

# Assessment of genetic variability, heritability, and genetic advance for important traits in *Pisum sativum* L.

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## ABSTRACT

This study aimed to assess genetic parameters for four distinct traits - days to 50% flowering, pod length (cm), pod diameter (cm), and plant height (cm) in the *rabi* seasons of 2021 and 2022. The investigation encompassed 40 pea genotypes, and a pooled analysis of variance indicated significant variations in all the examined traits. The findings of the current study lead to the conclusion that plant height in peas is primarily influenced by additive gene action, implying that this trait can be enhanced through straightforward selection methods. In contrast, both additive and non-additive approaches are necessary for the improvement of pod length and pod diameter. Specifically, days to 50% flowering is predominantly governed by non-additive gene action, indicating that the enhancement of this trait would be better achieved through heterosis breeding techniques. These insights into the genetic control mechanisms of these traits provide valuable guidance for breeding strategies, emphasizing the importance of selecting appropriate methods tailored to the underlying genetic architecture of each trait for optimal improvement outcomes.

**Key words :** Genetic variability, Heritability, *Pisum sativum*

## Introduction

Pea (*Pisum sativum* L.) is a versatile leguminous crop that serves as a model organism in plant genetics and breeding research. Peas are widely consumed across various nations, either in their fresh vegetable form or as dry seeds. Renowned for their versatility, peas offer a substantial nutritional profile. Rich in carbohydrates, peas also provide significant amounts of dietary fiber, protein, and an array of essential vitamins. Notable vitamins found in peas include vitamin A, C, K, and various B complex vitamins like folic acid, pantothenic acid, niacin, thiamine, and pyridoxine. In addition to vitamins, peas are a source of essential minerals such as iron, magnesium, phosphorus, and zinc. Furthermore, they

contain lutein, a yellow carotenoid pigment known for its visual benefits. This nutritional diversity makes peas not only a flavorful addition to meals but also a valuable component of a balanced and health-conscious diet.

The exploration of variability in pea genotypes is pivotal for several reasons. First and foremost, understanding the genetic basis of variability allows for the identification of key traits that contribute to the adaptability and resilience of pea plants in diverse environmental conditions. Additionally, variability studies in pea genotypes provide valuable information for plant breeders aiming to develop cultivars with enhanced performance and adaptability.

The success of a crop improvement program relies on the genetic variability within the plant material. Sometimes, selecting phenotypes based solely on their performance may prove insufficient, as these genotypes may exhibit poor performance in subsequent segregating generations. Hence, it becomes crucial to choose genotypes based on their genetic merit, specifically considering heritability and genetic advance (Hamouda *et al.*, 2016). Assessing genetic variability alongside heritability estimates allows for a determination of the potential genetic gain through selection (Burton, 1952; Swarup and Chaugle, 1962). Information on variability and heritability serves as a valuable tool in establishing selection criteria for enhancing yield and its component traits in any vegetable crop. Notably, heritability estimates, in conjunction with genetic advance, are more insightful in predicting gains under selection compared to heritability estimates alone (Paul *et al.*, 2006). Considering these factors, the present study aimed to assess the extent of genetic variability, heritability, and genetic advance over the mean for some important horticultural traits in 40 accessions of garden peas. Furthermore, the examination of these genotypes across two distinct environments introduces the crucial aspect of genotype  $\times$  environment interaction, shedding light on how genetic factors respond to and interact with specific environmental conditions.

## Materials and Methods

The current investigation was conducted during the rabi seasons of 2020-21 and 2021-2022 at the Experimental Farm of the School of Biotechnology, SKUAST-Jammu. The study involved 40 pea genotypes (Table 1). The seed material was sown in the experimental fields of the School of Biotechnology, SKUAST-J Chatha. Standardized agricultural practices were employed throughout the experiment. The seed material was evaluated using a Completely Randomized Block Design (RBD) with three replications over two consecutive years during the rabi seasons of 2019-2020 and 2020-2021. Each trial plot consisted of six rows, with 15 plants per row. The plants were sown with a gap distance of 45 cm  $\times$  10 cm plant-to-plant spacing. Standard horticultural practices were uniformly applied to all experimental units. Data on days to 50% flowering, pod length (cm), pod diameter (cm), and plant height (cm) were recorded from five randomly selected plants within each accession. Bartlett's test (Snedecor and Cochran, 1989) was used to test if data for both the years have equal variances. Equal variances across samples is called homogeneity of variances. Collected data was subjected to pooled analysis of variance using appropriate computer software (Gopinath *et al.*, 2021). Genotypic coefficient (GCV) and phenotypic coefficient of variation

