



Genetic Variability in Garden Pea (*Pisum sativum* L.): A Review

Suraj Luthra ^{a++}, Budhesh Pratap Singh ^{b+++*}, Rajat Singh ^{b++},
Badri Lal Nagar ^{c++} and Shivam Kumar Singh ^d

^a Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, U.P., India.

^b Department of Vegetable Science, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur, U.P., India.

^c Department of Vegetable Science, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior, M.P., India.

^d Crop Improvement Division, IIVR, Varanasi, U.P., India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/IJECC/2023/v13i113566

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/109016>

Review Article

Received: 05/09/2023

Accepted: 12/11/2023

Published: 28/11/2023

ABSTRACT

The estimation of variability parameters, particularly heritability and genetic gain, holds significant importance in assessing the potential for character improvement through selection. It is observed that selection based on highly heritable traits tends to yield more successful outcomes. Hence, the utilization of heritability, in conjunction with other measures of variability, enables the prediction of gains under specific selection intensities. Additionally, the concept of predicted genetic gain provides insight into the degree of change achievable in a trait through simple selection. However, the process of selecting for features related to yield and quality can be enhanced by having access to information regarding the correlation between these traits. This can be further improved by doing a path coefficient analysis to gain a deeper knowledge of the relationship between the important

⁺⁺ Ph. D. Research Scholar;

*Corresponding author: E-mail: bs119135@gmail.com;

characteristics. In order to enhance the traits that did not exhibit a favorable response to selection, it becomes necessary to divide the non-additive component of genetic variance through the process of hybridization, which can be accomplished by conducting genetic divergence studies.

Keywords: Variability; heritability; genetic gain; improvement.

1. INTRODUCTION

Pea (*Pisum sativum* L.) is a significant legume crop that holds considerable importance in the field of genetic study, owing to its extensive historical background. This may be traced back to the pioneering contributions of *Gregor J. Mendel*, widely regarded as the founder of genetics. Pea, classified as one of the six primary pulse crops grown on a global scale, ranks as the second most productive legume worldwide, following the common bean (*Phaseolus vulgaris* L.). The common pea, scientifically referred to as *Pisum sativum* var. Hortense L. ($2n=2x=14$), is considered to be one of the earliest cultivated crops in human history [1]. The plant in question is a perennial herbaceous crop belonging to the Fabaceae or Leguminosae family. It falls under the Genus *Pisum*, subfamily Faboideae, and tribe Fabeae. Blixt et al. [2] assert that the Mediterranean region serves as the principal locus of diversity, with Ethiopia being identified as a secondary origin.

The name "pea" has the potential to denote either a little spherical seed or the pod in which it is contained. Peas are commonly consumed in several nations either as fresh veggies or in the form of dry seeds. Peas possess a significant carbohydrate content, alongside notable quantities of dietary fiber, protein, and several vitamins (including vitamin A, C, K, and B complex vitamins such as folic acid, pantothenic acid, niacin, thiamine, and pyridoxine). Additionally, peas contain essential minerals such as iron, magnesium, phosphorus, and zinc, as well as lutein, a yellow carotenoid pigment that confers visual benefits. The dry weight of the substance consists of around 25% protein and 25% carbs, primarily composed of sugars. Peas are cultivated as a winter season vegetable in low-lying areas and as a summer season crop in mountainous regions. Legumes have the ability to engage in a symbiotic relationship with a type of bacteria known as *Rhizobium*, which enables them to convert atmospheric nitrogen into a usable form. This process not only enhances the soil's physical characteristics, but also provides protection against fungal infections [3]. The

process of nitrogen fixation by *Rhizobium leguminosarum* enhances soil fertility by supplying nitrogen to subsequent crops, hence eliminating the need for additional expenditures on supplementary fertilizers. Based on recent statistics provided by the National Horticultural Board (NHB) [4], it is observed that the cultivation of peas in India during the 2021-22 period encompassed an area of 549,000 hectares, resulting in a production of around 5,680,000 metric tons. Uttar Pradesh is responsible for 49% of the overall pea production in India. Despite its significant economic significance, the productivity per unit area of peas remains very low in the country, particularly when cultivating varieties during the off-season. The primary factors contributing to this issue include the absence of high-yielding varieties that possess inadequate or no resistance to powdery mildew and Fusarium wilt. Therefore, it is imperative to conduct a comprehensive assessment of several genotypes in order to find pea varieties that exhibit high yield and outstanding characteristics. These identified varieties can then be directly released for commercial production or utilized in future crop improvement initiatives, focusing on enhancing yield and quality features.

