Review Article

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

ABSTRACT

Estimating the parameters of variability, especially heritability and genetic gain are important indicators for improvement of characters through selection whereas the selection for highly heritable characters is more effective. Therefore, heritability along with other parameters of variability can be used in predicting the gain for a given selection intensity and expected genetic gain further gives the idea of the extent of improvement in a character through simple selection. However, selection for yield and quality traits can be better achieved if the information with respect to correlation between such traits is also available followed by a better understanding of the association between the relevant characters provided through path coefficient analysis. Similarly, for improvement of those characters which didn't respond to selection, there is a need for partitioning of non additive component of genetic variance further by hybridization which is achieved through genetic divergence studies.

Keywords: variability, heritability, genetic gain, improvement

INTRODUCTION

Among legumes, pea (*Pisum sativum* L.) is an important crop with a rich history in genetic research dating back to the classical work by the father of genetics Gregor J. Mendel. Pea is one of the six major pulse crops cultivated globally and it is the second highest yielding legume in the world after common bean (*Phaseolus vulgaris* L.). The common pea (also known as the garden pea), botanically known as *Pisum sativum var*. *Hortense* L. (2n=2x=14) is one of the world's oldest domesticated crops (Ambrose, 1995). It is an annual herbaceous crop of the family *Fabaceae* or *Leguminosae* (Genus: *Pisum*, subfamily: *Faboideae* tribe: *Fabeae*). According to Blixt *et al*., (1970), the Mediterranean region is the primary centre of diversity with secondary origin in Ethiopia. According to (Zohary and Hopf, 1973) Archaeological evidences dates the existence of pea back to 10,000 B.C. in Near East and Central.

Comment [A1]: What do you want to convey

The term "pea" can refer to small spherical seed or to the pod. Peas are consumed as fresh vegetables or dry seeds in most of the countries. Peas are starchy but, high in fiber, protein, vitamins (vitamin A, C, K and B complex vitamins such as folic acid, pantothenic acid, niacin, thiamine and pyridoxine), minerals (iron, magnesium, phosphorus and zinc) and

lutein (a yellow carotenoid pigment that benefits vision). The dry pea seeds are rich source of proteins (about 19-27%) and are free of anti-nutritional substances (Petterson *et al*., 1997). Dry weight is about one-quarter protein and one-quarter carbohydrates, mostly sugars.Pea is grown as winter season vegetable in plains and summer season in hills. Legumes can interact symbiotically with the soil-borne bacteria called Rhizobium and allow them to fix atmospheric nitrogen then improve the physical property of the soil and protect them against fungal pathogens (Chakraborty *et al*., 2003). It improves soil fertility by providing nitrogen to successive crop (nitrogen fixation by *Rhizobium leguminosarum*) without the added expense of supplemental fertilizer. In India, garden pea is grown in an area of 0.55 million hectares with an annual production of 5.52 million tonnes and productivity of 10.03 t/ha (NHB, 2018-19).

Comment [A2]: Kindly provide latest data

In spite of such an economic importance, production per unit area of pea is still low in the country especially when varieties are grown during off-season and the major constraints attributed to this are lack of high yielding varieties with poor or no resistance to powdery mildew and *Fusarium* wilt. Hence, there is an urgent need to evaluate large number of genotypes, to identify high yielding and superior varieties of pea which can be released as such for commercial production or can be incorporated in the future crop improvement programmes like its yield and quality traits.

Genetic Variability in Garden Pea

The success of any crop improvement programme largely depends upon the nature and magnitude of genetic variability existing in the breeding material. This study on genetic variability elucidates information on genetic parameters. Genetic variability is the amount of genotypic variation present in a population, forms the basis of all the crop improvement programmes. A wide range of variability is available in pea genotypes which provide great scope for improving pod yield through systematic breeding. The improvement in any crop is proportional to the magnitude of its genetic variability present in the germplasm. Greater the variability in a population, greater is the chance for effective selection for desirable types (Vavilov, 1949). Estimation of genetic variability present in the germplasm of a crop is a pre-requisite for designing effective breeding programme (Parkash, 2012). Thus, improvement in any crop is based on the extent of genetic variation and the degree of improvement depends upon the magnitude of available beneficial genetic variability (Shirshat *et al.*, 2007). For any breeding work initiation, to assess the genetic variability present in the indigenous genotypes for yield and its components is necessary. Parameter of genotypic and phenotypic coefficient

of variations is useful in detecting the amount of variability present in the germplasm (Datta and Das, 2013).