**Table 1.** List of accessions alongwith their sources used in the study

| S. No. | Accession  | Source             | S. No. | Accession     | Source             |
|--------|------------|--------------------|--------|---------------|--------------------|
| 1      | IC-209125  | NBPGR, New Delhi   | 21     | PalamSumool   | CSK HPKV, Palampur |
| 2      | IC-218991  | NBPGR, New Delhi   | 22     | Line No. 14   | CSK HPKV, Palampur |
| 3      | IC-218993  | NBPGR, New Delhi   | 23     | IC-208366     | NBPGR, New Delhi   |
| 4      | IC-219002  | NBPGR, New Delhi   | 24     | IC-218988     | NBPGR, New Delhi   |
| 5      | IC-219008  | NBPGR, New Delhi   | 25     | IC-278261     | NBPGR, New Delhi   |
| 6      | IC-311065  | NBPGR, New Delhi   | 26     | EC-598757     | NBPGR, New Delhi   |
| 7      | IC-329410  | NBPGR, New Delhi   | 27     | EC-598816     | NBPGR, New Delhi   |
| 8      | IC-329586  | NBPGR, New Delhi   | 28     | 2480(S49)     | CSK HPKV, Palampur |
| 9      | IC-342029  | NBPGR, New Delhi   | 29     | Pb89          | PAU, Ludhiana      |
| 10     | IC-381453  | NBPGR, New Delhi   | 30     | J12302(S-127) | CSK HPKV, Palampur |
| 11     | IC-394027  | NBPGR, New Delhi   | 31     | Azad P-4      | CSAUAT, Kanpur     |
| 12     | NC-60950   | NBPGR, New Delhi   | 32     | Azad P-5      | CSAUAT, Kanpur     |
| 13     | DPPIV-2    | CSK HPKV, Palampur | 33     | ArkaSampoorna | IIHR, Bangalore    |
| 14     | DPEPP-2    | CSK HPKV, Palampur | 34     | ArkaAjit      | IIHR, Bangalore    |
| 15     | DPPMFWR-1  | CSK HPKV, Palampur | 35     | ArkaPriya     | IIHR, Bangalore    |
| 16     | DPPMFWR-4  | CSK HPKV, Palampur | 36     | ArkaKarthik   | IIHR, Bangalore    |
| 17     | DPPMFWR-27 | CSK HPKV, Palampur | 37     | Azad Pea 1    | CSAUAT, Kanpur     |
| 18     | DPPMR-09-1 | CSK HPKV, Palampur | 38     | Arkel         | NSC, New Delhi     |
| 19     | DPPM-65    | CSK HPKV, Palampur | 39     | Bonneville    | NSC, New Delhi     |
| 20     | DPPM-73    | CSK HPKV, Palampur | 40     | Lincoln       | NSC, New Delhi     |

(PCV) were calculated using Burton's formula (1952). PCV and GCV estimates were categorized as low (0-10%), moderate (10-20%), and high (>20%) based on Sivasubramanian and Madhavamenon's criteria (1973). Broad-sense heritability ( $h^2_b$ ) was calculated following the formulas proposed by Johnson *et al.* (1955) and Hanson *et al.* (1956). Genetic advance was estimated using the formulas by Johnson *et al.* (1955) and Allard (1960).

## Results and Discussion

The Bartlett test was employed to assess the homogeneity of variances for pooled ANOVA analysis of two years' data. The results of the Bartlett test indicated that error variances across the years were homogenous, suggesting non-significant differences for all four traits between the successive years. The combined ANOVA, considering genotypes as a source of variation for all the characters, yielded statistically significant results, indicating substantial variability among the genotypes (Table 2). This observed variability is likely attributed to differences in their respective places of collection. Furthermore, the impact of location, as indicated by the year as a source of variation, was found to be statistically significant for traits such as days to 50% flowering, pod length (cm), and pod width (cm).

