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# Multivariate Analysis for Early Genotypes of Garden Pea under Mid Hill condition of Himachal Pradesh

***Himani[1], Shivam Sharma[2]*, D.R. Chaudhary[3], Ankush Sharma[1] and Ketan[1]***
*[1]M.Sc. Scholar, Department of Vegetable Science and Floriculture, CSK HPKV, Palampur (Himachal Pradesh), India.*
*[2]Ph.D. Scholar, Department of Vegetable Science and Floriculture, CSK HPKV, Palampur (Himachal Pradesh), India.*
*[3]Professor and Head of the Department, CSK HPKV, Palampur (Himachal Pradesh), India.*

*(Corresponding author: Shivam Sharma*)*
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**ABSTRACT: The current study was conducted to assess yield and horticultural potency to identify the most promising 22 early genotypes of garden pea through multivariate analysis for 16 agro-morphological traits during *rabi* 2020-21 at CSK HPKV, Palampur. In the past, several high-yielding varieties of mid and late-maturing groups have been developed in the country but very little emphasis has been given for the development of high yielding early maturing genotypes as a result harnessing variability among pea genetic stock now-a-days became a major challenge for the pea improvement program. Mahalanobis $D^2$ statistic grouped 22 genotypes into five clusters. Overall, cluster I was the largest, containing 8 genotypes while cluster IV was solitary having a single genotype. The highest intra-cluster distance was observed in cluster II while inter-cluster distances between cluster I and cluster IV depicted the presence of broad-spectrum genetic diversity. Based on cluster mean analysis, cluster III was found best for pod yield per plant. About, 66.9% variation was explained by the first five principal components with which ascorbic acid (PC1) was the maximum contributor towards genetic divergence followed by pod diameter (PC2), pod yield per plant (PC3), shelling percentage (PC4) and pods per plant (PC5). Hence, pea genotypes belonging to cluster III can be utilized to get higher yield through further heterosis breeding programs. In addition, hybridization between cluster I and cluster IV genotypes could get more recombinants in the segregating generations.**

**Keywords:** Cluster means, diversity, inter-cluster distances, PCA.

## INTRODUCTION

Garden pea (*Pisum sativum* L.), grown on a commercial scale for its tender and immature seeds as a winter vegetable in Northern plains and during spring in high hills. Consumers prefer hill-grown peas because of their distinct flavor, crispness, sweetness, and freshness. Currently, India is the largest producer of pea in the world, and owing to its diverse agroclimatic condition, it is grown around the year and hence bringing handsome lucrative returns to the growers (Katoch *et al.*, 2016). Worldwide garden pea occupies an area of 2.53 million hectares, production of 19.86 million tonnes and with productivity of 7.84 t/ha (Anonymous, 2020) while India occupies an area of about 563 thousand hectares with an annual production of 5703 thousand metric tonnes (Anonymous, 2020). In Himachal Pradesh, it occupies an area of 24.37 thousand hectares with an annual production of 294.97 thousand metric tonnes (Anonymous 2018). Being a leguminous vegetable, it holds a prominent position among vegetables on account of its high nutritive value, especially proteins and various other health-building substances like carbohydrates, vitamin A, vitamin C, calcium, phosphorus, and essential amino acids, particularly lysine (Mamatha *et al*., 2022)

The green pods from hilly areas become available at a time (April-October) when these cannot be grown in the plains on account of adverse weather conditions especially high temperature (Singh *et al.*, 2022). As a result, the product sells at a premium, fetching lucrative returns to the growers. On account of its relatively higher economic importance, the productivity especially of early genotypes is still low owing mostly to the lack of varieties with stable, high-yielding potential and losses due to several biotic and abiotic stresses (Rahman *et al.* 2019). Hence, there is a need to explore genetic variability which is considered an important prerequisite for crop improvement programs to obtain high-yielding progenies (Sharma *et al.*, 2020).

The presence of variability among different genotypes in a wide range of crop species is known as genetic diversity. Unlike variability, diversity may or may not have observable phenotypic differences. The $D^2$ method of proposed by Mahalanobis (1936) is used to survey

hereditary differences in which intra and inter-cluster distances are evaluated and thereby play a mandatory role in the selection of geographically and genetically divergent parents for the further pea improvement program. Keeping this point of view, the current investigation was carried out to analyze genetic diversity among the genotypes of garden pea. Thus, the information on the nature and magnitude of genetic diversity present in the genetic stocks are of considerable use in selecting the suitable genotypes to be included in future pea improvement programs.

