



Genetic variability studies in field pea (*Pisum sativum* L.) for yield and associated characters

Kommineni Jagadeesh ✉

Department of Genetics and Plant Breeding, PJTSAU, Hyderabad, India

C.S. Mahto

Department of Genetics and Plant Breeding, BAU, Ranchi, India

Niraj Kumar

Department of Genetics and Plant Breeding, BAU, Ranchi, India

ARTICLE INFO

Received : 01 June 2022

Revised : 18 August 2022

Accepted : 06 November 2022

Available online: 07 March 2023

Key Words:

Heritability

Genetic advance

Yield

Crop improvement

ABSTRACT

The prime and foremost objective of the study was to estimate the genetic variability for yield and its associated characteristics among the 23 genotypes of field pea and also to engender information regarding genetic parameters like range, mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as a percentage over means for the 18 traits under consideration. It was disclosed from the results of the analysis of variance that there exists a difference among the 23 genotypes for all the 18 traits under consideration. The trait including primary branches per plant, secondary branches per plant, plant height, swelling capacity, swelling index, biological yield per plant, and seed yield recorded high amounts of GCV and PCV. High heritability combined with high genetic advance was documented for the trait's plant height and seeds per plant, whereas high heritability coupled with low genetic advance, was recorded for the trait's days to fifty % flowering, days to maturity, primary branches per plant, secondary branches per plant, pod length, 100 seed weight, percent disease incidence and seed yield per plant. The existing variability identified can be further exploited in crop improvement of field pea.

Introduction

Pisum sativum L. ($2n=2x=14$) could be a diploid annual autogamous crop that belongs to Leguminosae or Fabaceae family, taxon rosoid, dicot family, and tribe viciae. Field pea is native to southwest Asia and is extensively cultivated in temperate climates. It is an atmospheric condition crop that may withstand light-weight frost. The peas under cultivation are of two types i. e field pea (*Pisum sativum* L. var. arvense) which is additionally referred to as dry pea and the other is garden pea (*Pisum sativum* L. var. hortense) which is additionally referred to as table pea. Field peas are grown for a variety of uses, including seed, feed, silage, and green compost. It contains a lot of high-quality protein. It is a low-cost source of proteins (especially tryptophan and lysine; 21–25 percent), complex carbohydrates, high fiber (soluble and

insoluble), B vitamins, folate, and mineral content, including calcium, iron, and potassium, with 86–87 percent total digestible nutrients and very low sodium and fat content (Tiwari and Singh, 2012). Peas are also thought to be a good source of biologically active components with possible health benefits such as reducing the prevalence of colon cancer, coronary diseases, and type-2-diabetes (Kour *et al.*, 2020). Peas are an essential agricultural crop because of their beneficial characteristics such as high-value nutrient composition due to the presence of carbohydrates, proteins, vitamins, and minerals. Field pea is also having other desirable characteristics due to the presence of phytochemicals, antioxidants, anti-nutritional factors, and in-vitro digestibility (Kumari and Deka, 2021). But due to the restricted genetic base and low

Corresponding author E-mail: kommineni Jagadeesh1@gmail.com

Doi: <https://doi.org/10.36953/E.CJ.13172379>

This work is licensed under Attribution-Non-Commercial 4.0 International (CC BY-NC 4.0)

© ASEA

variability utilized for the improvement of the yield; the productivity of peas was low when compared to the world productivity. The existing degree of variability in the germplasm will have a significant impact on the progress of the crop improvement program. Genetic variability studies are required to properly utilize the existing variability and explore the unknown variability in various forms. Heritability is the measure of trait transmission from the parents to their progeny. It is used to determine the amount of the genetic component of total variability and the approach necessary for crop improvement through character selection. Heritability has a vital role in the selection of genotypes in which the resemblance of characters yields in their progeny. Once the study has been completed the genetically diverse genotypes are included in the breeding programs for yield enhancement.