Singh *et al*., (2003) estimated that the high value of genetic advance in per cent of mean was recorded for plant height, length of internodes, length of pods, days taken to first flower, number of pods per plant, number of seeds per pod, number of primary branches, shelling percent, seed yield per plant and pod yield per plant. The studies also revealed the medium value of heritability for number of seeds per pod, shelling per cent, number of primary branches, number of pods per plant, 100 seed weight and seed yield per plant. High estimates of broad sense heritability were recorded for 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% flowering (92.25%), whereas remaining characters revealed moderate heritability. Kalloo *et al*., (2005) reported the high genetic advance as percent of mean along with high heritability was obtained for green pod yield per plant (66.28), plant height (54.67), number of green pod per plant (38.28) and 100 green pod weight (32.07). They also reported high estimates of genotypic variability for yield and its contributing traits. Akhilesh *et al*., *(*2007) reported that the seed yield per plant, 100-seed weight, plant height and pods per plant exhibited high heritability along with high genetic advance for different traits. The high value of genetic advance in per cent of mean was recorded for plant height, length of internodes, length of pods, days taken to first flower, number of pods per plant, number of seeds per pod, number of primary branches, shelling percent, seed yield per plant and pod yield per plant Sharma *et al*.,(2009) estimated heritability ranged from 49.25% in shelling percent to 95.95% in pod breadth. High heritability along with more genetic gain was expressed by pod breadth (94.95% & 63.16%). Total phenols (g/100g) of leaves (94.37% & 84.30%) and high heritability with moderate genetic gain was recorded for number of pods/ plant (93.41% & 25.39%), node number at which first flower appears (94.93% & 23.68%) and pod yield per plant (79.17% & 22.96%) indicating presence of additive genes in governing these traits and the selection based on the phenotypic performance of the plants could prove to be very effective in the improvement of these characters which could be retained in further generations. Akansha *et al*., (2011) studied 20 F_2 segregating population of field pea for their nature and magnitude of genetic variability and observed maximum variability for plant height, number of pods per plant and grain yield per plant. They also reported higher values of PCV for grain yield per plant (45.32) and for number of pods per plant (33.17), whereas

low estimates of PCV were reported for days to maturity (4.14) and days to flowering (6.89). Maximum value of GCV was observed for plant height (21.22) and for grain yield per plant (18.11), Low GCV observed for days to maturity (3.93) and days to flowering (4.67). Moderate to high heritability (broad sense) coupled with moderate genetic advance as percent of mean was recorded for the character's plant height, pod length and 100 seed weight indicating role of additive gene action in the expression of these traits. Kumar *et al*., (2013) estimated the magnitude of genetic variability, heritability and genetic advance for ten yield contributing traits among fifteen genotypes of garden pea. They observed considerable amount of genetic variability for all the characters including seed yield per plant indicating wide spectrum of variation among the genotypes. The exhibited higher values of genotypic and phenotypic coefficient of variation were observed for plant height, number of pods per plants, pod length, number of seed per pod,100- seed weight and seed yield per plant, high estimates of heritability, genotypic coefficient of variation and genetic advance were observed for plant height, productive branches per plant, number of pods per plant, pod length, number of seed per pod, 100- seed weight and seed yield per plant showing the influence of additive gene action on these traits hence, may be, useful for effective selection. Siddika *et al*., (2013) while studying 26 advanced lines of vegetable pea indicated that the existence of significant variability for characters like days to flowering, plant height, number of pods per plant, pod length, 100 seed weight and seed yield per plant except number of seeds per pod. They also indicated that the phenotypic variance (σ_p) was higher than genotypic variance (σ_g) for the characters; days to flowering, plant height, number of pods per plant, pod length, 100 seed weight, and seed yield per plant. At the same time the phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the aforementioned agronomic characters. High heritability associated with high genetic advance was observed for plant height, pod length and seed yield per plot.