2. GENETIC VARIABILITY IN GARDEN PEA

The characteristics and degree of genetic diversity present in the breeding population have a major impact on how successful a crop development programme is. This genetic variability study provides important insights into genetic variables. Genetic diversity, or the degree of genotypic variety within a population, is the fundamental concept behind all crop improvement efforts. Pea genotypes are highly variable, which offers significant potential for increasing pod output through methodical breeding efforts. A crop's ability to improve is closely correlated with the level of genetic variety found in its germplasm. According to Vavilov's [5] theory, populations with higher levels of variety are more likely to successfully select for desirable traits. Evaluating the genetic diversity found in a crop's germplasm is an essential step

before developing successful breeding plans [6]. As a result, a crop's potential to advance depends on its level of genetic diversity, and its ability to improve depends on the amount of advantageous genetic variability that is available [7]. It is imperative to evaluate the genetic diversity among native genotypes concerning yield and its component parts before beginning any breeding endeavour. One useful technique for assessing the level of diversity in the germplasm is to apply the genotypic and phenotypic coefficient of variations [8].

A study by Singh et al. [9] estimated the genetic advancement in percentage of mean for a number of plant characteristics, including height of the plant, length of the internode, length of the pod, number of days until first flowering, number of pods per plant, number of seeds per pod, number of primary branches, percentage of shelling, number of seeds, and number of pods per plant. The aforementioned investigations also provided the median heritability values for a number of traits, including the number of seeds per pod, the percentage of shelling, the number of primary branches, the number of pods per plant, the weight of 100 seeds, and the number of seeds produced per plant. For many variables, including plant height (97.84%), days to first green pod picking (95.80%), 100 green pod weight (94.69%), green pod yield per plant (93.10%), and days to 50% blooming (92.25%), the projected values for broad sense heritability were found to be significant. On the other hand, the remaining traits showed a moderate degree of heritability. Exhibiting notable genetic improvements indicated as a percentage of the mean for a number of variables, including green pod yield per plant (66.28), plant height (54.67), number of green pods per plant (38.28), and 100 green pod weight (32.07), was the study carried out by Kalloo et al. [10]. There was also a noticeable heritability for these traits. Moreover, significant genotypic diversity has been found in relation to crop output and related traits by the researchers. Akhilesh et al. [11] research revealed that a number of traits, such as plant height, pod production per plant, 100-seed weight, and seed yield per plant, had noteworthy heritability and significant genetic advancement. Multiple traits, including plant height, internode length, pod length, days to first flower, pod count per plant, seed count per pod, major branch count, shelling percentage, seed yield per plant, and pod yield per plant, showed a significant increase in the percentage of mean genetic advancement. According to Sharma et al. [12],

heritability estimates varied depending on a number of parameters, with values for pod breadth ranging from 95.95% to 49.25% for shelling percent. The significant amount of phenotypic variation that may be attributed to genetic origins (94.95% and 63.16%) indicates that pod breadth has a high heritability. It was also observed that the diameter of the pod had a greater potential for genetic improvement. With a value of 94.37%, the total phenol content (g/100g) of the leaves showed a significant degree of heredity. Furthermore, a moderate genetic increase of 84.30% was detected for this feature. Similarly, significant heritability estimates were established for the number of pods per plant, with observed values of 25.39% and 93.41%. Likewise, 94.93% and 23.68% of the heritability estimates were found for the node number at which the first blossom occurs. Furthermore, it was shown that the pod yield per plant had heritability estimates of 22.96% and 79.17%. The study's findings suggest that additive genes exist and that they significantly affect how certain traits are regulated. Consequently, these favourable features can be greatly enhanced and passed on to future generations by carefully selecting plants based on their phenotypic performance. Akansha et al. [13] focused on the range and characteristics of their investigation in order to assess the genetic variability among a population of twenty F2 segregating field pea plants. The results of the study showed that plant height, the number of pods on each plant, and the amount of grain produced by each plant all showed notable variation. Moreover, higher values of the phenotypic coefficient of variation (PCV) were noted by the researchers for the number of pods per plant (33.17) and grain yield per plant (45.32). On the other hand, the PCV values for days to flowering and days to maturity that were recorded were 6.89 and 4.14, respectively. Plant height (21.22) and grain output per plant (18.11) were found to have the largest genetic coefficient of variation (GCV), while days to maturity (3.93) and days to flowering (4.67) had the lowest GCV values. Plant height, pod length, and 100 seed weight showed significant genetic advancement as a proportion of the average value, as well as significant heritability (broad sense). This suggests that the action of additive genes influences how these traits manifest. In a fifteen genotypes of garden peas, Kumar et al. [14] estimated the genetic diversity, heritability, and genetic advancement of 10 yield contributing variables. A thorough examination demonstrated a significant degree of genetic variation in every