## MATERIALS AND METHODS

The experimental material comprised 22 genotypes of garden pea (early group) received from the Indian Institute of Vegetable Research (IIVR), Varanasi as part of AICRP on Vegetable crops and other genotypes collected from IARI, New Delhi; PAU, Ludhiana, and CSK HPKV, Palampur. The experiment was designed in Randomized Complete Block Design (RBD) with three replications during *rabi* 2020-2021. Each experimental unit consisted of two rows of 1.8 m in length and plants were spaced at inter and intra-row spacing of 45 cm and 10 cm, respectively. The observations were recorded on 10 randomly selected competitive plants from each entry per replication for 16 traits *viz.*, days to 50 % flowering, days to first picking, harvest duration (days), pod length (cm),pod diameter (cm), average pod weight (g), seeds per pod, shelling percentage (%), branches per plant, nodes per plant, intermodal length (cm), plant height (cm), pods per plant, TSS ($^0$b), ascorbic acid (mg/100g) and pod yield per plant (g). Multivariate analysis was done as per the procedure formulated by Mahalanobis (1936); Rao (1952) using WINDOSTAT 8.0 statistical software.

## RESULTS AND DISCUSSION

The analysis of variance showed that the mean sum of squares due to genotypes were significant and thereby, found trustworthy to carry out further analysis. Genetic diversity using Mahalanobis $D^2$ statistic, categorized 22 genotypes into five different clusters (Table 1, Fig. 1). Overall, cluster I was the largest containing eight genotypes. Out of 5 clusters of 22 genotypes, cluster I comprised of maximum 8 genotypes (2019/PEVAR-1, 2019/PEVAR-5, 2018/PEVAR-7, 2019/PEVAR-2, 2019/PEVAR-4, 2019/PEVAR-7, 2019/PEVAR-10, 2018/PEVAR-2) followed by cluster V with 7 genotypes (2019/PEVAR-8, 2018/PEVAR-6, 2019/PEVAR-1, 2018/PEVAR-PEVAR-3, 2018/PEVAR-5, 2019/PMVAR-4, 2018/PEVAR-4) and cluster II and III having 3 genotypes while cluster IV remained solitary. Singh and Mishra (2008) also reported cluster I as the biggest one. The results were in conformity with the findings of Aman *et al.* (2021) who conducted diversity studies involving 57 genotypes and found five different clusters.

The highest intra-cluster distance was observed in cluster II followed by cluster V, cluster III, and cluster I cluster whereas, the inter-cluster distance was observed highest between cluster I and cluster IV followed by cluster IV and cluster V. However, inter-cluster distances were observed highest between cluster I and cluster IV indicated the presence of wide genetic diversity between the genotypes belonging to any two clusters than the genotypes within the cluster (Table 2, Fig. 2). Since the intra-cluster distance was less when compared with inter-cluster distances. Therefore, it is necessary to attempt hybridization between genotypes falling under different clusters as the selection of genotypes based upon large inter-cluster distances from all the clusters may lead to favorable broad-spectrum genetic variability. The results of Sekhon *et al.* (2017) observed a similar trend in which inter-cluster distance was higher than intra-cluster.

Based on cluster means (Table 3**)**, cluster I was found best for the traits, days to first picking, internodal length, and pod diameter; cluster II for days to 50% flowering and harvest duration; cluster III for TSS, ascorbic acid and pod yield per plant; cluster IV for shelling percentage, branches per plant, nodes per plant and plant height and cluster V for pod length, average pod weight, pods per plant and seeds per pod. The grouping pattern of the genotypes suggested no parallelism between genetic divergence and the geographical distribution of genotypes. Devi *et al.* (2010); Habtamu and Million (2013); Prasad *et al.* (2018) reported that genetic diversity was independent of geographical region.

The principal component analysis revealed that 66.9% variation was explained by the first five principal components with ascorbic acid (PC1) followed by pod diameter (PC2), pod yield per plant (PC3), shelling percentage (PC4) and pods per plant (PC5) were observed as the maximum contributors towards genetic divergence (Table 4, Fig. 3). The results are in agreement with Yadav *et al.* (2010) who reported that 61.6% of the total genetic variation was described by first four principal components.

