

Genetic Analysis of Yield and Yield Attributing Components in Pea

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ABSTRACT

The genetic analysis of pea (*Pisum sativum* L.) was carried out twenty-five germplasm lines under irrigated normal soil condition to determine mode of inheritance of yield and its contributing traits. The experiment was conducted to evaluate in Randomized Block Design (RBD) with three replication at Nidharia Agriculture Farm S.M.M.Town P.G. College, Ballia, U.P. The data was recorded on twelve characters viz, such as days to 50% germination, days to 50% 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 for all the characters. All the 25 genotypes showed vast range of variation for all the 12 characters under consideration. Genotypes such as 725-D, 940-D and ARPANA produced the highest seed yield and several out-yielder genotypes are also observed. The highest amount of genotypic and phenotypic coefficient of variations were observed for plant height, number of pods per plant and seed yield per plant. The maximum value of heritability (99) was reported for plant height and minimum value of heritability (29) was reported for the pod length while remaining characters expressed the heritability in decreasing order such as pods per plant (97), biological yield per plant (97), seed yield per plant (94), number of branches per plant (85), days to 50% germination (84), harvest index (80), days to 50% flowering (79), test weight (69), days to maturity (64) and number of seed per pod (94). The maximum value of genetic advance in percent of mean was found for the plant height (86.63) and minimum value was found for the days to maturity (3.889). The result revealed that these traits may serve as effective selection attributes during selection in breeding program for yield improvement.

KEYWORDS

pea (*Pisum sativum* L.), mean, viability, heritability, genetic advance

INTRODUCTION

Pea (*Pisum sativum* L.) also called "matar" is an important legume vegetable for temperate and sub-tropical regions of the world. Pea is the major pulse crop which contributes the soil improvement either as green manure crop or as cover crop. Botanically pea pods are fruits since they contain seeds and develop from the ovary. Pea (*Pisum sativum* L.) is an annual self-pollinated crop having diploid chromosomes number $2n=2x=14$, cool season or Rabi season crop, belongs to family leguminosae or fabaceae and sub family is papilionaceae. Pea is a multi-purpose crop consumed in the form of vegetables, salad, soup, chhola, besan, dal etc. It is also being used to make chapati after mixing with barley or wheat. Pea is processed (canned, frozen or dehydrated) for consumption in the off season. In some parts of the world, it is grown for grazing purposes. It has high protein content (20%) with all essential amino acids important for normal activity of living organisms. The seed of the pea may be spherical or wrinkled. The germination of the pea is hypogeal fashion not epigeal fashion and the cotyledon remaining below the ground surface. The pea plant is semi-erect, hollow, slender and succulent stem. Leaves are pinnately compound and each leaf has 1 to 3 pairs of leaflet and terminal branch tendrils. A

pair of leaf-like bracts or stipule is found at the base of petiole of each leaf. The inflorescence is an axillary raceme. The length of pod is 4 to 10 cm, and the shape of pod is inflated to almost cylindrical. Pea has high nutritive value and contains higher protein (20 - 25%), starch (25-50%), sugar (2-10%), minerals (5%) and water (10-15%) in their seed. Pea is rich in phosphorus and calcium and good source of vitamins like vitamin A and D. Pulse is rich in Lysine but deficient in sulphur containing amino acids like cysteine and methionine. Nutritional value of dry pea grain (%) are higher than the green pea grain. It also plays an important role in nitrogen fixation. Short duration and early varieties of pea have the potential to provide premium returns to the farmers as they can fetch a better price and can be used for multi-cropping. In India, total area under pulses was 146.00 lakh hectares in which area under pea crop occupied 9.45 lakh hectares during 2019. The genetic improvement of crop for quantitative traits requires reliable estimates of genetic variability, heritability and genetic advancement of breeding materials (Dudley and Moll, 1969). In the present study attempt has been made to study the genetics of important quantitative traits including yield.

ARTICLE INFO

Received on	:	12.01.2022
Accepted on	:	05.03.2022
Published online	:	16.03.2022



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MATERIALS AND METHODS

The experiment was conducted at Agriculture Farm Nidharia of Shri Murl Manohar Town P.G. College Ballia (U.P.) during winter season in November 2020 - 2021. The experiment was conducted to evaluate twenty-five germplasm lines under irrigated normal soil condition in Randomized Block Design (RBD). The entire experimental field was divided into 3 blocks of equal size and each block had twenty-five entries. The row to row spacing was 30 cm, plant to plant distance was 15 cm and treatment to treatment distance was 40 cm. All cultural practices essential for the good crop of pea were applied for obtaining healthy and competitive crop stand. Five plants from each plot were randomly selected for recording observations for all the quantitative characters except days to 50% germination, days to 50% flowering and days to maturity, which were recorded on line basis. Average of these five plants in respect of different plant characters were used for statistical analysis. Observations of twelve characters and yield attributing characters were recorded. The experimental data were compiled by computing the mean of each treatment was subjected to the statistical analysis: Analysis of Variance (ANOVA) by Fisher and Yates (1943), heritability (In broad sense) is calculated by the formula suggested by Hanson (1963) and genetic advance was calculated by the formula suggested by Johnson *et al* (1955).