measure, including seed production per plant, hence pointing to a broad range of variation across the genotypes. The results of the study demonstrated significant improvements in the genotypic and phenotypic coefficient of variation for several plant characteristics, including plant height, number of pods per plant, length of pods, number of seeds per pod, weight of 100 seeds, and number of seeds produced per plant. Strong estimates of heritability, genotypic coefficient of variation, and genetic progress were also found in plant height, productive branches per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, and seed output per plant. The study's findings suggest that these traits could be used in successful selection procedures and are influenced by additive genetic mechanisms. Siddika et al. [15] looked into a wide range of 26 advanced vegetable pea lines in their study. The scientists recorded considerable variation in a number of traits, including the amount of time until flowering, the height of the plants, the number of pods on each plant, the length of the pods, the weight of one hundred seeds, and the number of seeds produced by each plant. However, no significant difference was seen in the number of seeds in each pod. Additionally, it was demonstrated that for the following traits: days to flowering, plant height, number of pods per plant, pod length, 100 seed weight, and seed output per plant, the phenotypic variation (σ_p) exceeded the genotypic variance (σ_g). Meanwhile, for every one of the previously listed agronomic characteristics, it was observed that the phenotypic coefficient of variation (PCV) showed larger magnitudes than the genotypic coefficient of variation (GCV). Plant height, pod length, and seed yield per plot were found to be significantly and favourably correlated with a high degree of heritability and substantial genetic advancement.

In a study published in 2015, Kumar et al. [16] assessed 54 genotypes of garden peas, including four control groups. Their study's primary goal was to measure the variability parameters for pertinent aspects. According to the findings, there were substantial differences in the genotypic and phenotypic coefficients of variation for total soluble solids, total sugars, pod yield per hectare, and total phenols. Strong heredity is indicated by the heritability estimates for pod production (kg/plot), the number of pods per plant, the node at which the first blossom develops (number), and total phenols (g/100g), all of which point to a significant genetic influence. Furthermore, there is a notable level of

genetic improvement in these traits, ranging from substantial to modest. Jaiswal et al. [17] evaluated a set of 12 genotypes of field pea to investigate the variability analysis of different reproductive characteristics in connection to grain output. The genotypes showed significant variation in the number of pods per plant, days to 50% flowering, plant height, number of pods per pod, days to maturity, number of seeds per pod, length of the pod, 100-seed weight, and grain yield per plant. They also showed notable variation in heritability and genetic advancement in these traits. The results of the study showed that for the variables under investigation, the phenotypic variation was greater than the genotypic variance. This result suggests that the phenotypic component contributed more significantly to the variation overall. Plant height was most accurately estimated by the genetic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV), which measured 48.10 and 48.42, respectively. The seed yield per plant was then measured, and estimations of 24.36 (GCV) and 33.69 (PCV) were obtained. Furthermore, an evaluation of the number of seeds per pod produced values of 16.40 (GCV) and 20.36 (PCV). There are additive genetic components present based on the observed range of broad-sense heritability, which is 52.00% to 99.00%. Katoch et al. [18] examined three conventional checks and a collection of 45 genetically different pea recombinant inbreds in their investigation. The aim of the study was to evaluate the degree of genetic diversity, heritability, and genetic advancements linked to yield, in addition to several horticulture and quality attributes. The study's objective was to identify recombinants with superior features that are suitable for use in crop improvement initiatives. A significant degree of variability was found in this study among the many different features that were looked into. For every characteristic, the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV). Over the course of the two-year period, a significant amount of change was seen in the phenotypic and genotypic coefficients related to the protein content, ascorbic acid levels, plant height, and pod yield per plant. Plant height and pod yield per plant were shown to have a significant heritability, suggesting that additive gene activity was primarily responsible for controlling these variables. Moreover, it is noteworthy that both qualities shown notable genetic progress in the corresponding years, suggesting their potential for favourable selection responses. Gudadinni

