Original Research Article

Genetic variability, heritabilityand genetic advance studies in field pea (*Pisum sativum* L.) for yield and its attributing traits

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ABSTRACT

An investigation was carried out with 48 genotypes of pea obtained through line x tester analysis and were tested using a randomized block experimental design with three replications at Tirhut College of Agriculture, Dholi, Dr. Rajendra Prasad Central Agricultural University, Bihar, India. The result showed a highly significant difference for all the ~~fourteen~~ 14characters under study. The variability, heritability and genetic advance as percent mean were studied for all the characters.~~High~~ A high genotypic coefficient of variation was observed in the trait's number of secondary branches, plant height, number of pods per plant, harvest index, nodules fresh weight and nodules dry weight. High heritability coupled with high genetic advance estimates was recorded for the number of secondary branches, plant height, pod length, number of seeds per pod, number of pods per plant, 100 seed weight, grain yield per plant, harvest index, nodules fresh weight and nodules dry weight indicating the role of additive gene action and selection for these traits is reliable.

Keywords: ~~genetic~~ Genetic variability, genetic advance, heritability, traits, yield.

INTRODUCTION

Pulses play a crucial role, especially in developing nations like India where the majority of the population is vegetarian. Pulses belong to the family Leguminosaeand the subfamily Papilionoiaceae. For a vegetarian diet, ~~Pulses~~ pulses are an excellent substitute ~~of~~ forprotein as they are nutritive and economical. They are also rich sources of amino acids, especially lysine. Because of their simple digestion of the seeds, 22-24% protein content, and increased demand for amino-rich base substances for livestock feed or ancillary goods for human nutrition, these pulses are becoming important in day-to-day life (1).

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Pea (*Pisum sativum* L.), ~~that~~ whichis among the pulses, is a leguminous plant with in Papilionoiaceae subfamily and a member of the dicotyledons class, ~~.~~with 2n=14 is the chromosome number found in the pea. It is extensively cultivated in cooler climates and is native to South Western Asia. Due to the fact that it is primarily a cold-weather crop, it can endure light frost. Field peas (*Pisum sativum* L. *var. arvense*), also referred to as dry peas, and garden peas (*Pisum sativum* L. *var. hortens*), commonly known as table peas, are the two types of peas ~~which~~ thatare traditionally grown.

Genetic diversity in peas is still crucial for crop breeding programmes to be successful~~,~~ since the diversity of the crop influences the extent to which it may be improved through selection. Additionally, the relative magnitudes of the phenotypic and genotypic variation coefficients provide a solid indication of the degree of population diversity (2).Estimating the characteristics of variability, particularly heritability and genetic advance, are crucial indications for improving characters through selection~~.~~, ~~Though~~ though selection for highly heritable characters is more efficient for a successful breeding strategy. Considering this, an effort was made in the present research to evaluate the degree of variability, heritability, and genetic advance for various pea characteristics.

MATERIALS AND METHODS

The current study was conducted at Tirhut College of Agriculture, Dholi, Dr. RPCAU, Bihar, India ~~the research was carried out~~. The experiment was performed during the *rabi* of 2021–~~20~~22 to generate crosses and 2022–~~20~~23 to evaluate the parents and crosses. Dholi is 55 meters above MSL and is geographically located at 25.9 °~~°~~N latitude and 85.9 °E longitude. The soil condition is sandy loam with a modest level of organic matter and an alluvial origin. The weather during the growing season was ideal for the normal growth and development of field pea crop.

Seven lines (females) namely, VL 42, RFPG 111, TRCP 8, HUPT 1810, KPF 14-29, DDR-23~~,~~ and IPFD 19-9, and five testers (males) namely, IPF-18-7, PANT P 436, PANT P 462, APARNA and HFP 1545 of field pea were chosen due to their phenotypic variability.In *rabi* 2020–~~20~~21, 35 crosses were produced utilizing seven lines and five testers. Therefore, the 35 crosses and their ~~twelve~~ 12progenitors, including the popular check variety RACHANA, were utilized as the experimental materials.