The mean, variability, heritability, and genetic advance for each trait in the study are presented in Table 3. Considerable variation was observed in plant height (85.8-206.4 cm), followed by days to flowering (48 to 90 days), with the lowest observed for pod diameter weight (2.4-7.1g) and slightly higher for pod length (32.5-40.3%).

The results of combined ANOVA with genotypes/ treatments as a source of variation for all the

characters was found statistically significant which reflected the existence of sufficient variability among the genotypes (Table 2). This variability can be attributed to differences in their place of collection. The influence of location indicated by year as source of variation was found statistically significant for days to 50% flowering and pod width (cm).

The mean performance, range, and coefficient of variation for the studied genotypes with respect to different traits are given in Table 3. Mean for days to 50 % flowering was found to be 75.15 days, showing a considerable range from 60.30 to 89.00 days for the genotypes 'Arka Ajit' and 'IC-381453,' respectively. This variation of 28.67 days underscores the potential for creating earliness by selecting the optimal genotype, ultimately contributing to early maturity. In terms of pod length, a substantial diversity was observed, ranging from 10.65 cm (Palam Sumool) to 4.50 cm (EC-598757). Similarly, pod diameter exhibited variability, ranging from 0.93 cm (IC-209125) to 1.62 cm (DPEPP-2). The average plant height was recorded at 86.13 cm, with genotypes ranging from 49.50 cm (IC-208366) to 163.57 cm (IC-342029). These findings emphasize the extensive variability among the studied genotypes, highlighting the potential for trait improvement and the selection of genotypes with desirable characteristics.

Analysis of genotypic coefficient variance (GCV) and phenotypic coefficient variance (PCV) of different traits for both the years are given in (Table 3). The results indicated that phenotypic coefficient variances (PV) in both the years are slightly greater than the genotypic coefficient variances (GCV) for all the traits, this mean that the traits under study were not much influenced by the environment. Similar results on *Pisum sativum* were also reported by Nawab *et al.* (2008) and Jaiswal *et al.* (2013). The

**Table 2.** Pooled analysis of variance for horticultural traits among the 40 garden pea genotypes

| Source of variation          | df  | Mean Sum of Squares          |                       |                      |                         |
|------------------------------|-----|------------------------------|-----------------------|----------------------|-------------------------|
|                              |     | Days to<br>50 %<br>Flowering | Pod<br>Length<br>(cm) | Pod<br>Width<br>(cm) | Plant<br>height<br>(cm) |
| Location                     | 1   | 6.667*                       | 0.007                 | 0.323*               | 0.223                   |
| Treatment                    | 39  | 298.041*                     | 11.938*               | 0.087                | 8296.430*               |
| Replication with in location | 4   | 2.108                        | 0.119                 | 0.001                | 44.802                  |
| Location x Treatment         | 39  | 1.068                        | 0.145*                | 0.022*               | 9.910                   |
| Error                        | 156 | 1.284                        | 0.047                 | 0.003                | 21.340                  |
| CD for treatment comparison  |     | 1.803                        | 0.444                 | 0.174                | 3.676                   |
| CV                           |     | 1.207                        | 5.187                 | 12.620               | 3.655                   |

\* significant at  $p < 0.05$ , df = degree of freedom

highest GCV and PCV values were found particularly for plant height 43.13, 43.04, 43.26, 43.14, respectively for 2021 and 2022) followed by pod length, pod diameter and days to 50 % flowering (Table 3). The lowest GCV and PCV was observed for days to 50 % flowering, moderate for pod length and pod diameter whereas high GCV and PCV was observed for plant height, this is as per the criteria given by Sivasubramanian and Madhavamenon's (1973). The highest value of GCV and PCV shows as presences of high variability available in these traits. Whereas moderate GCV and PCV was recorded this indicates as the trait more influenced by environment. Low GCV and PCV (9.40, 9.31, 9.45 and 9.34, respectively for 2021 and 2022) for days to 50 % flowering shows less variability exist in these characters, but slightly higher PCV than GCV which mean less influenced by the environment.