and colleagues [19] carried out an experimental investigation to obtain a better comprehension of genetic diversity, heritability, and genetic advancement in a set of twenty-six genotypes that included a control group consisting of garden pea samples. Information was obtained regarding several aspects of agricultural productivity and the variables affecting it. All of the parameters under investigation showed statistically significant heterogeneity, according to the analysis of variance, with the exception of the number of primary branches per plant. Yumkhaibam et al. [20] carried out research to find out how genetic diversity and heritability relate to various plant traits. Plant height, the number of primary branches per plant, the number of days until the first flowering and pod harvesting, ascorbic acid, protein content, pod weight, shelling percentage, internodal length, and other yield-related traits were all included in this list. The study's conclusions showed that a considerable amount of the observed plant features were shaped by inheritance. The genetic advance of days to first pod harvest was found to be the lowest, whereas the genetic advance of plant height, internodal length, and number of primary branches per plant were found to be the highest. Elevated heritability and significant genetic progress were found in important combinations in the variables of plant height, internodal length, and number of main branches per plant. Thus, based on the previously described findings, it may be inferred that the traits that have been seen are influenced by additive genetic components. Therefore, adopting the strategy of selecting superior genotypes based on these qualities will help crops be effectively improved, resulting in increased yield and superior yield attributes. The study carried out by Kanwar and colleagues [21] aimed to evaluate the genetic variability, heritability, and genetic gain in a population of peas that consisted of thirty genotypes. The experiment's findings showed that the pea genotype JP-54 produced the most pods per plant and the best pod yield overall. Based on the data gathered, the Swarna Mukti variety showed the most branches per plant and the maximum plant height. The genotype Arka Karthik showed the greatest values for plant spread, pod length, and protein content that have ever been measured. The cultivar with the greatest average pod weight and moisture content was AP-5. The very minimum number of days that Pusa Pragati needed to start flowering was noted. Rachna achieved the highest recorded fibre content ever recorded. All of the

features under investigation showed statistically significant variation, according to the analysis of variance, suggesting a greater chance of finding genotypes with favourable attributes. Significant genetic heterogeneity was found by LongKumer and Chaturvedi [22] for all variables evaluated in *Pisum sativum*. The study's conclusions also showed that, for every characteristic under investigation, the phenotypic coefficient of variation (PCV) continuously outperformed the genotypic coefficient of variation (GCV), suggesting the impact of environmental factors on these traits.

In a sample of ten genotypes of pea (*Pisum sativum* L.), Ali et al. [23] investigated the variability, heritability, genetic progress and correlation coefficient relevant to yield and yield-related features. There were notable differences in a number of important parameters, including the amount of time it took for fifty percent of the plants to bloom, the number of main branches per plant, the height of the plants, the time until maturity, the number of pods per plant, the length of the pods, the percentage of fresh pods that could be shelled, the weight of one hundred fresh and dry seeds, the number of seeds per pod, and the total number of seeds produced per plant. Sultan performed better than the other genotypes evaluated in terms of fresh pod shelling percentage, days to maturity, and 50% flowering. The highest values for plant height, number of pods per plant, and seed output per plant were found in the PL-4 genotype. In a study published in 2021, Pujari et al. [24] assessed the genetic variables linked to eleven distinct phenotypes in a sample of 21 field pea genotypes. Significant variability was found in the genotypes that were examined in the analysis of variance. There were significant differences in the genotypic and phenotypic coefficients of variation (PCV and GCV) for the characteristics number of primary branches per plant, number of pods per plant, and plant height (in centimetres) that were calculated. Yadav et al. [25] observed that for all the traits they looked at in vegetable pea, the phenotypic coefficients of variation (PCV) were larger in size than the genotypic coefficients of variation (GCV). In terms of both genotypic and phenotypic variance, the principal branches of each plant exhibited the largest coefficients of variation. The factors listed earlier were then measured, including nodes to first bloom appearance, nodes to first pod appearance, and pod production per plant. The highest phenotypic and genotypic coefficient of variations was found in the node to first pod appearance trait. This