Estimation of heritability

Heritability in a broad sense was estimated following the formula as suggested by Johnson *et al.* (1955):

$$\text{Heritability } (h^2)\ (\%) = \frac{\sigma^2 g}{\sigma 2p} \times 100$$

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Heritability in a narrow sense was calculated according to the formula

$$\text{Heritability (ns) (\%)} = \frac{2\sigma2gca}{2\sigma2gca + \sigma2sca + \sigma2e} \quad x\ 100$$

Where,

$\sigma2g$ = genotypic variance
$\sigma2\ p$ = phenotypic variance
$\sigma2e$ = environment variance

As suggested by (3) heritability (h^2) estimates were categorized as:

Low: 0 - 30%; Medium: 30 – 60 %; High: Above 60%

As suggested by Robinson (1966) ~~for~~ narrow sense heritability ~~were~~ wascategorized as:

Low: 5-10%; Medium: 10-30%; High: more than 30%

Genetic Advance (GA)

Genetic advance refers to the expected gain or improvement in the next generation by selecting superior individuals under a certain amount of selection pressure. From the heritability estimates the genetic advance was estimated.

$$GA = h^2(bs).\ \sigma p.\ K$$

Where,

h^2(bs) = ~~Heritibility~~ Heritability in broad sense

K = Selection differential, a constant value is 2.06 at 5% selection intensity

σp= Phenotypic Standard Deviation

Genetic Advance as percent of Mean (GAM)

In order to visualize the relative utility of genetic advance among the characters, genetic advance as percent of mean was computed.

$$GAM = \frac{GA}{\overline{X}} \quad x\ 100$$

Where,

GA = Genetic Advance

X = General mean of the character

The range of genetic advance as percent of the mean was classified as suggested by Johnson *et al.* (1955)

Low = less than 10%; Moderate = 10-20%; High = more than 20%

RESULTS AND DISCUSSION

The analysis of variance (Table 1) for 48 pea genotypes with regards to yield traits~~has~~ revealed ~~that~~ their significant amount of variation that could be further used in the breeding programmes. The mean sum of squares of all the ~~fourteen~~ 14characters included in the study revealed to be highly significant among the treatments ~~that~~ whichindicates there is variation and these genotypes can be selected further. Whereas the replication mean sum of squares of all the traits revealed to be non-significant which indicates that there is a reduction in the experimental error among the genotypes. Various genetic variability parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability, genetic advance (GA) and genetic advance as a percentage of mean (GAM) for ~~fourteen~~ 14 characters are represented in ~~the~~ Table 2.

Days to 50% flowering: For the following trait PCV and GCV values were found to be 3.90 and 4.21, respectively. Heritability value (85%) was found to be very high whereas genetic advance value was low (4.98). The GAM value was found to be low (7.46).

Number of primary branches: Moderate values of GCV and PCV for the above trait ~~was~~ wereobserved to be 10.07 and 13.56, respectively. Moderate level of heritability (55%) and low level of genetic advance (1.11) values were observed. The GAM value was found to be moderate (15.42).

Number of secondary branches: High values of GCV and PCV for the above trait ~~was~~ wereobserved to be 21.35 and 22.65, respectively. Very high levels of heritability (88%) and low levels of genetic advance (6.19) values were observed. The GAM value was found to be high (41.45).

Plant height: High values of GCV and PCV for the above trait ~~was~~ wereobserved to be 38.08 and 38.46, respectively. Very high level of heritability (98%) and high level of genetic advance (70.40) values were observed. The GAM value was found to be high (77.67).

Days to maturity: Low values of GCV and PCV for the above trait ~~was~~ wereobserved to be 2.81 and 4.09, respectively. Medium levels of heritability (47%) and low levels of genetic advance (4.71) values were observed. The GAM value was found to be low (3.99).