Analysis of genotypic coefficient variance (GCV) and phenotypic coefficient variance (PCV) was calculated for different traits across the two year data (Table 3). The findings reveal that the phenotypic coefficient variances (PCV) for all traits in both years were slightly greater than the genotypic coefficient variances (GCV), suggesting that the traits under investigation exhibit limited influence from the environment. This aligns with earlier reports on *Pisum sativum* by Guleria *et al.* (2009). The lowest GCV and PCV was observed for days to 50 % flowering, moderate for pod length and pod diameter whereas high GCV and PCV was observed for plant height, this is as per the criteria given by Sivasubramanian and Madhavamenon's (1973). Specifically, plant height demonstrated the highest GCV and PCV values (43.13, 43.04, 43.26, 43.14, respectively for 2021 and

2022), followed by pod length, pod diameter, and days to 50% flowering (refer to Table 3). These results are consistent with previous studies conducted by (insert reference), which highlighted similar trends. This implies that plant height is characterized by significant genetic and environmental influences, aligning with the criteria. The highest GCV and PCV values signify substantial variability in these traits, while moderate values indicate a notable environmental influence. Conversely, low GCV and PCV (9.40, 9.31, 9.45, and 9.34, respectively for 2021 and 2022) for days to 50% flowering suggest limited variability in these characteristics. Notably, the slightly higher PCV than GCV for this trait implies a minor impact of the environment. These results collectively provide valuable insights into the genetic and environmental factors influencing trait variability, contributing to a comprehensive understanding of the studied *Pisum sativum* genotypes.

Heritability serves as a valuable indicator of the transmission of traits from parents to offspring and is classified into low (below 30%), medium (30%–60%), and high (above 60%) categories. In the present study, all traits consistently exhibited high heritability (greater than 92.63 across both years). It is essential to note that high heritability does not imply trait fixation or immunity to environmental influences; instead, it underscores the substantial contribution of genetic factors to observed variations. Traits with high broad-sense heritability are deemed more predictable in breeding programs, as selecting individuals with desirable phenotypes increases the likelihood of similar traits in offspring. These findings align with previous studies of Deepika *et al.* (2017) emphasizing heritability as a

**Table 3.** Mean, range, coefficient of variation, heritability and genetic advance as per cent of mean for different traits in garden pea across the years

| Traits | Pooled Mean<br>(2021 & 2022) | Range (Pooled) |        | Year | GCV   | PCV   | h <sup>2</sup> | GA    |
|--------|------------------------------|----------------|--------|------|-------|-------|----------------|-------|
|        |                              | Min.           | Max.   |      |       |       |                |       |
| DTF    | 75.15                        | 60.30          | 89.00  | 2021 | 9.40  | 9.45  | 99.11          | 19.29 |
|        |                              |                |        | 2022 | 9.31  | 9.34  | 99.17          | 19.09 |
| PL     | 7.34                         | 4.50           | 10.65  | 2021 | 19.23 | 19.29 | 99.30          | 39.47 |
|        |                              |                |        | 2022 | 19.31 | 19.39 | 99.13          | 39.61 |
| PD     | 1.18                         | 0.93           | 1.62   | 2021 | 12.12 | 12.33 | 96.67          | 24.55 |
|        |                              |                |        | 2022 | 9.88  | 10.27 | 92.63          | 19.59 |
| PH     | 86.13                        | 49.50          | 163.57 | 2021 | 43.13 | 43.26 | 99.40          | 88.58 |
|        |                              |                |        | 2022 | 43.04 | 43.14 | 99.57          | 88.48 |

DTF = Days to 50% Flowering; PL = Pod Length (cm); PD = Pod Diameter (cm); PH = Plant Height (cm), GCV = genotypic coefficient of variance; PCV = phenotypic coefficient of variance; h<sup>2</sup> = Heritability (broad sense); GA = Genetic advance as % age of mean

reliable index for character transmission from parents to progeny.

