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Analysis of Genetic Variability and Genetic Divergence for Polygenic Traits in Field Pea (*Pisum sativum* L.)

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Abstract

A study was planned with 15 pea genotypes to estimation the available genetic variability and diversity in these genotypes. The experiment trial was conducted at Agriculture Research Farm of B.R.D.P.G. College (Campus), Deoria with three replications in a Randomized block design during rabi 2021-22. The observations were noted for eleven metric traits viz., days to 50% germination, days to 50% flowering, days to maturity, plant height (cm), branches per plant, pod length (cm), number of seeds per pod, weight of 100 seeds/test index (g), seed yield per plant (g), biological yield per plant (g) and harvest index (%). The results showed a substantial amount of genetic diversity among these genotypes. High heritability along with high genetic advance was noted for the traits pod length (42.55), branch per plant (35.37), seed yield per plant (27.50), test weight (23.97), biological yield per plant (23.94), seed per pod (21.20). Which showed that these traits were governed by additive gene action. The D^2 analysis made two separate non overlapping clusters of these genetic materials. The cluster I had the highest mean for days to 50% flowering (75.07), days to maturity (108.55), seed per pod (4.66), 100-seed weight (15.08) and harvest index (43.69). The highest (D = 91.82) inter cluster distance was observed between cluster I and II.

Key words : *genetic variability, heritability, genetic advance, genetic diversity, coefficient of variation.*

Introduction

Around 7 to 10 percent of the nation's total food grain production comes from pulses, which occupy about 20 percent of the land planted to food grains. With around 25–28% of the global production and 35% of the global area, India is the world's largest producer and consumer of pulses. Since pulses are mostly cultivated in India under rain fed conditions in regions with considerable rainfall variability, the productivity of pulses in India is less than half that of the USA and Canada. By 2050, the UK will need to import 39 million tonnes of pulses, meaning that production would have to increase by 2.2% annually. With the significant place in pulses map of the world, India has also been the largest importer of pulses from the world.

Leguminosae (Fabaceae) is a family that includes the field pea (*Pisum sativum* L.). Growing legume vegetables in the cooler months is crucial. It is primarily planted in the temperate part of the planet because it is a cool season crop. Its cultivation is only permitted during the milder winter months in tropical and subtropical regions. A high supply of protein, amino acids, and carbs is the field pea. Peas can be combined with other vegetables or consumed on their own. In the fields of North Indian conditions, it is primarily grown as a winter crop, and in the bumpy area, as a late spring food (1). Pea originated in the Mediterranean region, with Ethiopia and the Near East being its secondary origin regions (2).

The pea (*Pisum sativum* L.), a cool-season or rabi crop with diploid chromosomes numbering 2n=2x=14, belongs to the family Leguminosae. Peas are grown for a variety of reasons. The young peas are consumed as veggies, frozen food, or food in cans. In order to produce soup, dry pea grains are split (3).

In India, total area under pulses was 146.00 lakh hectares in which area under pea crop occupied 9.45 lakh hectares during 2019 (4). The major growing region are Uttar Pradesh, Madhya Pradesh, Jharkhand, Punjab, Himachal Pradesh, Haryana, West Bengal and Bihar etc. Uttar Pradesh stands at rank 1st in production of pea in India (5).

The genetic variability subsisting among different cultivars of a crop species is known as genetic diversity. Variability differs from diversity in such a way that variability shows observable phenotypic differences whereas diversity may or may not having observable phenotypic differences, latter may or may not have such an expression. The method of surveying hereditary difference is the D^2 measurement proposed by (6).

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Table-1 : Analysis of variation for 11 characters in pea (*Pisum sativum* L.).

Source of variation	Replications	Treatments	Error
	2 df	14 df	28 df
Day to 50% germination	0.29	1.47**	0.29
Days to 50% flowering	0.42	17.78**	1.57
Days to 50% maturity	0.6	43.94**	1.31
Plant height	0.33	1798.76**	1.49
Branch per plant	0.64	5.22**	0.23
Pod length	0.07	3.23**	0.04
Seed per pod	0.38	1.17**	0.16
Test weight	0.01	11.98**	0.79
Biological yield	0.55	67.94**	1.12
Harvest index	0.47	21.15**	1.28
Seed yield per plant	0.4	17.40**	0.38

*, ** significant at 5% and 1% level, respectively.