Pod length: Moderate values of GCV and PCV for the above trait ~~was~~ wereobserved to be 13.35 and 15.22, respectively. High levels of heritability (76%) and low level of genetic advance (1.56) values were observed. The GAM value was found to be high (24.13).

Number of seeds per pod: Moderate value of GCV (18.85) and a high value of PCV (22.8) for the above trait ~~was~~ wereobserved respectively. High levels of heritability (68%) and low levels of genetic advance (1.58) values were observed. The GAM value was found to be high (32.10).

Number of pods per plant: High values of GCV and PCV for the above trait ~~was~~ wereobserved to be 27.81 and 28.31 respectively. Very high levels of heritability (96%) and moderate levels of genetic advance (15.16) values were observed. The GAM value was found to be high (56.29).

100 Seed weight: Moderate value of GCV (18.94) and a high value of PCV (20.19) for the above trait ~~was~~ were observed respectively. Very high levels of heritability (87%) and low levels of genetic advance (5.26) values were observed. The GAM value was found to be high (36.60).

Grain yield per plant: Moderate values of GCV and PCV for the above trait ~~was~~ wereobserved to be 15.48 and 17.02, respectively. Very high levels of heritability (82%) and low levels of genetic advance (5.04) values were observed. The GAM value was found to be high (29.03).

Harvest index: High values of GCV and PCV for the above trait ~~was~~ wereobserved to be 22.92 and 24.50, respectively. Very high levels of heritability (87%) and moderate levels of genetic advance (13.18) values were observed. The GAM value was found to be high (44.19).

Number of nodules per plant: Low value of GCV (9.79) and moderate value of PCV (11.32) for the above trait was observed respectively. High levels of heritability (74%) and low levels of genetic advance (3.41) values were observed. The GAM value was found to be moderate (17.46).

Nodules fresh weight: High values of GCV and PCV for the above trait ~~was~~ wereobserved to be 39.45 and 40.29 respectively. Very high levels of heritability (95%) and low levels of genetic advance (1.26) values were observed. GAM value was found to be high (79.58).

Nodules dry weight: High values of GCV and PCV for the above trait ~~was~~ wereobserved to be 38.64 and 39.33 respectively. Very high levels of heritability (96%) and low levels of genetic advance (0.38) values were observed. The GAM value was found to be high (78.20).

Based on the above categorization, all the ~~fourteen~~ 14 traits are divided and the findings revealed that high PCV and GCV values are recorded in characters like number of secondary branches, plant height, number of pods per plant, harvest index, nodules fresh weight and nodules dry weight suggesting for substantial improvement through selection of these traits in later generations. These findings are in ~~a~~ line ~~to~~ withthe findings reported by (4,5,6).

Similarly, moderate PCV and GCV values are recorded in traits like the number of primary branches, pod length, number of seeds per pod, 100 seed weight, grain yield per plant, and number of nodules per plant suggesting a considerable amount of variability among the genotypes. These findings are in ~~a~~ line ~~to~~ withthe findings reported by (7,8,9,10).

Low magnitude of PCV and GCV was noted for the characters like days to 50% flowering and days to maturity representing the existence of low variability and selection of these traits are may not be worthwhile in early generations. These findings are in ~~a~~ line ~~to~~ withthe findings reported by (11,12,13,14).

High heritability coupled with high genetic advance estimates was recorded for number of secondary branches, plant height, pod length, number of seeds per pod, number of pods per plant, 100 seed weight, grain yield per plant, harvest index, nodules fresh weight and nodules dry weight indicating the role of additive gene action and selection for these traits is reliable.These findings are in ~~a~~ line ~~to~~ withthe findings reported by (15, 16, 17).