Kumar *et al*., (2015) evaluated the fifty-four genotypes of garden pea including four checks to estimate the parameters of variability of important characters. They revealed that the genotypic and phenotypic coefficients of variation were high for total soluble solids, total sugars, pod yield per hectare and total phenols. High heritability estimates coupled with high to moderate genetic gain observed for pod yield (kg/plot), node at which the first flower appear (number), number of pods per plant and total Phenols (g/100g).Jaiswal *et al*., (2015) evaluated a collection of 12 genotypes of field pea to estimate variability analysis of some reproductive characters on grain yield. The genotypes showed moderate to high level of

genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), heritability and genetic advance were observed for days to 50% flowering, plant height, number of pods per plant, days to maturity, number of seed per pod, pod length, 100-seed weight and grain yield per plant. The magnitudes of the phenotypic variance of these traits were higher than the genotypic variance, indicating that the phenotypic component was the major contributor to total variance. Among all traits, plant height exhibited high estimates of GCV and PCV (48.10 and 48.42) followed by seed yield per plant (24.36 and 33.69) and number of seed per pod (16.40 and 20.36). High broad-sense heritability (52.00% - 99.00%) indicated the presence of additive gene effects.Katoch *et al.,* (2016) taken Forty-five diverse pea recombinant inbreeds and three standard checks were studied to ascertain genetic variability, heritability and genetic advances among yield, and other horticultural and quality traits, and identification of superior recombinants for their utilization in crop improvement programme. Wide range of variability was observed for most of the characters under study. The magnitude of phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits. High phenotypic and genotypic coefficient of variation were recorded for protein content, ascorbic acid, plant height and pod yield per plant for both the years. Pod yield per plant and plant height exhibited high heritability associated with high genetic advances in the respective years indicating the additive gene action for their expressions and are likely to respond better to selection.Gudadinni *et al.,* (2017) conducted an experiment to derive information on genetic variability, heritability and genetic gain in the twenty-six genotypes including check in garden pea. The observations were recorded on various yield and yield contributing characters. Analysis of variance showed the significant variability for all the studied characters expect number of primary branches per plant. Tabalique *et al.,* (2019) studied the genetic variability and heritability results revealed that, heritability exerts at high degree for all the plant characters studied *viz.* plant height, days to first flowering, days to first pod harvesting, ascorbic acid, protein content, pod weight, shelling percentage, internodal length, number of primary branches per plant, pod yield per plant, pod yield per hectare as well for other yield attributing characters. Plant height, internodal length and number of primary branches per plant showed highest genetic advance and lowest for days to first pod harvest. High heritability coupled with high genetic advance was observed for plant height, internodal length and number of primary branches per plant. Therefore, from the above obtained results it can be concluded that the characters studied are governed by additive gene effect. Hence, adoption for selection of elite genotype on the basis of these characters will result in effective crop improvement for higher

Comment [A3]: Missing in reference part

yield and yield attributing characters.Kanwar *et al.,* (2020) studied the genetic variability, heritability and genetic gain in the 30 genotypes of pea. The results from experiment revealed that pea genotype JP-54 recorded maximum pod yield per plant and maximum number of pods per plant. Swarna Mukti recorded maximum number of branches per plant and plant height. Maximum protein content, pod length and plant spread were recorded in genotype Arka Karthik. AP-5 recorded highest average pod weight and moisture content in pod. Pusa Pragati recorded minimum days to first flowering. Rachna recorded maximum fiber content. Analysis of variance revealed significant difference for all the characters under study, indicating more scope for selection of promising genotypes. LongKumer and Chaturvedi (2020) observed significant variation among the genotypes for all the character studied in pea. The studies also revealed that the PCV were higher than the GCV for all the characters studied indicating the influence of environmental effect.

