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Studies of genetic variability, heritability and genetic advance for yield contributing traits in field pea (*Pisum sativum* L.)

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Abstract

Twenty-nine diverse genotypes of field pea were evaluated at agricultural research farm Nidharia of S.M.M. Town Post Graduate College, Ballia during *Rabi* 2015-2016 in a randomized block design (RBD) with three replication to study of genetic variability, heritability, genetic advance. The data was recorded on five randomly selected plants for nine characters. Analysis of variance (ANOVA) express significant for all characters. The highest mean value was observed for test weight (149.46) followed by days to maturity (97.35) and plant height (82.92). The estimates of phenotypic coefficients of variation (PCV) were slightly higher than genotypic coefficients of variation (GCV) for maximum traits. Highest genotypic coefficient of variance (GCV) and phenotypic coefficient of variance was recorded for number of pods per plant followed by number of seeds per plant. High heritability coupled with high genetic advance for plant height (99.50), seed yield per plant (98.60), number of pods per plant (98.10) and number of seeds per plant (97.20). The results revealed that these traits may serve as effective selection attribute during selection in breeding program for yield improvement in wheat.

Keywords: Pea (*Pisum sativum* L.), ANOVA, h^2 , genetic advance

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- Viciae, order-Fabales, family-Leguminosae (Fabaceae), sub-family-Papilionaceae, genus-*Pisum* and species-*sativum* having chromosomes, $2n = 2X = 14$. The origin of field pea was, probably, western Asia. Pea is one of the most important *rabi* season pulse crops cultivated mainly in U.P., M.P., Bihar, Rajasthan, Odessa, Maharashtra. As per FAO report, India is one of the largest producers of field pea in the world and stands at the fifth place. Yet, it had only seven percent of world production that is 7.8 Lakh tonnes. In India, U.P. is the highest producer of the pea accounted 60 per cent of the country production. The area, production and productivity of Ballia district in 2015-16 was 973 ha, 887 metric tonnes and 9.12 q/ha, respectively. (District Agriculture office information).

Field pea is rich in high quality protein and also good source of phosphorus, calcium and vitamins specifically vitamin A and D. Peas are highly nutritive having high percentage of protein (6.2g/100g of fresh weight) and carbohydrates (16.9g/100g of fresh weight) along with essential minerals, vitamins A, B and C (Makasheva, 1983) [7] and provide a major portion of the nutritive proteins to the poor masses, majority of which are vegetarian.

The development of an intensive breeding and improvement program needs detailed biological information and an understanding of genetic variation for yield and its components. There, must be a thorough knowledge of the existence of genetic variability, the mode of inheritance of economic characters, heritability, the kind of gene action and the relative magnitude of additive, dominance and total genotypic and phenotypic variance of the population. Considering the availability of genetic variability, there is scope of yield and quality improvement and there by develop export potential of field peas. Hence, the present investigation is carried out for various economic traits and to measure the extent of variability, heritability, genetic advance and their genetic makeup in field peas.

Materials and Methods

The experiment of present investigation was conducted to evaluate the twenty nine diverse field pea germplasm in Randomized Block Design at Agricultural Research Farm, Nidharia, S.M.M. Town Post Graduate College, Ballia (U.P.).

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These genotypes exhibited wide spectrum of variation for various agronomical and morphological characters. The experimental field was divided into three replications. Each germplasm consisted of two rows of 3 m length with spacing of plant to plant 15 cm and 30 cm between the rows. The recommended cultural practices were followed to raise a good crop. The observations were recorded on five randomly selected plants from each plot except days to 50% flowering and days to maturity. Five competitive plants from each plot were randomly selected for recording observations for all the quantitative characters except days to flowering and maturity, which was recorded on the plot basis. The data were recorded for the following characters; days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of seeds per plant, number of pods per plant, number of seeds per pod, test weight (1000-seed weight) (g) and seed yield per plant (g). Statistical analysis was carried out according to standard statistical procedure. The analysis of variance was done as suggested by Panse and Sukhatme (1978) [9]. The genotypic and phenotypic coefficients of variation were worked out according to the given by Robinson *et al.*, (1949) [10]. Heritability in broad sense and expected genetic advance on the basis of percent of mean were worked out according to the method advocated by Burton and Devane (1953) [11] and Johnson *et al.*, (1955) [4], respectively.

Results and Discussion

Analysis of variance was carried out separately for all characters are presented in (Table 1). The mean sum of squares due to treatments were highly significant for all the characters. In other words, the performances of the genotypes with respect to these characters were statistically different; suggesting that, there is ample scope for selection in the available genotypes of field pea. The results are with conformity of earlier researcher like, Sirohi *et al.* (2006) [11] and Chaudhary *et al.* (2010) [2].