High heritability and moderate genetic advance were recorded for number of primary branches and number of nodules per plant indicating the presence of both additive and non-additive gene action.These findings are in ~~a~~ line ~~to~~ withthe findings reported by (18,19). While high level of heritability and low genetic advance for days to 50% flowering and days to maturity indicating the role of non- additive genes in the inheritance of these traits. These findings are in ~~a~~ line ~~to~~ withthe findings reported by(20,21,22)and improvement of these traits through mere selection is not useful therefore breeder should go for heterosis breeding or recurrent selection for improvement of these characters.

CONCLUSION

As all the traits under evaluation significantly differed from one another, the current study on variance revealed significant variability among all the genotypes.The characters *viz.*, number of secondary branches, plant height, pod length, number of pods per plant, nodule fresh weight and nodules dry weight showed high value for GCV, heritability and genetic advance as percentage of mean. Therefore, additive gene effects control these traits. Thus, when selecting pea cultivars to increase yield, these traits should be taken into consideration.

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Table 1. Analysis of variance for fourteen characters in field pea

S. No	Character	Range		Mean sum of squares			C.V. %
		Min	Max	Replication (d.f = 2)	Treatments (d.f = 47)	Error (d.f = 94)	
1	Days to 50% flowering	61.66	73.33	1.89	21.58**	1.12	1.58
2	Number of primary branches	5.33	9.33	1.02	2.03**	0.43	9.08
3	Number of secondary branches	8.33	20.33	3.88	31.82**	1.28	7.57
4	Plant height	49.66	162.33	6.88	3598.93**	24.04	5.41
5	Days to maturity	110	124.66	13.77	45.55**	12.32	2.97
6	Pod length	4.93	8.9	0.05	2.47**	0.22	7.31
7	Number of seeds per pod	3.33	6.66	1.02	3.01**	0.40	12.85
8	Number of pods per plant	15	47.66	4.69	170.54**	2.03	5.28
9	100 seed weight	9.89	21.55	2.55	23.25**	1.01	7.00
10	Grain yield per plant	11.74	24.78	1.69	23.28**	1.51	7.06
11	Harvest index	17.9	50.24	18.44	147.12**	6.66	8.64
12	Number of nodules per plant	15.93	23.8	1.13	12.27**	1.23	5.67
13	Nodules fresh weight	0.35	2.95	0.039	1.21**	0.02	8.17
14	Nodules dry weight	0.17	0.92	0.004	0.11**	0.001	7.34

** Significant at p = 0.01% level

Table 2. Estimates of variability parameters in fourteen field pea genotypes

S. No	Character	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)	Heritability (%)	Genetic Advance	Genetic Advance as % of mean
1	Days to 50% flowering	6.8220	7.9447	3.9081	4.2174	85	4.9858	7.4601
2	Number of primary branches	0.53	0.96	10.07	13.56	55	1.11	15.42
3	Number of secondary branches	10.18	11.45	21.35	22.65	88	6.19	41.45
4	Plant height	1191.63	1215.66	38.08	38.46	98	70.40	77.67
5	Days to maturity	11.07	23.39	2.81	4.09	47	4.71	3.99
6	Pod length	0.75	0.97	13.35	15.22	76	1.56	24.13
7	Number of seeds per pod	0.86	1.27	18.85	22.8	68	1.58	32.10
8	Number of pods per plant	56.17	58.19	27.81	28.31	96	15.16	56.29
9	100 seed weight	7.41	8.42	18.94	20.19	87	5.26	36.60
10	Grain yield per plant	7.25	8.76	15.48	17.02	82	5.04	29.03
11	Harvest index	46.82	53.47	22.92	24.50	87	13.18	44.19
12	Number of nodules per plant	3.67	4.91	9.79	11.32	74	3.41	17.46
13	Nodules fresh weight	0.39	0.41	39.45	40.29	95	1.26	79.58
14	Nodules dry weight	0.035	0.036	38.64	39.33	96	0.38	78.2

Where, GCV- ~~genotypic~~ Genotypic coefficient of variance, PCV - ~~phenotypic~~ Phenotypic coefficient of variance.

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