Table-2 : Estimation of heritability, genetic advance and coefficient of variation in field pea genotypes.

Character	Mean	Min	Max	var (g)	var (p)	Herit-ability (%)	GA	GA% mean	GCV (%)	PCV (%)
Day to 50% germination	9.49	8.33	10.33	0.39	0.68	57.67	0.98	10.34	6.61	8.71
Day to 50% flowering	74.91	70.33	77.33	5.41	6.97	77.55	4.22	5.63	3.10	3.52
Day to maturity	108.20	103.33	114.33	14.21	15.52	91.53	7.43	6.87	3.48	3.64
Plant height	65.91	43.33	148.77	599.09	600.58	99.75	50.36	76.41	37.14	37.18
Branch per plant	7.05	5.13	9.93	1.67	1.89	87.96	2.49	35.37	18.31	19.52
Pod length	4.89	3.85	7.85	1.06	1.11	95.96	2.08	42.55	21.08	21.52
Seed per pod	4.63	3.80	5.80	0.34	0.50	67.65	0.98	21.20	12.51	15.21
Test weight	15.08	11.23	19.07	3.73	4.52	82.49	3.61	23.97	12.81	14.11
Biological yield per plant	39.62	32.45	49.21	22.27	23.40	95.19	9.49	23.94	11.91	12.21
Harvest index	43.60	38.80	47.62	6.62	7.90	83.82	4.85	11.13	5.90	6.45
Seed yield per plant	17.28	14.54	23.44	5.67	6.05	93.73	4.75	27.50	13.79	14.24

Keeping the above points in view, the present investigation has been carried out to estimate the amount of genetic variability and diversity in field pea genotypes.

Materials and methods

Experimental site : The field experiment under present investigation was conducted during *rabi* 2021-22 at Agriculture Research farm of Baba Raghav Das Post Graduate College, Deoria (U.P.). Geographically, this College is located in the east part of Uttar Pradesh, India. The site of experiment is located at 26.5°N latitude, 83.79°E longitude and 68 meter (223 feet) above the mean sea level. The climate of district Deoria is semi-arid with hot summer and cold winter nearly 80% of total rain fall is received during the monsoon (only up to September) with a few showers in the winter.

Experimental materials and methods : The experimental material for the present investigation comprised of 15 field pea genotypes including one check from indigenous collection available at Department of Genetics and Plant Breeding, B.R.D.P.G. College, Deoria (U.P.) were sown in Randomized Block Design with three replications during *rabi* 2021-22. The recommended packages and practices were followed during cropping period to grow a good crop. The row-to-row distance was maintained at 30 cm and plant to plant 10 cm.

Observation recorded : To observe the yield, contributing traits and seed characteristics, five plants were randomly tagged to record these observations. By taking the average, the mean value for the treatment was computed. The characters studied and techniques adopted to record the observations are given below: days to 50% germination, days to 50% flowering, days to maturity, plant height (cm), branches per plant, pod length (cm), number of seeds per pod, weight of 100 seeds/test index (g), seed yield per plant (g), biological yield per plant (g) and harvest index (%).

Statistical analyses : The experimental data collected the respect of 11 characters on 15 field pea genotypes and one check were compiled by taking the mean values of selected plants in each plot and subjected for following statistical analyses: Analysis of variance (7), Estimation of Heritability (8), Genetic advance as per cent of mean (9) and Genetic diversity (D^2) analysis (6).

Results and Discussion

Analysis of variance : Analysis of variance (ANOVA) for Randomized Block Design (RBD) was conducted for 11 characters such as days to 50% germination, days to 50%

Table-3a : Number of genotypes in each cluster of field pea genotypes.

Clusters	No of genotypes	Genotypes
I	14	Rachana, Aarkel, HUW¬15, GS-10, AZAD-AP-3, PANT-25, PANT-74, JP-885, B-22, KPMR-400, PANT-P-5, KPMR-522, IPFD99-13, IPF99-25
II	1	Aparna

Table-3b : Intra and inter cluster distance between the genotypes.

