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Study of genetic variability and heritability in various germplasm of field pea (*Pisum sativum* sub sp. *arvense* L.)

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Abstract

The present investigation was carried out with 13 genotypes during *Rabi* 2018 in CRD having 3 replication at field experimentation center of Department of Genetics and Plant Breeding, PDDUIAS Utlou. Significant differences were observed in the genotypes for all the 12 characters. Phenotypic coefficients of variation was higher than genotypic coefficient of variation indicating environmental influence on the traits. High heritability couple with high genetic advance as a percent of mean were observed for seed yield per plant (gm), biological yield(gm), plant height (cm), seed weight (gm), harvest index and number of pods per plant.

Keywords: Field pea, Variability, h^2 , GA, GCV, PCV

1. Introduction

Field pea is one of the world's oldest domesticated crops which is an economically valuable pulse crop grown around the globe for its protein rich seed and other soil restorative purposes (Mc Phee, 2003) [8]. It is the fourth leading legume in terms of consumption in the world. They are consume as fresh vegetables or dry seeds in most of the country. Field pea occupies about 0.73 million hectares area in India with a production of 0.72 million tone. About 90% of its area and production is limited to Uttar Pradesh alone. Other field pea growing states are Rajasthan, Haryana, Punjab and Jammu and Kashmir.

In any crop improvement programme, assessment of Genetic variability is prerequisite for effective selection of desired trait. In most of pea breeding programmes, the major traits of interest to pea breeders are yield and its component traits. The estimates of heritability help in selection of elite genotypes from diverse populations whereas the genetic advance is the measure of genetic gain under selection. Thus, genetic advance denotes the improvement in the mean genotypic value of selected population. Estimates of heritability along with genetic advance are more beneficial in yield improvement that can be made in a crop by selecting the best genotype for various related characters from the mixed parental populations or segregating populations. Realizing the importance of the above mentioned aspects in this important crop, the present study was undertaken to estimates the genetic variability, heritability and genetic advance for various quantitative characters of field pea.

2. Materials and Methods

The present investigation was conducted at the Department of Genetics and Plant Breeding Experimentation field, Pandit Deen Dayal Upadhyay Institute of Agriculture Sciences, Utlou, Bishnupur District, Manipur during the *Rabi* season of the year 2018-19. The experiment was laid out in a completely randomized design with 3 replications. Recommended dose of N:P:K was applied and all the recommended agronomic practices were followed to raise a healthy crop. Observation were recorded for 12 characters *viz.*, days to 50% flowering, days to maturity, plant height(cm), number of branches per plant, number of cluster per plant, number of pods per plant, pod length (cm), number of seeds per pod. Seed yield per plant (g), 100 seed weight (Test weight), Biological yield (g) and Harvest index (%). The data recorded on the above characters were subjected to the following statistical procedures namely analysis of variance as per Panse and Sukhatme (1985) [11], phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) were obtained by the formulae suggested by Burton

and Devane (1952) [5], heritability in broad sense (h^2) and genetic advance by using the procedure given by Allard (1960) [11].

3. Result and Discussion

The analysis of variance revealed significant differences among the 13 genotypes for all the 12 characters studied viz., days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of cluster per plant,

number of pods per plant, pod length(cm), Number of seeds per pod, seed yield per plant, 100 seed weight, biological yield (cm),harvest index(%).The analysis shows that there is great extend of variability among the genotypes regarding yield and yield components. So it is clear that, selection for all the traits among genotypes have a great impact and good scope of improvement. The results of the study were in agreement with the results reported by Benti *et al.* (2017) [12] and Bhuvanewari *et al.* (2016) [13].

Table 1: Analysis of variance for 12 characters in field pea

S.no.	Characters	Mean sum of square		'F'Value
		Genotype	Error	
		(d.f. = 12)	(d.f. = 26)	
1.	Days to 50% flowering	236**	42.61	5.53
2.	Days to maturity	66.15**	11.46	5.77
3.	Plant height (cm)	1644.3**	8.82	186.41
4.	Number of branches per plant	1.84**	0.35	5.13
5.	Number of cluster per plant	3.02**	0.56	5.36
6.	Number of pods per plant	25.35**	2.33	10.86
7.	Pod length (cm)	1.05**	0.12	8.62
8.	Number of seeds per pod	1.52**	0.38	3.97
9.	Seed yield per plant (gm)	188.87**	0.27	682.69
10.	100 seed weight	128.19**	1.81	70.81
11.	Biological yield (gm)	1366.07**	2.58	529.38
12.	Harvest index (%)	48.00**	0.83	57.79

d.f. = Degree of freedom, * = Significant at 1% level of significance, ** = Significant at 5% level of significance