was followed by the number of seeds per 250 g, number of pods per 250 g, and total soluble solids. The goal of Kumar et al [26]. current study from 2022 was to investigate the genetic variability and connections between various agronomic parameters in different genotypes of *Pisum sativum* L., also known as pea. All six of the pea genotypes under investigation showed significant statistical variations. According to the study's findings, genotypes carrying the G6 genotype exhibited superior performance in terms of fresh pod shelling percentage, days to maturity, and 50% blooming. When it came to plant height, pod count, and seed yield per plant, the genotype known as G2 showed the highest values. With a maximum of 100 seeds, genotype G9 had the highest fresh and dry weight. While the genotype G8 had the greatest values for both pod length and quantity of seeds per pod, the genotype G5 showed noticeably more primary branches per plant. The study by Tasnim et al. [27] aimed to investigate the genetic relationship between certain quantitative traits relevant to the commercial production of peas. Moreover, their aim was to evaluate the suitability of these traits as selection criteria in a pea breeding programme. A sample of five inbred parents served as the experiment subjects in this study. For every characteristic under study, the phenotypic coefficients of variation (PCV) closely matched the genotypic coefficients of variation (GCV), suggesting that selection showed significant promise and that the influence of environmental factors was minimal.

3. CONCLUSION

Traits such as the number of branches per plant, number of leaves per plant, pod yield per plant, and pod length exhibited notable levels of additive components, including increased estimates of heritability. Additionally, these traits displayed a high genetic advance as a percentage of mean (GAM), as well as the presence of a high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). The genetic modification of garden peas can be achieved by the practice of selective breeding, utilizing the existing germplasms for the afore mentioned characteristics.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Ambrose MJ. From Near East center of origin the prized pea migrates throughout world. *Diversity*. 1995;11:118-119.
2. Blixt OH, Frankel, Bennet E. (*Pisum sativum*): Genetic resources in plants- their exploration and conservation. International Biological Programme, Blackwell Scientific Publishers, Oxford. 1970;321-326.
3. Chakraborty U, Sarkar B, Chakraborty BN. Protection of soybean root rot by bradyrhizobium japonicum and Trichoderma harzianum, associated changes in enzyme activities and phytoalexin production. *Journal of Mycology and Pathology*. 2003;33:21-25.
4. Anonymous. Indian horticulture data base. Published by National Horticulture Board, Gurgaon; 2022.
5. Vavilov NI. The origin, variation, immunity and breeding of cultivated plants. *Chronic. Bot*. 1951;13:1-366.
6. Parkash C. Estimation of genetic variability and implications of direct effects of different traits on leaf yield in bathua (*Chenopodium album*). *Indian J. Agric. Sci. The complete*2012;82:71–74.
7. Shirshat SS, Giritammannavar VA, Patil SJ. Analysis of genetic variability for quantitative traits in chilli. *Karnataka J. Agric. Sci.* 2007;20(1):29-32
8. Datta S, Das L. Characterization and genetic variability analysis in *Capsicum annum* L. germplasm. *SAARC J. Agric.* 2013;11(1):91-103.
9. Singh G, Singh M, Singh V, Singh, B. Genetic variability, heritability and genetic advance in pea (*Pisum sativum* L.). *Prog. Agri.* 2003;3:70-73.
10. Kalloo G, Rai M, Singh J, Verma M, Kumar R, Rai GK, Vishwanath. Morphological and biochemical variability in pea (*Pisum sativum* L.). *Veg. Sci.* 2005;32:19-23.
11. Akhilesh S, Meenakshi S, Ashwini R, Yudhvir S. Genetic variability and association studies for green pod yield and component horticultural traits in garden pea under high hill dry temperate conditions. *Ind. J. Hort.* 2007;64:349-354.
12. Sharma MK, Chandel A, Kohli UK. Genetic evaluation, correlations and path analysis in garden pea (*Pisum sativum* var. hortense L.). *Ann. of Horti.* 2009;2:33-38.
13. Akansha S, Shalini S, Dayal Prasad Babu J. Heritability, character association and path analysis studies in early segregating