RESULTS AND DISCUSSION

Success of any plant breeding program depends upon the amount of variability present in the population. In the experiment, Randomized Block Design (RBD) was used to estimate the genetic variability and its further interpretation in the form of other genetic components. The analysis of variance of treatment (Table 1) being significant for all the characters paves way for research work due to the amount of genetic variability and diversity present in the population. Mean of the population sample (Table 2) provides an idea about the central tendency of variability for all the traits. All the 25 genotypes showed vast range of variation for all the 12 characters under consideration. Genotypes such as 725-D, 940-D and ARPANA produced the highest seed yield and several out-yielder genotypes are also observed. These genotypes can be used as donor parent in breeding programme and can be beneficial for transferring the desired gene. In this term, several other genotypes can be used for their importance in enhancing the respective characters such as 974 for days to 50% germination, 940-D for days to 50% flowering, 942-D for days to maturity, 883-T for plant height, 944-T for number of branches per plant and test weight, 725-D for number of pods per plant, and biological yield, 966-D for pod length, DDR-13 for number of seed per pod and 890-D for harvest index.

Table 1: Analysis of variation for 12 characters in pea (*Pisum sativum* L.)

Source of variation	d.f	Days to 50% germination	Days to 50% flowering	Days to Maturity	Plant Height (cm)	No. of Branches/Plant	Pod/PlantPod Length (cm)	seed/pod	Test Weight (g)	Biological yield/plant(g)	Harvest index (%)	Seed yield per plant (g)	
Replication	2	1.973	14.29	3.253	1.42	0.023	0.52	0.165	0.328	0.521	1.833	0.173	0.691
Treatment	24	9.364**	35.07**	25.424**	4523.07**	0.56**	161.89**	0.341**	0.480**	5.659**	159.60**	105.28**	28.346**
Error	48	0.542	2.751	3.989	2.96	0.030	1.133	0.152	0.074	0.730	1.269	7.69	0.578

** Significant at 1% level of significance

The Range, Grand mean, coefficient of variation (CV) and CD of 12 characters was expressed in Table 3. The grand mean recorded for days to 50% germination was 11.83 days. Genotype 944-T and 974 (9.33) have lowest mean while the genotype 522-D (17.00) has highest mean value. Genotypes 944-T and 974 showed earlier germination over the all treatment. Coefficient of variation for this trait was reported 6.23. The general mean for days to 50% flowering was recorded 79.91 while minimum and maximum range for this character was recorded 71.33 days (940- D) and 84.67 days (Sapna-D,913) respectively. However, genotypes 940-D show the early flowering (71.33 days) and genotypes Sapna-D and 913 showed the late flowering. Coefficient of variation was recorded 2.08

for days to 50% flowering. The mean value for days to maturity was recorded 113.41 days while the range varies from 105.67 (942-D) to highest 119.33 (816- D) for this trait. Coefficient of variation was estimated at 1.76 for days to maturity. The plant height recorded from lowest to highest was 51.68 (966-D) and 166.22 (883-T). However, the general mean for plant height was estimated at 92.21 cm. Coefficient of variation for plant height was 1.87. The minimum number of branches per plant was counted for genotype 974 (2.73) while the maximum number of branches per plant was counted for genotype 944-T (4.33). However, the grand mean for this trait was 3.60. Coefficient of variation was observed for this trait 4.86.