Genetic advance serves as a valuable indicator, reflecting the effectiveness and efficiency of the selection process within the base population. In the current study, the lowest genetic advance as a percentage of the mean was observed in days to 50% flowering (19.29 and 19.09) followed by pod diameter (24.55 and 19.59), pod length (39.47 and 39.61), and plant height (88.58 and 88.48) for both the years, 2021 and 2022, respectively. Heritability estimates, when combined with the genetic advance, offer a more comprehensive understanding. In this study, traits with high heritability and significant genetic advance (>50) were noted for plant height, indicating the predominance of additive gene action. This underscores the effectiveness of selection in improving this trait. Conversely, days to 50% flowering exhibited high heritability with low genetic advance, suggesting non-additive gene action. Pod length and pod diameter displayed high heritability with moderate genetic advance, implying the involvement of both additive and non-additive gene actions in the inheritance of these traits.

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**Conflict of Interest-** None

## References

- Allard, R. W. 1960. Principles of plant breeding. *John Willey and Sons. Inc. New York*, 485.
- Burton, G.W. 1952. Quantitative inheritance in grasses. In: *Proceedings of 6th International Grassland Congress*, Pennsylvania State College, USA, 23 August, 1952. 277-283.
- Deepika, Mahajan R., Padma, L., Sharma, P., Salgotra, R.K. and Sharma, S. 2017. Assessment of Genetic Variability, Heritability and Genetic Advance among *Pisum* Accessions. *Vegetos- An International Journal of Plant Research* 30: (Special Issue) <http://dx.doi.org/10.5958/2229-4473.2017.00125.2>.
- Gopinath, 2021. grapesAgri1: Collection of Shiny Apps for Data Analysis in Agriculture. *Journal of Open Source Software*. 6(63): 3437, <https://doi.org/10.21105/joss.03437>.
- Hamouda, F.E., Bashirand, S.G.E. and Ginaro, M.K. 2016. Phenotypic and genotypic coefficients of variation and other growth attributes in sesame genotype under rainfed conditions. *Advances in Agriculture Science*. 2(3): 79-84.
- Hanson, C.H., Robinson, H.F. and Comstock, R.E. 1956. Biometrical studies on yield in segregating population of Korean lespedeza. *Agron. J.* 48: 268-272.
- Jaiswal, N.K., Gupta, A.K., Dewangan, H. and Lavanya, G.R. 2013. Genetic Variability Analysis in Field Pea (*Pisum sativum* L.). *International Journal of Science and Research (IJSR)*. 4(1): 2006-2007.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybeans. *J Agron.* 47(7): 314-8.
- Guleria, S., Chongtham, N. and Dua, S. 2009. Genetic variability, correlation and path analysis studies in pea (*Pisum sativum* L.). *Crop Research (Hisar)*. 38:179-183.
- Nawab, N.N., Subhani, G.M., Mahmood, K., Shakil, Q. and Saeed, A. 2008. Genetic variability, correlation and path analysis studies in garden pea (*Pisumsativum* L.). *Journal of Agricultural Research*. 46: 333-340.
- Paul, A.K.M..A., Islam, M.J., Hasan, M.M.H. and Chowdhury, A.Z.M.K.A. 2006. Genetic variation of some morpho physiological characters in *Triticum durum* wheat. *International Journal for Sustainable Agricultural Technology*. 2(8): 11-14.
- Sivasubramanian, S. and Madhavamenon, P. 1973. Genotypic and phenotypic variability in rice. *Madras Agricultural Journal*. 60: 1093-1096.
- Snedecor, George, W. and Cochran, William G. 1989. *Statistical Methods*, Eighth Edition, Iowa State University Press.
- Swarup, V. and Chaugle, B.S. 1962. Studies on genetic variability in sorghum; phenotypic variation and heritable component in some quantitative characters contributing towards yield. *Indian Journal of Genetics and Plant Breeding*. 22: 31-36.
- Vaishnav, P. and Pandey, R.L. 2001. Genetic relationship of growth and developmental traits with seed yield in dwarf field pea. *Indian J. Plant Genet. Res.* 14: 52-54.