Material and Methods

The study was steered at a research farm, department of genetics and plant breeding, Birsa agricultural university, Kanke, Ranchi, in the Kharif season of the year 2020-2021. The material to be analyzed i.e., 23 genotypes was collected from various agricultural universities and research stations located throughout India (Table-1). The experiment was carried out in three replications in a randomized block design. The genotypes were grown in a plot having 6 rows each of 4meter length. The Row to row spacing was 45cm, while plant-to-plant spacing was 15cm. During the crop growth, all agronomic measures were followed to ensure a healthy crop. During the period of the experiment, observations were documented for 18 traits, i.e., Days to fifty percent flowering, days to pod initiation, days to maturity, primary branches per plant, Secondary branches per plant, plant height, pods per plant, pod length, seeds per pod, seeds per plant, 100 seed weight, swelling capacity, swelling index, protein content, harvest index, biological yield per plant and seed yield per plant. The mean values of 5 randomly selected plants from each treatment were utilized for statistical analysis such as analysis of variance. The magnitude of genetic variability was estimated following the standard procedures and the phenotypic (PCV) and genotypic (GCV) coefficients of variation were estimated as suggested by Singh and Chaudhary

(1985) whereas heritability (broad sense) as followed by Allard (1960) and genetic advance were estimated by the methods given by Johnson *et al.* (1955). The modified Micro-Kjeldahl technique was used to determine the quantity of protein present in field pea seeds of all samples. The distilled samples were titrated against 0.1N hydrochloric acid until a violet tint appeared as the endpoint. The titration value was used to calculate the percent Nitrogen, which was then used to estimate total protein concentration using a conversion factor of 6.25 percent.

Nitrogen % =

$$\frac{\text{Normality} \times (\text{Volume of hydrochloric acid} - \text{Volume of blank}) \times 14 \times 100}{\text{Sample weight (gm)} \times 1000}$$

Table 1: Name and Source of 23 Genotypes of Field pea (*Pisum sativum* L.)

S. No.	ENTRY	SOURCES
1	HFP 1607	CCS HAU, Hisar
2	HFP 1702	CCS HAU, Hisar
3	Pant P 498	Pantnagar, GPUAT
4	Pant P 501	Pantnagar, GPUAT
5	Pant P 497	Pantnagar, GPUAT
6	VL 72	VPKAS, Almora
7	RFPG 180	RARS, Durgapura
8	RFPG 181	RARS, Durgapura
9	KPMR 937	CSAUA&T, Kanpur
10	RFP 2010-1	Raipur
11	RFP 2010-4	Raipur
12	IPF 20-17	IIPR, Kanpur
13	IPF 20-21	IIPR, Kanpur
14	IPF 20-11	IIPR, Kanpur
15	TRCP-11	Agartala
16	RFP 12-08	BAU, Ranchi
17	TRCP 8	Agartala, Tripura (ICAR)
18	VL 42	VPKAS, Almora
19	SKNP 04-09	SDAU, SK Nagar
20	IPF 16-13	IIPR, Kanpur
21	HUDP-15 (ZC)	BHAU, Varanasi
22	Dantewada FP-1(LC)	SDAU, SK Nagar
23	Aman (NC)	IIPR, Kanpur

Results and Discussion

The existence of significant differences among the 23 genotypes of field pea for all the traits under consideration had been revealed from the results of the analysis of variance (Table2). The existing

substantial quantity of genetic variability can be utilized in crop improvement programs.

The values of PCV, GCV, Heritability, Genetic advance, and Genetic advance as % of the mean are represented in the table 2.

Table 2: ANNOVA showing means squares for 18 characters in 23 genotypes of Field pea (*Pisum sativum* L.)

Source	D.f	Days to 50% flowering	Days to Pod initiation	Days to Maturity	Plant height (cm)	Primary Branches Per Plant	Secondary branches per plant	Pods Per Plant	Plant Height (cm)	Pod Length (cm)	Seeds Per Pod
		1	2	3	4	5	6	7	8	9	10
Replication	2	0.17	0.88	40.43**	0.095	0.036	0.17	22.50*	237.82	0.38**	0.22
Genotype	22	12.12**	3.17**	12.26**	0.57**	0.72**	12.12**	18.85**	1351.79**	1.30**	1.77**
Error	44	0.003	0.54	2.18	0.04	0.04	0.003	5.52	98.36	0.082	0.25

Table-2. (Contd.)