**Table 1: Grouping of pea genotypes into different clusters based on Mahalanobis $D^2$ cluster analysis.**

| Cluster No. | No of genotypes | Genotypes |
|---|---|---|
| I | 8 | 2019/PEVAR-1, 2019/PEVAR-5, 2018/PEVAR-7, 2019/PEVAR-2, 2019/PEVAR-4, 2019/PEVAR-7, 2019/PEVAR-10, 2018/PEVAR-2 |
| II | 3 | Palam Triloki, Matar Ageta, Pusa Shree |
| III | 3 | 2019/PEVAR-3, 2019/PEVAR-9, 2019/PEVAR-6 |
| IV | 1 | 2019/PMVAR-8 |
| V | 7 | 2019/PEVAR-8, 2018/PEVAR-6, 2019/PEVAR-1, 2018/PEVAR-PEVAR-3, 2018/PEVAR-5, 2019/PMVAR-4, 2018/PEVAR-4 |

**Table 2: Average intra and inter cluster distances among garden pea genotypes.**

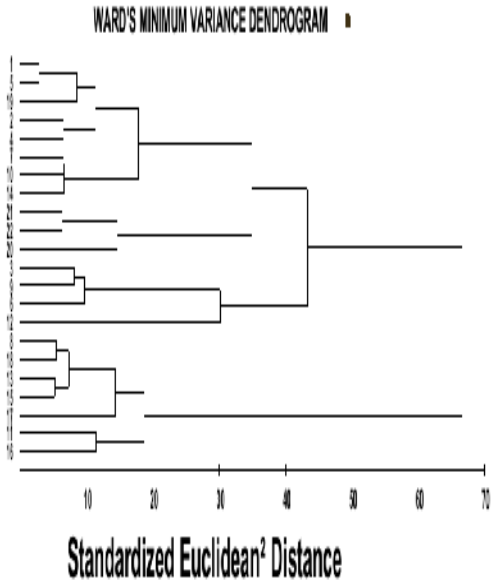
| | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V |
|---|---|---|---|---|---|
| Cluster I | **17.14** | 30.44 | 27.30 | 59.31 | 32.89 |
| | (4.14) | (5.52) | (5.23) | (7.70) | (5.74) |
| Cluster II | | **20.88** | 39.49 | 51.98 | 43.38 |
| | | (4.57) | (6.28) | (7.21) | (6.59) |
| Cluster III | | | **17.87** | 46.21 | 33.49 |
| | | | (4.23) | (6.80) | (5.79) |
| Cluster IV | | | | **0.00** | 56.21 |
| | | | | (0.00) | (7.50) |
| Cluster V | | | | | **20.80** |
| | | | | | (4.56) |

**Table 3: Cluster means of five clusters for different traits of 22 garden pea genotypes.**

| Cluster No. | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V |
|---|---|---|---|---|---|
| Days to 50% flowering | 78.46 | 75.33 | 76.44 | 80.63 | 81.33 |
| Days to first picking | 120.08 | 123.33 | 122.77 | 124.33 | 124.28 |
| Harvest duration (days) | 17.45 | 21.89 | 16.00 | 17.66 | 19.52 |
| Pod length (cm) | 9.02 | 8.68 | 10.32 | 10.35 | 10.53 |
| Pod diameter (cm | 3.68 | 3.65 | 3.31 | 3.30 | 3.60 |
| Average pod weight (g) | 5.73 | 4.66 | 6.05 | 3.62 | 6.63 |
| Seeds per pod | 6.77 | 6.81 | 7.00 | 6.83 | 7.73 |
| Shelling percentage (%) | 49.66 | 43.21 | 51.69 | 54.50 | 51.77 |
| Branches per plant | 1.20 | 1.34 | 1.26 | 1.53 | 1.319 |
| Nodes per plant | 15.61 | 16.96 | 15.91 | 22.40 | 17.27 |
| Inter nodal length (cm) | 4.62 | 4.16 | 4.38 | 3.47 | 4.49 |
| Plant height (cm) | 72.16 | 70.11 | 69.63 | 77.80 | 77.35 |
| Pods per plant | 11.24 | 11.79 | 10.92 | 10.58 | 11.97 |
| TSS ($^0$b) | 16.99 | 18.02 | 28.74 | 17.60 | 17.58 |
| Ascorbic acid (mg/100g) | 24.53 | 23.51 | 27.26 | 25.62 | 22.42 |
| Pod yield per plant (g) | 64.69 | 54.73 | 66.14 | 38.28 | 79.58 |

