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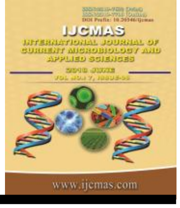

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Genetic Variability, Character Association and Path Analysis of Seed Yield and Its Contributing Traits in Field pea (*Pisum sativum* L. *var. arvense*)

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ABSTRACT

One hundred twenty field pea (*Pisum sativum* L. *var. arvense*) genotypes were evaluated with four check varieties *viz*., Ambika, Rachna, HFP 8909 and HUDP 15 to assess the genetic variability, association of different yield traits and direct & indirect effects of these traits on seed yield. Analysis of variance (ANOVA) revealed significant differences among all the genotypes for majority of the traits except number of primary branches per plant. The genotypes showed moderate to high level of genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV). The magnitudes of phenotypic coefficient of variance (PCV) for all the characters were slightly higher than their corresponding genotypic coefficient of variance (GCV), indicated very less environmental influence on the expression of the characters. Higher estimate of GCV (30.414) was recorded for number of seeds per pod followed by seed yield per plant (28.874). Correlation analysis indicated that seed yield per plant exhibited highly significant and positive correlation with harvest index, seeds per pod, pod length and 100-seed weight. Path analysis indicated that the highest positive and direct effect on seed yield per plant was exerted by harvest index and seeds per pod. Highly positive indirect effect on seed yield per plant was exerted by harvest index via seeds per pod, pod length and biological yield per plant. The characters identified above as important direct and indirect yield components can be used in formulation of selection strategy in field pea for selection of high yielding genotypes.

Keywords

Field pea (*Pisum sativum* L. *var. arvense*), Genetic variability, Character association and Path coefficient

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Introduction

Field pea (*Pisum sativum* L. *var*. *arvense*), is one of the most important pulse crops of India. It grows in winter season and belongs to tribe-Vicieae, order-Fabales, family-Leguminoceae (Fabaceae), sub-family-Papilionaceae, genus–*Pisum* and species–*sativum* having chromosomes, 2n = 2X = 14. Pea has versatile uses as food, feed and fodder. Pea (*Pisum sativum* L.) besides pulse, residues are nutritious feed for livestock and milch cattle and thus, offer an added advantage to the poor farmer families. There are two types of pea grown in India *viz*., vegetable type in which grains are very sweet when green and become wrinkled on drying and grain type where grains are generally dull white and round.

Green seeds of the grain type are not as sweet as vegetable type. The dry grains are consumed in various forms such as chat, chhola, dal, vegetable and flour. Green seeds are used as fresh, frozen or canned vegetable. Despite the inherent high productivity potential of pea, its production has been on decline and average productivity is miserably low, due to non-availability of input responsive, biotic and abiotic stress resistant varieties. Therefore, there is an urgent need to evolve high yielding varieties having high protein content and resistance to major biotic and abiotic stresses with suitability for different agro-climatic conditions and cropping systems. Since the scope of genetic improvement in any crops depends mainly on the extent of available genetic variability, this study was done to assess the genetic variability, association of different seed yield traits and direct & indirect effects of these traits on seed yield.

Materials and Methods

This study was designed to work out the status of genetic variability, association of different seed yield traits and direct & indirect effects of these traits on seed yield among one hundred twenty field pea genotypes with four check varieties *viz*., Ambika, Rachna, HUDP 15 and HFP 8909during Rabi 2015-16 at Genetics and Plant Breeding Research Farm of Narendra Deva University of Agriculture and Technology, Narendra Nagar, Kumarganj, Faizabad (U.P.).The seeds of different genotypes were available with Pulses Section of the University. The experiment was laid out in Augmented Block Design.

The entire experimental field was divided into 12 blocks of equal size and each block had 14 plots. Out of 14 plots in a block, 10 plots were used for accommodating the un-replicated test genotypes while 4 were allocated to the four check varieties. The four checks were randomly allocated along with the test genotypes in a block. Each plot consisted of a single row of 4 m length, following inter and intra row spacing 30 cm and 10 cm respectively. Recommended cultural practices were practiced to raise a good crop. The observations were recorded on randomly selected five competitive plants from each genotype for nine characters *viz*. Plant height (cm), number of primary branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight, biological yield per plant, harvest index and seed yield per plant (g), while two characters *viz*., days to 50 per cent flowering, days to maturity were recorded on the plot basis. The analysis of variance for augmented block design (Federer 1956), GCV and PCV (Burton and de Vane 1953), correlation coefficient (Searle 1961), path coefficient (Dewey and Lu 1959) were estimated.

Results and Discussion

The analysis of variance revealed highly significant differences among all the genotypes for all the characters under study except number of primary branches per plant, it indicated that high amount of variability was present among all the genotypes (Table 1). Phenotypic coefficient of variance (PCV) was higher than genotypic coefficient of variance (GCV), which indicated the effect of environment on the expression of characters (Table 2). Bashir *et al.*, (2017) and Meena *et al.*, (2017) also reported that relative magnitude of phenotypic coefficients of variation was higher than genotypic coefficients of variation for all the characters under study indicating environmental influence on the traits. Kumar (2008), Khan *et al.*, (2017), Pal and Singh (2012) and Ranjan *et al.*, (2006) also found that the genotypes differed significantly for all the traits except the number of branches per plant. Higher estimate of GCV was recorded for number of seeds per pod (30.414) followed by seed yield per plant (28.874).