Table 2: Mean value of different characters of pea

Sr. No	Characters	Days to 50% germination	Days to 50% flowering	Days To Maturity	Plant Height (cm)	No. of Branches/ Plant	Pod/Plant Length (cm)	seed/ pod	Test Weight (g)	Biological yield per plant(g)	Harvest index (%)	Seed yield/plant (g)	
1	522-D	17.00	82.33	114.67	53.71	3.87	17.80	5.83	4.20	18.83	24.00	40.17	9.64
2	DDR-13	13.00	84.00	116.00	76.62	3.33	17.53	5.93	5.20	14.37	25.43	44.74	11.39
3	914-T	10.67	79.00	113.33	133.07	4.13	28.00	5.61	4.27	16.30	41.01	35.55	14.59
4	947-T	10.67	83.33	116.00	59.57	3.93	17.67	6.10	4.47	16.93	22.89	36.65	8.39
5	944-T	9.33	80.00	110.67	141.32	4.33	20.80	5.51	4.00	19.83	34.49	29.22	10.06
6	945-D	12.67	80.67	112.67	58.65	3.93	20.93	6.03	4.80	17.27	25.70	39.38	10.11
7	915-D	12.33	79.00	114.00	92.64	3.40	11.77	5.61	3.80	17.07	29.73	27.36	8.11
8	SIKHA	11.00	79.00	113.00	128.39	3.67	27.47	5.11	4.15	16.93	35.19	34.23	12.05
9	883-T	10.67	76.67	112.33	166.22	4.27	29.87	5.11	3.73	18.40	36.56	34.37	12.56
10	RACHANA-T	10.33	75.33	114.67	108.17	3.00	34.33	4.88	3.93	16.20	38.25	39.80	15.55
11	937	12.33	82.33	117.33	135.14	4.07	29.47	5.58	4.40	19.07	44.29	34.33	15.19
12	913	12.33	84.67	114.67	61.15	3.13	12.60	5.56	4.00	16.67	20.63	31.74	6.53
13	957-T	10.33	78.33	116.00	161.57	4.13	21.40	5.47	4.13	16.33	29.98	31.93	9.57
14	974	9.33	82.00	117.00	154.51	2.73	19.13	5.87	5.07	19.23	40.69	34.11	13.88
15	940-D	10.33	71.33	112.00	64.34	3.53	30.33	5.98	4.73	17.53	38.49	42.79	16.45
16	SWATI	12.00	74.00	108.67	80.69	3.47	23.13	5.65	4.67	15.63	30.13	39.98	12.04
17	400-D	11.33	81.33	111.33	62.05	4.00	23.40	5.56	4.67	16.97	27.83	45.67	12.68
18	942-D	10.33	75.00	105.67	72.78	3.53	28.10	6.02	4.67	17.43	35.73	38.82	13.85
19	815-D	12.67	81.33	112.67	53.93	3.00	18.00	5.73	4.33	18.80	27.16	37.79	10.26
20	890-D	11.67	80.00	110.67	61.19	3.40	27.57	6.21	4.73	15.80	31.45	47.45	14.93
21	SAPNA-D	13.67	84.67	114.00	63.43	3.00	20.73	5.65	4.07	16.17	31.02	36.56	11.35
22	725-D	11.33	79.33	114.00	128.81	3.63	37.33	5.63	4.27	18.07	51.22	33.05	16.91
23	816-D	13.33	82.67	119.33	64.58	3.67	8.07	5.81	4.73	18.70	26.59	22.37	5.95
24	966-D	11.67	82.67	114.00	51.68	3.47	20.93	6.25	4.87	18.77	31.96	42.53	13.57
25	ARPANA	15.33	78.67	110.67	71.09	3.40	34.13	5.43	4.00	19.07	38.17	42.36	16.17
	Mean	11.83	79.91	113.41	92.21	3.60	23.22	5.68	4.40	17.45	32.74	36.92	12.07

The grand mean calculated for pods per plant was 23.22. The minimum value observed for this character was 8.07 (816-D) while maximum value was 37.33 (725-D). Coefficient of variation was found 4.59 for this trait. The mean value for pod length was recorded 5.68 while the pod length measured maximum for genotype 966-D (6.25) and minimum measured for genotype Rachna-T was 4.88. Coefficient of variation was observed 6.68 for this character. The grand mean for seeds per pod was recorded 4.40, while minimum and maximum value for this character was observed 3.73 (883-T) and 5.20 (DDR-

13). Top three lines are DDR-13, 974 and 966-D. The value of coefficient of variation was reported 6.20 for number of seeds per pod. For the test weight, mean value was recorded 17.45 while the highest and lowest value was estimated 19.83 (944-T) and 14.37 (DDR-13). The value of coefficient of variation was estimated 4.90 for test weight. The biological yield per plant having mean value 32.74 while the minimum and maximum value for this character were observed 20.63 (913) and 51.22 (725-D) respectively. The value of coefficient of variation was recorded 3.44 for this character. The minimum