Source	D.f	Seeds per Plant	100 Seed Weight (gm)	Swelling Capacity (ml/seed)	Swelling Index (%)	Biological Yield per Plant (gm)	Seed Yield per Plant (gm)	Harvest Index	Protein Content (%)
		11	12	13	14	15	16	17	18
Replication	2	35.10	1.79	0.002*	0.03	12.02	3.34*	0.02*	0.09
Genotype	22	739.94**	15.39**	0.003**	0.13**	176.48**	17.49**	0.01**	3.21**
Error	44	91.89	0.93	0.001	0.02	15.14	0.75	0.003	0.67

Phenotypic and Genotypic Coefficient of Variability:

Among the various traits considered for investigation, the traits like primary branches per plant (54.47), secondary branches per plant (49.63), pods per plant (23.711), plant height (24.96), swelling capacity (25.47), swelling index (36.63), harvest index (22.93), biological yield per plant (35.75), seed yield per plant (33.30) are having high values of phenotypic coefficient of variation. The characters like pod length (12.23), and 100 seed weight (14.36) recorded a moderate amount of phenotypic coefficient of variation. The phenotypic coefficient of variation was low in the traits like days to 50% flowering (4.65), days to maturity (3.83), seed per pod (8.79), and protein content (4.70). Higher values of genotypic coefficient of variation are recorded for traits like primary branches per plant (49.44), secondary branches per plant (45.81), plant height (22.46), swelling capacity (20.89), swelling index (34.22), biological yield per plant (31.57), seed yield per plant (31.27). The characters like Pods per plant (15.84), pod length (11.15), 100 seed Weight (13.15), and Harvest Index (17.88) had a moderate amount of genotypic coefficient of

variation. In the company of various traits days to 50% Flowering (4.36), days to maturity (3.57) seed per pod (6.37), and protein content (3.51) had a low amount of genotypic coefficient of variation. The characters primary branches per plant, secondary branches per plant, plant height, percent disease incidence, swelling capacity, swelling index, biological yield per plant, and seed Yield per plant recorded a high amount of GCV and PCV. The above traits are mostly under genetic control, which makes their phenotypic selection more reliable. These findings were in accordance with Sharma *et al.* (2003), Mehta *et al.* (2005), Kumar *et al.* (2013) and Saxesena *et al.* (2014), Ranjan *et al.* (2006). The traits pod length and 100 seed weight recorded a moderate amount of PCV and GCV but pods per plant and harvest index showed a moderate amount of GCV only. These results were in accordance with Lal *et al.* (2011). In the company of various traits days to 50% Flowering (4.3558), days to maturity (3.5720) seed per pod (6.3741), and protein content (3.5090) had a low amount of genotypic coefficient of variation. Thus, the selection for these traits may not be fruitful. These results were in acceptance by Singh *et al.* (2011), Patel (2012), and Yadav (2013).

Table 3: Genetic Parameters of 18 characters in 23 Genotypes of field pea

Characters	Genotypic Coefficient of variation	Phenotypic Coefficient of variation	Heritability in broad sense	Genetic Advance	Genetic advance as % of mean
Days to 50% flowering	2.54	3.011	71.09	3.276	4.41
Days to Pod initiation	1.07	1.36	62.08	1.520	1.73
Days to Maturity	3.26	3.53	85.37	6.796	6.120
Plant height (cm)	49.44	54.47	82.39	0.79	92.45
Primary Branches Per Plant	45.81	49.63	85	0.91	87.08
Secondary branches per plant	2.54	3.011	71.09	3.276	4.41
Pods Per Plant	15.84	23.71	44.6	2.90	21.78
Plant Height (cm)	22.46	24.96	80.94	37.88	41.62
Pod Length (cm)	11.15	12.23	83.04	1.188	20.93
Seeds Per Pod	14.99	18.28	67	1.21	25.34
Seeds per Plant	21.67	25.87	70.16	25.36	37.38
100 Seed Weight (gm)	13.15	14.36	83.86	4.13	24.81
Swelling Capacity (ml/seed)	20.89	25.47	67.22	0.05	35.27
Swelling Index (%)	17.42	22.67	59.17	0.31	27.59
Biological Yield per Plant (gm)	31.574	35.75	78.02	13.34	57.45
Seed Yield per Plant (gm)	31.271	33.30	88.17	4.57	60.49
Harvest Index	17.875	22.93	60.79	0.10	28.71
Protein Content (%)	3.509	4.702	55.69	1.41	5.40