Table 2: Estimates of genetic parameters for 12 characters in 13 field pea genotypes

S.no.	Characters	σ^2g	σ^2p	σ^2e	GCV	PCV	ECV	h^2 (b.s.) (%)	Genetic advance (5%)	Genetic advance as% of mean
1.	Days to 50% flowering	64.46	107.07	42.61	14.59	18.81	11.86	60.20	12.78	23.23
2.	Days to maturity	18.23	29.69	11.462	3.87	4.95	3.07	61.39	6.83	6.20
3.	Plant height (cm)	545.16	553.98	8.82	44.35	44.71	5.64	98.40	47.50	90.23
4.	Number of branches per plant	0.49	0.85	0.35	27.13	35.63	23.10	57.98	1.10	42.47
5.	Number of cluster per plant	0.82	1.38	0.56	26.95	35.02	22.35	59.24	1.43	42.69
6.	Number of pods per plant	7.67	10.007	2.33	28.35	32.37	15.63	76.74	4.99	51.14
7.	Pod length (cm)	0.30	0.43	0.12	8.02	9.48	5.04	71.69	0.96	13.97
8.	Number of seeds per pod	0.38	0.76	0.38	6.14	14.09	9.98	49.80	0.89	14.44
9.	Seed yield per plant (gm)	62.86	63.14	0.27	45.51	45.61	3.01	99.56	16.28	93.49
10.	100 seed weight	42.12	43.93	1.81	25.63	26.17	5.31	95.88	13.08	51.65
11.	Biological yield (gm)	454.49	457.07	2.58	34.70	34.80	2.61	99.43	43.77	71.26
12.	Harvest index (%)	15.72	16.55	0.83	14.32	14.69	3.29	94.98	7.95	28.72

The magnitude of phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters studied indicating environmental influence on the traits. Similar findings were also reported by Sunil *et al.* (2017) [14], Naveen *et al.* (2015) [10], Meena *et al.* (2017) [9], Brijesh *et al.* (2017) [4] and Vaibhav *et al.* (2018) [15]. The estimates of genotypic and phenotypic variances was highest for plant height(545.16, 553.98) followed by biological yield (454.49, 457.07) and days to 50% flowering (64.46, 107.07).

Heritability(broad sense) estimates ranged from 49.80 to 99.56. Seed yield per plant (99.56) showed the highest value of heritability followed by biological yield (99.43), plant height (98.40), 100 seed weight (95.88) and harvest index (94.98). Number of pods per plant (76.74), has high value of heritability followed by pod length (71.69) and days to maturity (61.39). Number of seeds per pod (49.80) has the moderate value of heritability followed by number of branches per plant (57.98), number of cluster per plant (59.24) and days to 50% flowering (60.20).

The estimates of genetic advance as a percent of mean ranged between 6.20 to 93.94. Seed yield per plant (93.49) showed

the highest value of genetic advance. Plant height (90.23), biological yield (71.26), 100 seed weight (51.65), number of pods per plant (51.14), number of cluster per plant (42.69), number of branches per plant (42.47), harvest index (28.72) and days to 50% flowering (23.23) also had high value of genetic advance. Number of seeds per pod (14.44) and pod length (13.97) has moderate value of genetic advance. The value of genetic advance was found least in days to maturity (6.20).

Moderate value of heritability with high value of genetic advance are found in days to 50% flowering (60.20/23.23), number of cluster per plant (59.24/42.69) and number of branches per plant (57.98/42.47). High heritability with low genetic advance was observed in days to maturity (61.39/6.20). Ravi *et al.* (2014) [12] also reported high heritability coupled with high genetic advance for plant height and moderate for days to 50% flowering. Lal *et al.* (2011) [7] also observed high broad sense heritability for plant height, biological yield and number of pods per plant suggesting that these traits would respond to selection owing their high genetic variability and transmissibility. High expected genetic

advance couple with high heritability estimates were predicted for seed yield per plant, pods per plant and plant height indicating least influence by the environmental variation also revealed by Singh and Singh (2006)^[13]. Similar findings was also reported by Hafiz *et al.* (2014)^[6].

4. Conclusion

From the experimental results it can be concluded that considerable genetic variability was found amongst all the 13 genotypes for all the characters studied indicating that selection would be effective in further breeding programme. The characters with high heritability coupled with high genetic advanced as percent of mean i.e seed yield per plant, biological yield, plant height, 100 seed weight, harvest index and number of pods per plant should be given top priority during selection for further utilization in breeding programme.

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