and maximum range for harvest index were estimated 22.37 (816-D) and 47.45 (890-D) respectively. While grand mean observed for this character was 36.92. The value of coefficient of variation was reported 7.51 for harvest index. The grand mean for seed yield per plant was observed 12.07 while the minimum and maximum range for this character was reported 5.95 (816-D) and 16.91 (725-D) respectively. Coefficient of variation was found 6.30 for seed yield per plant. Genotypes such as 725-D, 940-D and ARPANA produced the highest seed yield and several out-yielder genotypes are also

observed. These genotypes can be used as donor parent in breeding programme and can be beneficial for transferring the desired gene. In this term, several other genotypes can be used for their importance in enhancing the respective characters such as 974 for days to 50% germination, 940-D for days to 50% flowering, 942-D for days to maturity, 883-T for plant height, 944-T for number of branches per plant and test weight, 725-D for number of pods per plant, and biological yield, 966-D for pod length, DDR-13 for number of seed per pod and 890-D for harvest index.

Table 3: The Range, Grand mean, coefficient of variation (CV) and CD of 12 characters of pea

Sr. No.	Characters	Range		Grand mean	Coefficient of Variation (CV)	Critical Differences (CD)
		Min.	Max.			
1	Days to 50% germination	9.33	17.00	11.83	6.23	1.21
2	Days to 50% flowering	71.33	84.67	79.91	2.08	2.72
3	Days to maturity	105.67	119.33	113.41	1.76	3.28
4	Plant height	51.68	166.22	92.21	1.87	2.83
5	Branches per plant	2.73	4.33	3.60	4.86	0.29
6	Pods per plant	8.07	37.33	23.22	4.59	1.75
7	Pod length (cm)	4.88	6.25	5.68	6.86	0.64
8	Seeds per pod	3.73	5.20	4.40	6.20	0.45
9	Test weight (100 seeds)	14.37	19.83	17.45	4.90	1.40
10	Biological yield per plant (g)	20.63	51.22	32.74	3.44	1.85
11	Harvest index (%)	22.37	47.45	36.92	7.51	4.55
12	Seed yield per plant (g)	5.95	16.91	12.07	6.30	1.25

It is well known fact that the genotypic coefficient of variation (GCV) is comparatively more important than phenotypic coefficient of variation (PCV) because a high amount of genetic variation helps in the formation of effective breeding programme for crop improvement (Table 4). Hence, the emphasis should be given on genotypic variation in comparison to phenotypic variation. In this experiment the highest amount of genotypic and phenotypic coefficient of variations were observed for plant height, number of pods per plant and seed yield per plant. Result indicates that selection of desired plants can easily be done on the basis of these three characters (plant height, number of pods per plant and seed yield per plant) taking into consideration for developing desirable and high yielding varieties. In general, the phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) due to the environmental effect added into it. Similar results were reported by Singh (1985), Rao (1994), Kumaran *et al* (1995), Sardana *et al* (2007), Jeberson *et al* (2016). Coefficient of heritability in broad sense or the degree of genetic determination is the ratio of

Vg/Vp expresses the extent to which phenotypes are determined by their respective genotypes. Heritability and genetic advance are important elements to estimate the heritable variation present in the population. In other words, the fundamental requirement of selection for any character is the heritable value of the genotype which is to be taken into consideration. The heritability is always expressed in percentage. The expected genetic advance is the prediction of a breeder that is upto which extent a character can be improved in the next generation when 5-10% of superior genotypes are selected. High heritability was reported for plant height, number of pods per plant, biological yield per plant and seed yield per plant which concludes the idea that these characters show maximum response to selection and superior genotype can be evolved through selection unexpression of these characters. Few characters showed moderate level of heritability and gave a fair chance of selection for better genotype with respect to these characters. Pod length had discouraging result and will not be taken into consideration.

Table 4: Estimates of phenotypic variance , genotypic variance and environmental variance for twelve characters in pea

Characters	Phenotypic variance	Genotypic variance	Environmental variance	PCV	GCV	Heritability (h ²) (%)	Genetic advance (5%)	Genetic advance in percent of(5%) mean
Days to 50% germination	3.4833	2.9406	0.5428	15.781	14.4995	84	3.246	27.443
Days to 50% flowering	13.5244	10.7728	2.7517	4.6023	4.1075	79	6.034	7.552
Days To Maturity	11.1344	7.145	3.9894	2.9422	2.3569	64	4.411	3.889
Plant Height (cm)	1509.6671	1506.7024	2.9647	42.1362	42.0948	99	79.883	86.63
Branches/Plant	0.2087	0.178	0.0307	12.6839	11.7138	85	0.803	22.285
Pod/Plant	54.7192	53.5855	1.1336	31.8572	31.5255	97	14.923	64.266
Pod Length (cm)	0.2151	0.063	0.1521	8.1578	4.416	29	0.28	4.925
seed/pod	0.2095	0.1353	0.0741	10.4136	8.3702	64	0.609	13.859
Test Weight (100 seeds)	2.3736	1.6432	0.7305	8.8267	7.3439	69	2.197	12.587
Biological Yield per plant(g)	54.0472	52.7782	1.269	22.4517	22.1866	97	14.789	45.165
Harvest index (%)	40.2243	32.5321	7.6921	17.1788	15.4491	80	10.567	28.621
Seed Yield / Plant(g)	9.8345	9.256	0.5785	25.9809	25.2052	94	6.08	50.372