Heritability, Genetic advance, and genetic advance as % of mean:

The traits possessing a high amount of heritability are days to 50% flowering (0.88), days to maturity (0.87), primary branches per plant (82), secondary branches per plant (85), plant height (0.81), pod length (0.83), 100 seed weight (0.84), swelling index (0.87), biological yield per Plant (0.78), seed yield per Plant (0.88). The traits with a moderate amount of heritability are seed per pod (0.53), swelling capacity (0.67), protein content (0.56), and harvest index (0.61). Finally, the only trait with a low amount of heritability is pods per plant (0.45). The genetic advance recorded among the various characters under consideration are as days to 50% flowering (6.31), days to maturity (7.53), primary branches per plant (0.80), secondary branches per

plant (0.91), days to pod initiation(1.52), pods per plant (2.90), plant height (37.89), pod length (1.19), seed per pod (0.11), seeds per plant (25.36), 100 seed weight (4.13), swelling capacity (0.05), swelling index (0.66), protein content (1.41), harvest index (90.10), biological yield per plant (13.34), seed yield per plant 94.57). It was evident from the results of the analysis represented in table-3, that a high magnitude of Genetic advance as a percentage of mean was documented for the characters like primary branches per plant (92.45), secondary branches per plant (87.08), pods per plant (21.78), plant height (41.61), pod length (20.93), 100 seed weight (24.81), percent disease incidence (67.39), swelling capacity (35.27), swelling index (35.27), harvest Index (28.71), days to 50% flowering (8.40), days to pod initiation, days to maturity (6.87),

biological yield per plant (57.45), seed yield per plant (60.49). There was no character with a moderate amount of genetic advance as a percentage of the mean among the considered ones. A low amount of genetic advance as a percent of the mean was observed for the characters like days to 50% flowering (8.40), days to maturity (6.87), and days to pod initiation (1.73).

High heritability and high genetic advance were recorded for the trait's plant height and seeds per plant.

These traits are less impacted by environmental fluctuations. Selection is simple since the above qualities are mediated by additive gene activity. These results were in accordance with Katoch *et al.* (2016) and Tambolkar *et al.* (2016). High heritability coupled with low genetic advance was recorded for the trait's days to fifty % flowering, days to maturity, primary branches per plant, secondary branches per plant, pod length, 100 seed weight, and seed yield per plant. Heterosis breeding was desirable for the improvement of these traits. These results were in accordance with Saxesena *et al.* (2014) and Sharma *et al.* (2013). Low heritability along with high genetic advance was observed in the case of pods per plant. The traits with a moderate amount of heritability with low genetic advance were observed in the case of the traits days to pod initiation, seeds per pod, swelling capacity, swelling index, protein content, and harvest index.

High heritability and moderate genetic advance were recorded for the trait biological yield per plant

High heritability with high genetic advance as % of mean was recorded for the trait's primary branches per plant, secondary branches per plant, plant height, seeds per plant, pod length, 100 seed weight, biological yield per plant, and seed yield per plant. Further improvement for the above traits can be made through selection using the above breeding lines. Traits possessing high heritability with low genetic advance as % of the mean are days to fifty % flowering and days to maturity. The traits with moderate heritability and high genetic advance as % of the mean are seeds per pod, swelling capacity, swelling index, and harvest index. Moderate heritability with low genetic advance as % of mean was observed in the traits days to pod initiation and

protein content. Low heritability along with high genetic advance as % of mean was recorded by pods per plant. These results were in accordance with Dar *et al.* (2013).