Ali et al.,(2021) conducted an experiment to study the variability, heritability, genetic advance and correlation coefficient for yield and yield related traits in 10 pea (*Pisum sativum L.*) genotypes. Highly significant differences were observed for days to 50% flowering, primary branches per plant, plant height days to maturity, pods plant per plant, pod length, fresh pod shelling percentage, 100-seeds fresh and dry weight, number of seeds per pod and seed yield per plant. Among the genotypes, Sultan was observed best for 50% flowering, days to maturity and fresh pod shelling percentage. Genotype PL-4 had maximum plant height, number of pods plant per plant and seed yield per plant. Pujari *et al*., (2021) evaluated genetic parameters for eleven characters with 21 genotypes of field pea. The analysis of variance had large variability present among the genotypes studied. High to moderate PCV and GCV estimates for the traits viz; number of primary branches per plant, pods per plant, and plant height (cm) was noted. Yadav *et al.* (2021) reported the phenotypic coefficients of variations (PCV) were higher than genotypic coefficients of variations (GCV) for all the characters of vegetable pea. The highest phenotypic as well as genotypic coefficients of variation were observed in case of primary branches per plant followed by pod yield per plant, pods per plant, nodes to first flower appears and nodes to first pod appears. The highest phenotypic and genotypic coefficient of variations were observed for node to first pod appear followed by number of seeds per 250 g, number of pods per 250 g and total soluble solid. Kumar *et al.,* (2022) studied genetic variability and association among agronomic characters of pea (*Pisum sativum* L.) genotypes. Highly significant differences were found 6 among the tested pea genotypes. The results obtained revealed that genotypes (G6) were best for 50%

flowering, fresh pod shelling percentage and days to maturity. Genotype (G2) had highest plant height, number of pods plant per plant and seed yield per plant. Genotype (G9) had maximum 100-seed fresh and dry weight. Genotype (G5) had more primary branches per plant whereas genotype (G8) showed maximum pod length and seeds pod per plant. *Tasnim et al.* (2022*)* studied the genetic relationship between different quantitative traits for commercial cultivation and to assess selection criteria in pea breeding program in five inbred parents. Phenotypic coefficients of variation (PCV) were close to genotypic coefficients of variation (GCV) for all the characters indicating less impact of the environment and potentiality of selection.

REFERENCES

Akansha,S., Shalini S., and J. Dayal Prasad Babu. (2011). Heritability, character association and path analysis studies in early segregating population of field pea (*Pisum sativum* L. var. arvense). *Inter. J. Pt. Breed. Gene*., 5(1): 86-92.

Akhilesh, S., Meenakshi, S., Ashwini, R. and Yudhvir, S. (2007). 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.*, 64: 349-354.

Ali, B., Kumar, S. and Ahmed, W. (2021). Genetic variability, heritability and correlation coefficient in production traits of pea (*Pisum sativum* L.) Genotypes. International Journal of Genetics and Genomics, 9(4):78.

Ambrose, M. J. (1995). From Near East center of origin the prized pea migrates throughout world. *Diversity*, 11: 118-119.

Blixt, O.H., Frankel and Bennet, E. (1970). (*Pisum sativum*): Genetic resources in plants-their exploration and conservation. International Biological Programme, Blackwell Scientific Publishers, Oxford, 321-326.

Chakraborty, U., Sarkar, B. and Chakraborty, B. N. (2003). Protection of soybean root rot by *bradyrhizobium japonicum* and *Trichoderma harzianum*, associated changes in enzyme activities and phytoalexin production. *Journal of Mycology and Pathology*, 33: 21-25.

Datta, S. and Das, L. (2013). Characterization and genetic variability analysis in *Capsicum annuum* L. germplasm. *SAARC J. Agric.*, 11(1): 91-103.

Gudadinni, P., Bahadur, V., Ligade, P., Topno, S.E. and Prasad V.M. (2017). Study on genetic variability, heritability and genetic advance in garden pea (*Pisum sativum* var. *hortense*L.). *Int. J. Curr. Microbiol. App. Sci.*, 6(8): 2384-2391.

Jaiswal, N.K., Gupta, A.K., Dewangan, H. G. and Lavanya, R. G. (2015). Genetic variability analysis in field pea (*Pisum sativum* L.). *Inter. J. Sci. Res.*, 4(1): 2006-2007.

Kalloo, G., Rai, M., Singh, J., Verma, M., Kumar, R., Rai, G.K. and Vishwanath. 2005. Morphological and biochemical variability in pea (*Pisum sativum* L.). *Veg. Sci.*, 32:19-23.

Kanwar, P. S., Toppo, S. and Sahu, S. (2020). Evaluate the performance of genotypes of pea in terms of growth, yield and quality attributes. *Journal of Pharmacognosy and Phytochemistry*, 9(3): 2117-2120.