Similarly higher genetic advance was estimated for plant height, number of pods per plant and biological yield per plant predicting better chances for selection of these characters.

Heritability from a very long time has been the basis of argument leading to selection. Here, heritability is not a stable parameter in any genotype due the variations found in it because of environmental effect. Heritability (broad sense) did not give better information for expected genetic advance due to the fact that the numerator used for calculating heritability included dominance as well as epistasis. The value of dominance and epistasis did not retain in the next generation. Thereby heritability (narrow sense) is considered more useful in breeding programmes which include only the additive component of the variation which is heritable. High heritability coupled with high genetic advance indicated that these characters were mainly governed by the additive nature of gene action and can easily be exploited in selection and

be carried in further generations. The results are in conformity with the findings of Sureja and Sharma (2000), Lal *et al* (2011), Meena *et al* (2017) and Kumar *et al* (2019).

CONCLUSION

In general, the present investigation suggest that the sufficient variability exist in the present pea breeding material. Studies of variation indicated that considerable variation in plant height, number of pods per plant, seed yield per plant, biological yield per plant, harvest index and days to 50% germination would be used for bringing an improvement through the breeding programme. Studies on heritability and genetic advance indicated that the plant height, biological yield per plant, number of pods per plant, seed yield per plant, branches per plant and days to 50% germination bear considerable importance for supporting in crop improvement.

REFERENCES

- Dudley JW and Moll RH. 1969. Interpretation and use of estimates of heritability and genetic variances in plant breeding 1. *Crop science* 9:257-262.
- Fisher RA and Yates F 1943. Statistical tables for biological, agricultural and medical research.
- Hanson WD. 1963. *Heritability*. In: *Statistical Genetics and Plant Breeding* 125-140.
- Jeberson MS, Shasidher KS and Iyanar K. 2016. Estimation of genetic variability expected genetic advance, correlation path analysis in field pea. *Pisum sativum L.*. *Electronic Journal of Plant Breeding* 7(4):1074-1078.
- Johnson HW, Robinson HF and Comstock RE. 1955. Estimates of genetic and environmental variability in soyabean. *Agron. J* 45:314-318.
- Kumar TNV, Alloli TB, Hadimani HP, Ajjappalavar PS, Satish D, Kareem A and Hanchinamani CN. 2019. Studies on correlation and path analysis in garden pea (*Pisum sativum L.*) varieties. *Int. J. Curr. Microbiol. App. Sci* 8(12):3024-3031.
- Kumaran SS, Natrajan S and Thamburaj S 1995.
- Lal GM, Meena ML, Chandra K and Singh CM. 2011. Assessment of genetic variability and interrelation on between yield and its contributing components in field pea. *Pisum sativum L.*. *Envt and Eco* 29:3-1235.

- Meena BL, Das SP, Meena SK, Kumari R, Devi AG and Devi HL. 2017. Assessment of GCV, PCV, heritability and genetic advance for yield and its components in field pea (*Pisum sativum* L.). *Int. J. Curr. Microbiol. App. Sci* 6(5):1025-1033.
- Rao SK. 1994. *Agriculture Science Digest* (2):129-130.
- Sardana S, Mahajan RK, Gautam NK and Ram B. 2007. Genetic variability in pea (*Pisum sativum* L.) germplasm for utilization. *SABRAO J. Breed. Genetics* 39(1):31-41.
- Singh RK. 1985. Genotypic and phenotypic variability and correlation in pea (*Pisum sativum* L.). *Indian J. Agri. Sci* 55(3):147-150.
- Sureja KP and Sharma AK. 2000. Genetic variability correlation and path coefficient analysis in garden pea. *Pisum sativum* L.). *Current Res* 9(1):43-45.

Citation:

Singh B and Prakash R. 2022. Genetic Analysis of Yield and Yield Attributing Components in Pea. *Journal of AgriSearch* 9(1): 6-11