**Table 4: Eigen vectors for the first five prinipal components of different traits.**

| Variable | Eigen vector | | | | |
|---|---|---|---|---|---|
| | PC1 | PC2 | PC3 | PC4 | PC5 |
| Eigen values (Root) | 3.49 | 2.42 | 2.08 | 1.58 | 1.14 |
| Variation (%) | 21.80 | 15.10 | 13.10 | 9.90 | 7.10 |
| Cumulative variation (%) | 21.80 | 36.90 | 49.90 | 59.80 | 66.90 |
| Days to 50% flowering | 0.30 | 0.01 | -0.09 | -0.10 | -0.34 |
| Days to first picking | 0.25 | -0.25 | -0.06 | -0.20 | 0.26 |
| Harvest duration (days) | 0.16 | -0.06 | -0.49 | -0.09 | -0.13 |
| Pod length (cm) | 0.38 | -0.18 | -0.27 | 0.14 | -0.07 |
| Pod diameter (cm) | 0.04 | 0.36 | 0.35 | -0.02 | -0.15 |
| Average pod weight (g) | 0.40 | 0.32 | -0.12 | 0.20 | -0.03 |
| Seeds per pod | 0.34 | 0.08 | -0.05 | 0.18 | -0.14 |
| Shelling percentage (%) | 0.01 | -0.17 | -0.13 | 0.25 | 0.40 |
| Branches per plant | 0.17 | -0.43 | 0.19 | -0.09 | 0.13 |
| Nodes per plant | 0.17 | -0.49 | 0.19 | -0.10 | -0.23 |
| Inter nodal length(cm) | 0.05 | 0.38 | -0.12 | -0.53 | 0.29 |
| Plant height(cm) | 0.23 | -0.04 | 0.07 | -0.63 | 0.10 |
| Pods per plant | 0.26 | 0.02 | 0.32 | 0.10 | 0.47 |
| TSS ($^0$b) | -0.17 | -0.06 | -0.32 | 0.15 | 0.43 |
| Ascorbic acid (mg/100g) | 0.43 | 0.25 | 0.06 | 0.21 | 0.18 |
| Pod yield per plant (g) | 0.09 | -0.05 | 0.47 | 0.13 | 0.03 |




**1** 2019/PEVAR-1 **2** 2019/PEVAR-2 **3** 2019/PEVAR-3 **4** 2019/PEVAR-4 **5** 2019/PEVAR-5
**6** 2019/PEVAR-6 **7** 2019/PEVAR-7 **8** 2019/PEVAR-8 **9** 2019/PEVAR-9 **10** 2019/PEVAR-10
**11** 2019/PMVAR-4 **12** 2019/PMVAR-8 **13** 2018/PEVAR-1 **14** 2018/PEVAR-2 **15** 2018/PEVAR-3
**16** 2018/PEVAR-4 **17** 2018/PEVAR-5 **18** 2018/PEVAR-6 **19** 2018/PEVAR-7 **20** Pusa Shree
**21** Palam Triloki **22** Matar Ageta