Clusters	I	II
I	19.86	
II	91.82	0.00

Table-3c : Average mean performance of clusters of field pea genotypes.

Clusters	Days to 50% germination	Days to 50% flowering	Days to maturity	Plant height	Branch per plant	Pod length	Seed per pod	100-seed weight	Biological yield per plant	Harvest index	Seed yield per plant
I	9.48	75.07	108.55	59.99	6.84	4.89	4.66	15.08	38.96	43.69	17.03
II	9.67	72.67	103.33	148.77	9.93	4.89	4.27	14.97	48.97	42.34	20.74

flowering, plant height, days to maturity, pod length, branches per plant, number of pods per plant, number of seed per plant, biological yield per plant, test weight, harvest index and seed yield per plant. The variation in treatment for all characters was found significant (Table-1). Earlier researchers namely (10) have also reported significant amount of variability in the genetic material for all the characters studied in field pea.

Estimation of variability, heritability and genetic advance : Variability in germplasm is a prerequisite for effectiveness of selection in plant breeding. The germplasm due to selection in quantitative characters depends primarily on nature and magnitude of genetic variability present on the population to be improved. Genotypic variation is due to the different genotypic constitution of the individuals in a population. Variability due to environment or environmental variance, which embraces all variations of non-genetic origin, can have a great variety of cause and its nature depends very much on the character and the organism studied. The estimates of phenotypic variance and genotypic variance along with their phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) and heritability in broad sense, genetic advance, and genetic advance in percent of 5% mean for 11 characters are expressed in table 2. The PCV and GCV were recorded highest for the traits plant height (cm) was recorded 37.18 and 37.14 respectively, followed by pod length which was 21.52 and 21.08 respectively. Remaining characters existed moderate to low coefficient of variation such as for days to 50% germination PCV and GCV was 8.71 and 6.61 respectively; for days to 50% flowering PCV and GCV was 3.52 and 3.10 respectively; for days to maturity PCV and GCV was recorded 3.64 and 3.48 respectively; for branches per plant PCV and GCV was recorded 19.52 and 18.31 respectively; PCV and GCV were recorded for seed per pod 15.21 and 12.51 respectively; PCV and GCV were recorded for test weight 14.11 and 12.81 respectively; PCV and GCV for biological yield per plant (g) was recorded 12.21 and 11.91 respectively; PCV and GCV for harvest index was observed 6.45 and 5.90 while PCV and GCV for seed yield per plant was recorded 14.24 and 13.79 respectively. Earlier researchers also observed high amount of PCV and GCV values for number of primary branches per plant per plant (11). Moderate estimates for PCV and GCV were also observed by previous workers for days to 50% flowering (12), pod length (13), pods per plant (14), seeds per pod (14), shelling percentage (14) and seed yield per plant (15). The variance (p) and variance(g) were recorded for the different traits such as for days to 50% germination variance (p) and variance(g) was 0.68,0.39 respectively; for days to 50% flowering variance (p) and variance(g)was 6.97 and 5.41 respectively; for days to maturity variance (p) and variance(g) was recorded 15.52 and 14.21 respectively; for plant height (cm) variance (p) and variance(g) was recorded 600.58 and 599.09 respectively; for branches per plant variance (p) and variance(g) was recorded 1.89 and 1.67 respectively; variance (p) and variance(g) for pod length was 1.11 and 1.06; variance (p)and GCV were recorded for seed per pod 0.50 and 0.34 respectively; variance (p) and variance(g) were recorded for test weight 4.52 and 3.73 respectively; variance (p) and variance(g)for biological yield per plant (g) was recorded 23.40 and 22.27 respectively; variance (p) and variance(g) for harvest index was observed 7.90 and 6.62 while variance (p) and variance(g) for seed yield per plant was recorded 6.05 and 5.67 respectively. Most of the results are in accordance with the previous reports of (16).

