices of seed yield. Mahanta *et al.* (2001), Tiwari *et al.* (2001), Singh and Srivastava (2001), Singh and Mishra (2002), Singh *et al.* (2003), Arya *et al.* (2004), Singh and Singh (2005) and Singh and Singh. (2006) emphasized the importance of number of pods per plant in determining seed yield in field pea. Several workers including Singh and Singh (1999), Tiwari *et al.* (2001), Singh and Srivastava (2001), Arya *et al.* (2004), Singh and Singh (2005) and Singh and Singh.(2006) reported the inter association of plant height with seed yield per plant. Singh and Singh (1999), Mahanta *et al.* (2001), Arya *et al.* (2004), Singh and Singh (2004), Gul *et al.* (2005) and Patel *et al.* (2006) reported similar finding that is 100 seed weight exhibited significant and positive association with grain yield per plant.

Number of pods per plant exerted highest direct effect on seed yield, also reported by Mahanta *et al.* (2001), Tiwari *et al.* (2001), Singh and Srivastava (2001), Singh and Mishra (2002), Singh *et al.* (2003), Arya *et al.* (2004), Singh and Singh (2005), Singh and Singh (2006), Avci and Ceyhan (2006) in field pea. This indicates that number of pods per plant is highly reliable component on yield.

Another important character with high direct effect on seed yield is plant height showed positive direct effect on seed yield, which were earlier reported by Tiwari *et al.* (2001), Singh and Srivastava (2001), Arya *et al.* (2004), Singh and Singh (2005) and Singh and Singh (2006). Data analysis reveals that number of pods per plant had the highest genotypic correlation coefficient and direct effect on seed yield and the corresponding indirect effect through plant height and 100 seed weight. Hence, number of pods per plant should be given prior attention in fieldpea improvement programme because of its major influence on yield.

In conclusion, most of the characters under study except for days to emergence show highly significant differences from the variance analysis. Plant height, pod length, 100 seed weight and number of clusters per plant exhibited moderately high heritability with moderate genetic advance as percent of mean. Estimate of GCV was also high for these traits indicating presence of additive gene effects, thus, these traits may be improved by mass, progeny or family selection and should

be considered in field pea improvement programme, whereas days to maturity showed high heritability coupled with low genetic advance as percent of mean and character number of primary branches per plant showed moderate heritability coupled with low genetic advance as percent of mean, suggesting that biparental mating, followed by progeny selection would be suitable for the selection of transgressive segregants and good recombinants. The significant genotypic and phenotypic correlation between days to flowering and days to maturity, can be used as a criterion for selecting lines with short life span. Number of pods per plant had the highest genotypic correlation coefficient and direct effect on seed yield and its indirect effect through plant height and 100 seed weight. Hence number of pods per plant serves as most important selection indices of seed yield.

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