Table.1 Analysis of variance of augmented block design for 11 characters in field pea genotypes

S.V.	d f	Days of 50 per cent flowering	Days to maturity	Plant height (cm)	Number of pods/ plant	Pod length (cm)	Number of primary branches/ plant	Number of seeds/ pod	100- Seed weight (g)	Biological yield/ plant (g)	Seed yield /plant (g)	Harvest index (%)
Blocks (ignoring Treatments)	11	38.383**	33.383**	3339.912**	16.654**	4.035**	0.747**	5.076**	11.367**	53.927**	25.134**	86.862**
Checks	3	40.076 **	51.028 **	11884.360 **	9.629 **	0.449**	0.180	0.541**	11.369**	7.847**	1.604**	40.878**
ERROR	33	2.864	4.088	248.028	0.087	0.008	0.067	0.005	0.074	0.188	0.024	0.773

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

Table.2 Range, mean, coefficient of variance and least significant differences for 11 characters of field pea genotypes

LSD_1 = difference between adjusted yield of two genotype in the same block.
LSD_2 =difference between two check means.
LSD_3 = difference between adjusted mean of two genotypes in the different block.
LSD_4 = difference between adjusted yield of genotype and check mean.
PCV = phenotypic coefficient of variance.
GCV = genotypic coefficient of variance.

Characters	**Range (Min-Max)**	**Mean Value**	**Coefficient of variance (%)**			**Range of parameters**			
			PCV	**GCV**	**Coefficient of variance (%)**	**LSD_1**	**LSD_2**	**LSD_3**	**LSD_4**
						5%	**5%**	**5%**	**5%**
Days to 50 per cent flowering	61.188-77.938	71.458	5.524	4.989	6.377	1.406	4.870	5.444	4.007
Days to maturity	111.875-130.375	122.415	3.169	2.703	3.768	1.679	5.818	6.504	4.787
Plant height (cm)	12.700-139.650	74.659	35.597	28.690	38.197	13.081	45.313	50.662	37.286
Number of primary branches /plant	0.718-2.697	1.433	28.317	21.789	29.253	0.215	0.746	0.834	0.614
Number of pods/ plant	10.885-26.060	15.282	14.571	14.442	16.863	0.245	0.850	0.950	0.699
Number of seeds/ pod	1.738-8.411	4.261	30.460	30.414	34.181	0.060	0.207	0.231	0.170
Pod length (cm)	3.005-9.018	5.293	22.786	22.720	25.659	0.076	0.263	0.294	0.216
100-seed weight (g)	10.872-27.432	18.348	14.463	14.386	16.163	0.226	0.783	0.875	0.644
Biological yield/plant(g)	15.999-38.913	26.101	15.047	14.955	17.107	0.360	1.247	1.394	1.026
Harvest index (%)	23.039-61.684	43.405	17.639	17.522	19.795	0.730	2.530	2.828	2.082
Seed yield/plant(g)	4.801-22.496	11.554	28.906	28.874	32.606	0.129	0.448	0.501	0.369

Table.3 Simple correlation coefficients between different characters in field pea genotypes

Characters	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of primary branches /plant	Number of pods / plant	Number of seeds / pod	Pod length (cm)	100-Seed weight	Biological yield/ plant	Harvest index (%)	Seed yield/ plant (g)
Days to 50 per cent flowering	**1.0000**	0.9412**	-0.1105	-0.1376	-0.1485	-0.0499	-0.0662	0.0176	-0.1773*	-0.0624	-0.1234
Days to maturity		**1.0000**	-0.0885	-0.1305	-0.1466	-0.0470	-0.0678	0.0485	-0.1526*	-0.0409	-0.0998
Plant height(cm)			**1.0000**	0.1887*	0.4387**	-0.2515**	-0.1829*	-0.1717*	0.0410	-0.2878**	-0.1487
Branches / plant				**1.0000**	0.4879**	-0.2380**	-0.1819*	-0.0712	0.0836	-0.1353	-0.0498
Pods / plant					**1.0000**	-0.4787**	-0.4199**	-0.0946	0.0519	-0.2130**	-0.0958
Seeds / pod						**1.0000**	0.9287**	-0.0334	0.6719**	0.7347**	0.7952**
Pod length(cm)							**1.0000**	-0.0503	0.6117**	0.6696**	0.7241**
100-Seed weight (g)								**1.0000**	0.1932*	0.4583**	0.3812**
Biological yield/ plant(g)									**1.0000**	0.5598**	0.8439**
Harvest index (%)										**1.0000**	0.9057**
Seed yield/plant (g)											**1.0000**

*, **Significant at 5% & 1% probability level Respectively.