Heritability estimates along with genetic advance are normally more helpful in predicting the grain under selection than heritability estimates alone. The estimate of heritability can be utilized for the prediction of genetic gain, which indicates the genetic improvement that would result from the selection of best individual. Hence, the maximum value of heritability (99.75) was reported for plant height and minimum value of heritability (57.67) was reported for the day to 50% germination while remaining characters expressed the heritability in decreasing order such as pods length (95.96), biological yield per plant (95.19), seed yield per plant (93.73), day to maturity (91.53), branch per plant (87.96), harvest index (83.82), test weight (82.49), day to 50% flowering (77.55), seed per pod (67.65) day to 50%germination (57.67). High heritability estimates were also reported for days to first flowering (Ali *et al.* 2018), days to 50% flowering (11), primary branches per plant (17), plant height (18), seeds per pod (16), pods per plant (19) and pod yield per plant (16).

Genetic advance is the improvement in the mean genotypic value of selected individual over the parental population. High heritability accompanied with high genetic advance indicated that the heritability is due to additive genetic effect and selection may be effective while high heritability coupled with low genetic advance indicates pre-dominance of non-additive gene action while low heritability is exhibited due to influence of environmental interaction rather than genotypic selection for such characters may not be rewarding. The maximum value of genetic advance in percent of mean was found for the plant height (76.41) and minimum value was found for the day to 50% flowering (5.63) however, the value for the rest characters was found in decreasing order pod length (42.55), branch per plant (35.37), seed yield per plant (27.50), test weight (23.97), biological yield per plant (23.94), seed per pod (21.20), harvest index (11.13), day to 50% germination (10.34), days to maturity (6.87) and day to 50% flowering (5.63). High degree of genetic advance was also revealed for days to first flower by 17; for days to 50% flowering by (18); for number of primary branches per plant per plant (17); for seeds per pod (19); for pods per plant by (19); for pod yield per plant by (16).

Genetic divergence : The analysis of variance revealed highly significant differences among genotypes for all the twenty characters under investigation. These differences suggest the existence of considerable divergence among the material under study.

D^2 analysis : Based on the estimates of genetic divergence, all the fifteen varieties of field pea were grouped into two different clusters as shown in Table 3(a). Generalized distance was estimated through Mahalanobis' D^2-statistic. Among the two clusters, cluster I was largest including 14 genotypes followed by II had one variety.

The intra and inter-cluster average distance : The average distance within and between clusters and average inter and intra cluster D^2 values are presented in Table-3b. In this table, the diagonal values are mean intra cluster and off the diagonal values are inter cluster distances. The only and highest (D=91.82) inter cluster distance was observed between cluster I and II indicating wide diversity between genotypes in these clusters. The highest (D=19.86) intra-cluster distance was found for cluster I followed by cluster II (0.00).

Cluster means : Clusters means of all 11 characters are presented in Table-5. The cluster I had the highest mean for days to 50% flowering (75.07), days to maturity (108.55), seed per pod (4.66), 100-seed weight (15.08) and harvest index (43.69). For remaining traits, it had the minimum mean performance.

The cluster II had the highest mean values for days to 50% germination (9.67), plant height (148.77), branch per plant (9.93), pod length (4.89), biological yield per plant (48.97) and seed yield per plant in cluster II (20.74) and lowest for cluster I (17.03). The crosses between genotypes belonging to the clusters separated by low inter cluster distances are unlikely to throw promising recombinants in the segregating generations. A perusal of Table 3(c) reveals that significant existence of different clusters in respect of intra-cluster group means for eleven characters, the crossing between entries belonging to cluster pairs separated by large inter-cluster distances and having high cluster means for one or other characters to be improved likely to be more fruitful. (20) also reported maximum intra-cluster distances in their respective genetic stock used.

Conclusions

Pea is an important pulse crop and hold a strong position in the Indian economy. Poor and rural people of India mostly use this crop as their daily diet due to their lower economic condition and at low-cost availability of this crop. Pod length, number of branches per plant, seed per pod and seed yield per plant are ultimate economic traits. High heritability along with high genetic advance was noted for the traits pod length, branch per plant, seed yield per plant, test weight, biological yield per plant and seed per pod. Which showed that these traits were governed by additive gene action and had a substantial amount of variability among these genotypes. Selection will be rewarding for the improvement of these traits in our breeding program.

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