Katoch, V., Singh, P., Devi, M. B, Sharma, A., Sharma, G.D. and 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. *Leg. Res.*, 39(2): 163-169.

Kumar, D., Malik, S., Singh, S. K. and Kumar, M. (2013). Genetic variability, heritability and genetic advance for seed yield and yield components in garden pea (*Pisum sativum* L.). *Vegetos-An Inter. J. Pt. Res.*, 26(1): 182-184.

Kumar, R., Kumar, M., Dogra R. K. and Bharat N. K. (2015). Variability and character association studies in garden pea (*Pisum sativum* var. hortense L.) during winter season at mid hills of Himachal Pradesh. *Legume Res*., 38(2): 164-168.

Kumar, S., Ali, B., Ahmed, W., Islam, R., Rahman, M. M., Chakma, M. and Miah, M. S. (2022). Assessment of the genetic variability for various agronomic traits of pea (*Pisum sativum* L.) genotypes. *Plant Archives*, 22(1): 87-94.

Longkumer, K. and Chaturvedi, H. P. (2020). Genetic variability, correlation and path coefficient studies in pea (*Pisum sativum* L.) genotypes under foothill condition of Nagaland. *Journal of Plant Science Research*, 36 (1): 125-130.

NHB (2018-19), National Horticultural Board (2018-19), 1st advance estimates. National Horticulture Board, Gurgoan, Haryana.

Parkash, C. (2012). Estimation of genetic variability and implications of direct effects of different traits on leaf yield in bathua (*Chenopodium album*). *Indian J. Agric. Sci.*, 82: 71–74. The complete

Petterson, D. S., Sipsas, S. and Mackintosh, J. B. (1997).

Pujari, P. K., Salam, J. L., Sao, A., Mandavi, N. C. and Singh, D. P. (2021). Study of genetic variability in field pea (*Pisum sativum* L.) *Journal of Pharmacognosy and Phytochemistry*, 10(1): 1053-1055.

Comment [A4]: Write the reference correctly

Comment [A5]: Write the complete reference

Sharma, M.K., Chandel, A. and Kohli, U.K. (2009). Genetic evaluation, correlations and path analysis in garden pea *(Pisum sativum var. hortense* L.). *Ann. of Horti.*, 2: 33-38.

Shirshat, S.S., Giritammannavar, V.A. and Patil, S.J. (2007). Analysis of genetic variability for quantitative traits in chilli. *Karnataka J. Agric. Sci*., 20(1): 29-32

Siddika A., Islam, A.K.M.A., Rasul, M.G., Mian M.A.K. and Ahmed J.U. (2013). Genetic variability in advanced generations of vegetable pea (*Pisum sativum* L.). *International Journal of Plant Breeding*, 7(2): 124-128.

Singh G, Singh M, Singh V, Singh, B. (2003). Genetic variability, heritability and genetic advance in pea (*Pisum sativum* L.). *Prog. Agri.*, 3: 70-73.

Tasnim, S., Poly, N. Y., Jahan, N. and Khan, A. U. (2022). Relationship of quantitative traits in different morphological characters of pea (*Pisum Sativum* L.) *Journal of Multidisciplinary Applied Natural Science*, 2(2): 103-114.

The chemical composition and nutritive value of Australian grain legumes (2nd edn.) Grain Research and Development Corporation, Canberra, Australia.Wiley and Sons, Inc., New York.

Vavilov, N.I. (1951). The origin, variation, immunity and breeding of cultivated plants. *Chronic. Bot.*, 13: 1-366.

Yadav, P., Ram, C. N., Yadav, G. C., Nath, S. and Kumar, S. (2021). Studies on genetic variability, heritability and genetic advance in garden pea (*Pisum sativum* L. var. *hortense*). *The Pharma Innovation Journal*, 10(7): 1146-1148.

Yumkhaibam, T., Deo, C., Ramjan, M.d., Bidyaleima, N.C., and Semba, S., (2019). 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.*, 8(3): 4034-4039.

Zohary, D. and Hopf, M. (1973). Domestication of pulses in the old World: Legumes were companions of wheat and barley when agriculture began in the Near East. Science, 182(4115): 887-894.

Comment [A6]: Write the reference properly