- population of field pea (*Pisum sativum* L. var. arvense). Inter. J. Pt. Breed. Gene. 2011;5(1):86-92.
14. Kumar D, Malik S, Singh SK, Kumar M. Genetic variability, heritability and genetic advance for seed yield and yield components in garden pea (*Pisum sativum* L.). Vegetos-An Inter. J. Pt. Res. 2013; 26(1):182-184.
 15. Siddika A, Islam AKMA, Rasul MG, Mian MAK, Ahmed JU. Genetic variability in advanced generations of vegetable pea (*Pisum sativum* L.). International Journal of Plant Breeding. 2013;7(2):124-128.
 16. Kumar R, Kumar M, Dogra RK, Bharat NK. Variability and character association studies in garden pea (*Pisum sativum* var. hortense L.) during winter season at mid hills of Himachal Pradesh. Legume Res. 2015;38(2):164-168.
 17. Jaiswal NK, Gupta AK, Dewangan HG, Lavanya RG. Genetic variability analysis in field pea (*Pisum sativum* L.). Inter. J. Sci. Res. 2015;4(1):2006-2007.
 18. Katoch V, Singh P, Devi MB, Sharma A, Sharma GD, Sharma JK. 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. Leg. Res. 2016;39(2):163-169.
 19. Gudadinni P, Bahadur V, Ligade P, Topno SE, Prasad VM. Study on genetic variability, heritability and genetic advance in garden pea (*Pisum sativum* var. hortense L.). Int. J. Curr. Microbiol. App. Sci. 2017;6(8):2384-2391.
 20. Yumkhaibam T, Deo C, Ramjan Md, Bidyaleima NC, Semba S. Estimation of genetic variability, heritability and genetic advances for yield and its component traits of garden pea (*Pisum sativum* L.) in North East India. J. Phar. Phyt. 2019;8(3):4034-4039.
 21. Kanwar PS, Toppo S, Sahu S. Evaluate the performance of genotypes of pea in terms of growth, yield and quality attributes. Journal of Pharmacognosy and Phytochemistry. 2020;9(3):2117-2120.
 22. Longkumer K, Chaturvedi HP. Genetic variability, correlation and path coefficient studies in pea (*Pisum sativum* L.) genotypes under foothill condition of Nagaland. Journal of Plant Science Research. 2020;36(1):125-130.
 23. Ali B, Kumar S, Ahmed W. Genetic variability, heritability and correlation coefficient in production traits of pea (*Pisum sativum* L.) Genotypes. International Journal of Genetics and Genomics. 2021;9(4):78.
 24. Pujari PK, Salam JL, Sao A, Mandavi NC, Singh DP. Study of genetic variability in field pea (*Pisum sativum* L.) Journal of Pharmacognosy and Phytochemistry. 2021;10(1):1053-1055.
 25. Yadav P, Ram CN, Yadav GC, Nath S, Kumar S. Studies on genetic variability, heritability and genetic advance in garden pea (*Pisum sativum* L. var. hortense). The Pharma Innovation Journal. 2021;10(7): 1146-1148.
 26. Kumar S, Ali B, Ahmed W, Islam R, Rahman MM, Chakman M, Miah MS. Assessment of the genetic variability for various agronomic traits of pea (*Pisum sativum* L.) genotypes. Plant Archivez. 2022;22(1):87-94.
 27. Tasnim S, Poly NY, Jahan N, Khan AU. Relationship of quantitative traits in different morphological characters of pea (*Pisum Sativum* L.) Journal of Multidisciplinary Applied Natural Science. 2022;2(2):103-114.

© 2023 Luthra et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:
The peer review history for this paper can be accessed here:
<https://www.sdiarticle5.com/review-history/109016>