Conclusion

The characters primary branches per plant, secondary branches per plant, biological yield per plant, and seed yield per plant recorded high phenotypic and genotypic coefficients of variation. These characters also possess high heritability coupled with high genetic advance as % of the mean which made the phenotypic selection based on these characters highly fruitful. Even though high heritability with high genetic advance as % of mean was recorded by the character plant height, seeds per plant, pod length and 100 seed weight, selection will be less beneficial as these traits possessed moderate and low phenotypic and genotypic coefficient of variations. Therefore, the selection criteria of the genotypes should be based not only on the genotypic and phenotypic coefficient of variation. But it is their combination with heritability and genetic advance as a percentage of the mean which is highly fruitful.

Conflict of interest

The authors declare that they have no conflict of interest.

References

- Allard, R. W. (1960). Principles of plant breeding. John Willey and Sons. Inc. New York, 485.
- Dar, S. A., Ishfaq, A., Ali, G., Pir, F. A., & Manzar, A. (2013). Study on genetic variability, heritability and genetic advance in pea (*Pisum sativum* L.). *Annals of Horticulture*, 6(1), 161-163.
- Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans 1. *Agronomy journal*, 47(7), 314-318.
- Katoch, V., Singh, P., Devi, M. B., Sharma, A., Sharma, G. D., & Sharma, J. K. (2016). Study of genetic variability, character association, path analysis and selection parameters for heterotic recombinant inbred lines of garden peas (*Pisum sativum* var. hortense L.) under mid-hill conditions of Himachal Pradesh, India. *Legume Research*, 39(2), 163-169.

- Kumari, T., & Deka, S. C. (2021). Potential health benefits of garden pea seeds and pods: A review. *Legume science*, 3(2), e82.
- Lal, G. M., Meena, M. L., Chandra, K. U. N. J., & Singh, C. M. (2011). Assessment of genetic variability and interrelation between yield and its contributing components in field pea (*Pisum sativum* L.). *Environment and Ecology*, 29(5), 1235-1239.
- Nayik, G. A., & Gull, A. (Eds.). (2020). *Antioxidants in Vegetables and Nuts-Properties and Health Benefits*. Springer.
- Roy, F., Boye, J. I., & Simpson, B. K. (2010). Bioactive proteins and peptides in pulse crops: Pea, chickpea and lentil. *Food research international*, 43(2), 432-442.
- Saxeena, R. R., Vidyakar, V. I. D. Y. A. P. A. T. I., Vishwakarma, M. K., Yadav, P. S., Meena, M. L., & Lal, G. M. (2014). Genetic variability and heritability analysis for some quantitative traits in field pea (*Pisum sativum* L.). *The Bioscan*, 9(2), 895-898.
- Singh, A., Singh, S., & Babu, J. D. P. (2011). Heritability, character association and path analysis studies in early segregating population of field pea (*Pisum sativum* L. var. arvense). *International Journal of Plant Breeding and Genetics*, 5(1), 86-92.
- Sing, R. K., & Chaudhary, B. D. (1985). *Biometrical Methods in Quantitative Genetic Analysis* Kalyani publishers. New Delhi, Ludhiana, 318.
- Tambolkar, B. B., Chavan, N. H., & Vidhate, S. B. (2016). Variability studies in pea (*Pisum sativum* L.) with respect of growth, yield and yield attributes parameters. *International Journal of Tropical Agriculture*, 34(6), 1765-1769.
- Tiwari, B. K., & Singh, N. (2012). *Pulse chemistry and technology*. Royal Society of Chemistry.
- Yadav, K., Singh, B. D., Srivastava, C. P., Chand, R., & Yadav, A. (2010). Analysis of genetic divergence in pea (*Pisum sativum* L.) using quantitative traits and RAPD markers. *Indian Journal of Genetics and Plant Breeding*, 70(4), 363.

Publisher's Note: ASEA remains neutral with regard to jurisdictional claims in published maps and figures.