Table.4 Direct and indirect effects of different characters on seed yield in fieldpea genotypes

Characters	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of primary branches / plant	Number of pods / plant	Number of seeds/ pod	Pod length (cm)	100-Seed weight (g)	Biological yield / plant(g)	Harvest index (%)	Seed yield / plant(g)
Days to 50 per cent flowering	**0.0145**	0.0137	-0.0016	-0.0020	-0.0022	-0.0007	-0.0010	0.0003	-0.0026	-0.0009	-0.1234
Days to maturity	-0.0113	**-0.0120**	0.0011	0.0016	0.0018	0.0006	0.0008	-0.0006	0.0018	0.0005	-0.0998
Plant height (cm)	-0.0011	-0.0009	**0.0102**	0.0019	0.0045	-0.0026	-0.0019	-0.0017	0.0004	-0.0029	-0.1487
Number of primary branches /plant	0.0014	0.0013	-0.0019	**-0.0102**	-0.0050	0.0024	0.0018	0.0007	-0.0008	0.0014	-0.0498
Number of pods/plant	-0.0097	-0.0096	0.0287	0.0319	**0.0654**	-0.0313	-0.0275	-0.0062	0.0034	-0.0139	-0.0958
Number of seeds/pod	-0.0068	-0.0064	-0.0342	-0.0324	-0.0651	**0.1360**	0.1263	-0.0045	0.0914	0.0999	0.7952
Pod length(cm)	0.0013	0.0013	0.0036	0.0035	0.0082	-0.0181	**-0.0195**	0.0010	-0.0119	-0.0131	0.7241
100 seed weight (g)	0.0008	0.0023	-0.0081	-0.0034	-0.0045	-0.0016	-0.0024	**0.0471**	0.0091	0.0216	0.3812
Biological yield/ plant (g)	-0.0769	-0.0662	0.0178	0.0363	0.0225	0.2915	0.2654	0.0838	**0.4339**	0.2429	0.8439
Harvest index (%)	-0.0356	-0.0233	-0.1641	-0.0772	-0.1214	0.4189	0.3818	0.2613	0.3192	**0.5702**	**0.9057**

R SQUARE = 0.9867, Residual factor = 0.1151, Bold figures indicate the direct effects

Correlation coefficients were worked out for different yield contributing characters in field pea (*Pisum sativum* L. *var*. *arvense*) genotypes (Table 3). The genotypic correlation coefficients between different characters were generally similar in sign and nature to the corresponding phenotypic correlation coefficients. However, in general the magnitudes of genotypic correlation coefficient were higher than their corresponding phenotypic correlation coefficient which suggested, a strong inherent relationship in different pair of characters. Similar, results have also been reported by Kumar *et al.,* (2003), Chaudhary and Sharma (2003) and Singh *et al.,* (2014). Seed yield per plant exhibited highly significant and positive correlation with harvest index followed by biological yield per plant, seeds per pod, pod length and 100-seed weight. However, seed yield per plant had negative and non-significant correlation with plant height followed by days to 50 per cent flowering, days to maturity, pods per plant and number of primary branches per plant. Singh *et al.,* (2014) also reported that biological yield per plant was highly significant with grain yield per plant. Earlier reports in fieldpea have also indicated existence of positive and highly significant association of weight of seeds per plant with the weight of pods per plant, biological weight per plant and harvest index recording (0.839, 0.694 and 0.505), respectively (Tofiq *et al.*, 2015). In addition Basaiwala *et al.,* (2013) also found that seed yield per plant was positively and significantly correlated with seeds per pod and harvest index. Another report in fieldpea also indicated that length and width of pod and 100-seed weight were associated positively and significantly with grain yield per plant (Singh *et al.*, 2008).

The direct and indirect effects of different characters on seed yield per plant are presented in Table 4. High positive direct contributions to seed yield per plant was exhibited by harvest index and biological yield per plant. However, seeds per pod, pods per plant, 100-seed weight, days to 50 per cent flowering and plant height exhibited considerable positive and direct effect on seed yield per plant. Tofiq *et al.,* (2015) also reported that biological weight per plant and harvest index exhibited maximum positive direct effect on weight of seeds per plant recording (0.630 and 0.456) respectively. Singh *et al.,* (2014) also reported that biological yield per plant, harvest index and plant height had positive and direct effect on grain yield per plant.

Similarly, days to 50 per cent flowering and pod length had positive and direct effect on grain yield per plant. Bashir *et al.,* (2017) also reported that 100-seed weight and number of seeds per pod had maximum direct effect on grain yield per plant. The occurrence of negative as well as positive indirect effects on seed yield by one or more characters present a complex situation where a compromise balance is required to attain proper balance of different yield components, for determining the ideotype of seed yield in field pea.

All over analysis indicated that high amount of variability was present in the genotypes under study which provides a better opportunity to select desirable genotypes for further utilization in breeding programme. Correlation and path analysis indicated that harvest index, biological yield per plant, number of seeds per pod, pod length and 100-seed weight, had true relationship with seed yield and they are the major yield contributing traits.

Hence, direct selection for these traits would be rewarding for yield improvement in field pea. Results obtained by Basaiwala *et al.,* (2013), Bashir *et al.,* (2017) have also in agreement with this finding.

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