**Fig. 1.** Dendrogram using Ward's Minimum Variance.

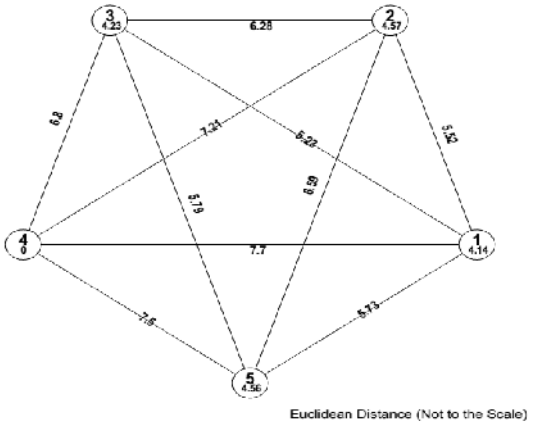



**Fig. 2.** Cluster diagram depicting inter and intra cluster distances (Mahalanobis Euclidean Distance).

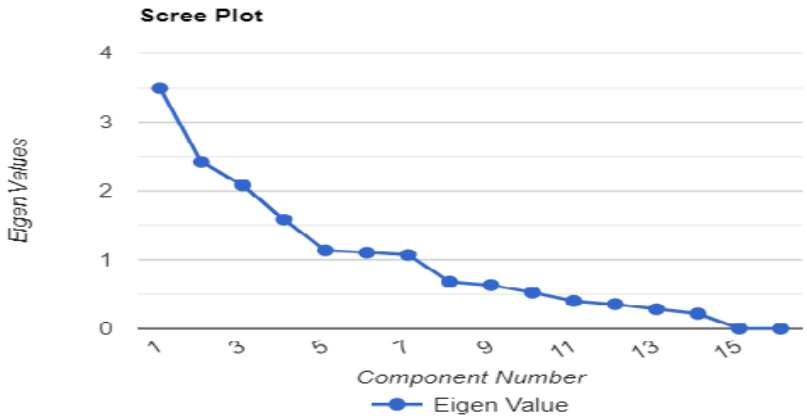



**Fig. 3**. Eigen values for various principal components.

## CONCLUSION

The highest inter-cluster distances indicated the presence of wide genetic diversity between the genotypes belonging to any two clusters than the genotypes within the cluster. Cluster III can be utilized to get higher yield through further heterosis breeding programs. The selection of genotypes based upon large cluster distances from all the clusters may lead to favorable broad-spectrum genetic variability, especially between cluster I and cluster IV, which could possibly get more recombinants in the segregating generations.

## FUTURE SCOPE

The multivariate analysis in garden pea can further be utilized in heterosis and transgressive breeding for specific agro-morphological traits improvement. Diversity studies using modern molecular markers might be helpful in deciding the selection of parents for bringing a revolution in the future's pea improvement program.

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**Conflict of Interest.** None.

## REFERENCES

Aman, F., Ara, N. and Shah S. M. A. (2021). Genetic diversity among pea (*Pisum sativum* L.) genotypes for maturity and yield traits. *Sarhad Journal of Agriculture*, *37*(2), 386-397.

Anonymous (2018). National Horticulture Board (NHB) http://www.nhb.gov.in

Anonymous (2020). FAOSTAT https://www.fao.org/faostat/

Devi, P., Pant, S. C., Rana, D. K. and Rawat, S. S. (2010). Genetic variability and selection parameters for different genotypes of pea (*Pisum sativum* L.) under valley condition of Uttarakhand. *Journal of Hill Agriculture*, *1*, 56-58.

Habtamu, S. and Million, F. (2013). Multivariate analysis of some Ethiopian field pea (*Pisum sativum* L.) genotypes. *International Journal of Genetics and Molecular Biology*, *5*, 78-87.

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. *Legume Research*, *39*(2), 163-169.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. *Proceedings National Academy of Sciences of India*, *22*, 49-55.

Mamatha, R. M., Sharma, R. K., Bhardwaj, A. and Kumar, R. (2022). Genetic diversity study among Garden Pea (*Pisum sativum* var. *hortense* L.) genotypes. *Biological Forum – An International Journal*, *14*(3), 911-915.

Prasad, D., Nath, S., Lal, K., Jaiswal, A. and Yadav, V. P. (2018). Evaluation of field pea (*Pisum satium* L. var. *arvense*) genotypes for genetic variability and divergence. *International Journal of Chemical Studies*, 6, 2288-2291.

Rahman, A., Katoch, V., Rathour, R., Sharma, S., Rana, S. S. and Sharma, A. (2021). Studies on genetic parameters, correlation and path coefficient analysis in er2 introgressed garden pea genotypes. *Legume research*, *44*(6), 621-626.

Rao, C. R. (1952). Advancedstatistical methods in biometrical research. John Wiley and Sons, p. 390.

Sekhon, B. S., Sharma, A., Katoch, V., Kapila, R. K. and Sood V. K. (2017). Assessment of genetic diversity in advanced breeding lines derived from intraspecific crosses of garden pea (*Pisum sativum* L.). *Legume Research*, *42*(2), 145-152.

Sharma, A., Sekhon, B. S., Sharma, S. and Kumar, R. (2020). Newly isolated intervarietal garden pea (*Pisum sativum* L.) progenies ($F_7$) under north western Himalayan conditions of India. *Experimental Agriculture*, *56*(1), 76-87.

Singh, D. and Mishra, V. K. (2008). Studies on genetic divergence in pea. *Agriculture Science Digest*, *28*(1), 77-78.

Singh, S., Singh, B., Sharma, V. R., Kumar, M. and Sirohi, U. (2022). Assessment of genetic diversity and population structure in Pea (*Pisum sativum* L.) germplasm based on Morphological traits and SSR Markers. *Legume Research*, *45*(6), 683-688.

Yadav, K., Singh, B. D., Srivastava, C.P., Chand, R. and 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), 363-369.

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