The mean performance of various genotypes has also showed good range of variability for various characters, which were studied in present investigation (Table 2). The range record for plant height (43.63-128.66), number of branches per plant (2.0-6.16), number of pods per plant (9.31-51.26), no of seeds per plant (30.83-157.40), number of seeds per pod (2.51-4.66), days to maturity (78.66-106.33), days to 50% flowering (48.33-67.33), test weight (95.29-185.54) and seed yield per plant (3.62-19.96). The estimates of phenotypic coefficients of variation (PCV) were slightly higher than genotypic coefficients of variation (GCV) for maximum traits. The

higher magnitudes of PCV over GCV for almost all traits were due to some influence of environment on phenotypic expression. The highest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values were observed for number of pods per plant (43.76 – 43.34) followed by number of seeds per plant (39.72 – 39.16) and seed yield per plant (37.23 – 36.96). Similar, findings were also reported by Srivastava *et al.* (1974) [15], Mehta *et al.* (2005) [8] and Lavanya *et al.* (2010) [6]. The result indicate that breeders have opportunity for selection of desirable plants through the attributes had higher magnitudes of PCV/GCV.

Heritability estimates and provides the information and assessment of amount of transmissible variability of a population/genotypes. It is one of the most important basic factors that determine the genetic improvement or response due to selection, especially superior plants of the population/genotypes. In the present investigation, the range of heritability values in broad sense was recorded from 42.5% to 99% for all the characters under study. High estimate of heritability were recorded for 7 characters *viz.* plant height (99.50), seed yield per plant (98.60), number of pods per plant (98.10), number of seeds per plant (97.20), number of branches per plant (95.70), days to maturity (93.80) and days to 50% flowering (90.30). The above estimates gave an indication that substantial genetic improvement can be achieved in these characters and indicating that these traits were little influenced by environment. These require low selection intensity for improvement. Similar results were also reported by Gupta *et al.* (2006) [3]. The estimates of genetic advance for 9 characters studied, which range from 0.66% to 62.39%. High genetic advance was recorded for number of seeds per plant (62.39), plant height (56.94). The moderate genetic advance was recorded for test weight (27.29), number of pods per plant (19.61). The low estimates genetic advance were observed for days to maturity (10.80), seed yield per plant (9.05), days to 50% flowering (8.51), number of branches per plant (1.94) and number of seeds per pod (0.66) suggesting there by that these traits could be considered as reliable indices for selection and higher responses of this trait could be expected from selection. Similar findings were also reported by Kumar *et al.* 1997 [5], Sharma *et al.* 2007 [13], Singh *et al.* 2011 [14] and Sharma and Sharma (2012) [12].

The genetic advance (as per cent per mean) varied from 14.225% to 113.340%. The higher genetic advance (as per cent of mean) was recorded for no of pods per plant (113.340%) followed by number of seeds per plant (101.946%), seed yield per plant (96.866%), whereas lower genetic advance was recorded for days to maturity (14.225%).

Table 1: Analysis of Variance for nine characters in 29 genotype of pea (*Pisum sativum* L.)

Source of Variation	d.f.	Days to 50% flowering	Days to Maturity	Plant height in (cm)	Number of branches/plant	Number of pods per plant	Number of seeds/plant	Number of seeds/pods	1000 seed test weight	Seed yield per plant
Replication	2	1.45	1.15	1.03	0.67	0.08	1.34	0.01	2.34	0.26
Treatment	28	89.94**	546.81**	628.26**	6911.52**	169.17**	125.44**	29.26**	6.88**	224.49**
Error	56	2.00	1.88	3.49	0.12	1.86	26.92	0.33	345.27	0.29
Total	86									

** P=0.01.

Table 2: Mean, Range, SE, CD and Genotypic and Phenotypic Coefficient of variation Heritability, Genetic advance and Genetic advance in per cent of mean in pea strains (*Pisum sativum* L.)

S. No.	Characters	Mean Value	Range	Standard error (SE)	Critical difference	Coefficient of Variation		Heritability h^2 (b.s)%	Genetic Advance (5%)	Genetic advance as % of mean % (5%)
						GCV	PCV			
1	Days to 50% flowering	61.24	48.33-67.33	0.821	2.32**	7.10	7.473	90.30	8.51	17.822
2	Days to maturity	97.35	78.66-106.33	0.801	2.26**	5.56	5.742	93.80	10.80	14.225
3	Plant height (cm)	82.92	43.63-128.66	0.081	3.06**	33.41	33.490	99.50	56.94	88.013
4	Number of branches per plant	3.62	2.00-6.16	0.118	0.33**	26.59	27.188	95.70	1.94	68.671
5	Number of pods/plant	22.18	9.31-51.26	0.774	2.19**	43.34	43.767	98.10	19.61	113.340
6	Number of seeds/plant	78.43	30.83-157.40	3.003	8.50**	39.16	39.723	97.20	62.39	101.946
7	Number of seeds/pod	3.77	2.51-4.66	0.332	0.940**	13.11	20.10	42.50	0.66	22.588
8	Test weight (g)	149.46	95.29-185.54	10.734	30.411**	12.50	17.63	50.30	27.29	23.404
9	Seed yield/plant	11.98	3.62-19.96	0.309	0.877**	36.96	37.23	98.60	9.05	96.866

R= 0.05 for CD

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