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# Studies on Genetic Diversity of Garden Pea (*Pisum sativum* L.)

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## A B S T R A C T

Genetic diversity in plant genetic resources provides opportunity for plant breeders to develop new and improved cultivars with desirable characteristics. Therefore, an attempt was made to determine the degree of divergence among 24 diverse genotypes of garden pea (*Pisum sativum* L.). Of genotypes, PB-01, PB-89 and Wasundra were carried from PAU, Ludhiana; VRPE-14, VRPE-24, VRPE- 32 and VRPE- 58 (IIVR, Varanasi); rest of the genotypes were the collection from Private Seed Company. These genotypes were evaluated in Randomized Complete Block Design with three replications in winter season during 2015-16 at Agriculture Farm of Lovely Professional University, Phagwara in Punjab. The findings revealed a considerable genetic diversity among genotypes which dispersed in 5 diverse clusters. Of these, cluster III, IV and V were mono-genotypic while cluster I had maximum genotypes. Among characters studied, pod yield contributed maximum towards diversity by 31.16%. Cluster mean analysis showed that intra-cluster distances ranged (0 – 168.79) indicated that collection of germplasm was highly divergent. Maximum inter-cluster distance (1430.70) was recorded between cluster III (i.e., Anmol) and cluster V (i.e., Shilpa-10) from mono-genotypic clusters those offer promise for their direct use as varieties and potential parents in future breeding programme.

***Key words*:** *Pisum sativum*, Genetic divergence, Hybrid, Genetic variability, Germplasm

Garden pea (*Pisum sativum L.*) belonging to family Leguminosae is cultivated its tender and immature seeds for use as vegetable and mature dry seeds for use as a pulse [1-2]. It is highly nutritive and contains high percentage of digestible proteins along with sugars, vitamins, minerals etc. [3]. It originated somewhere in the Ethiopia, Eastern Mediterranean region and south west Asia. Different centers of origin for pea were listed based on genetic diversity, area comprising Central Asia and the Mediterranean [4]. The first cultivation of peas appears to have been in western Asia, from where it spread to Europe, China and India. It is widely grown in temperate climate, but its cultivation is limited to winter season in the sub tropics and tropics.

Because of large diversity, the selection of varieties for growing in any locality is one of the most critical and most difficult tasks for the breeder. For further improvement, hybridization can prove as best technique which is helpful to combine early maturity with high yield and quality attributes in a hybrid. However, selection of parents is very important otherwise it would be costly effort resulting low heterosis. Moreover, the genotypes included in the diverse clusters can be used as promising parents for hybridization to obtain high heterotic response [5]. Multivariate analysis is considered as best tool while we have to choose the parental lines for hybridization [6-7]. Considering aforesaid problem, present investigation was formulated to assess genetic diversity among available germplasm of garden pea.

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## MATERIALS AND METHODS

Twenty-four diverse genotypes of garden pea obtained from various sources were tested at Agriculture Farm of Lovely Professional University, Phagwara (Punjab) during *rabi* season of 2015-2016. The experimental material viz. PB- 01, PB- 89 and Wasundra were carried from PAU, Ludhiana; VRPE-14, VRPE-24, VRPE- 32 and VRPE- 58 (IIVR, Varanasi); rest of the genotypes are the collection from Private Seed Company. The experiment was laid out in a randomized block design repeating each genotype into 3 blocks. The observations were recorded on five randomly selected plants for thirteen characters viz. including yield and quality attributes and subjected to statistical analysis. The experimental site is situated at 31°22'31.81" North Latitude and 75°23'03.02" East longitude, with an average elevation and with a mean sea level of 252 m. It is at a distance of 350 Kms from Delhi on Delhi-Amritsar the region falls under the agro climatic zone Central plain zone. This zone is characterized by mild winters and moderate summers associated with high relative humidity

during the rainy season. The maximum temperature (18-27°C) and minimum temperature (5-13°C) were favourable for the growth and development of crop during crop season. The soil of the experimental site was alkaline in reaction (pH= 7.46) containing organic carbon by 1.6%. The crop was raised in 4 m×1.5 m plot size. The seeds of vegetable pea genotypes were sown on November 2, 2015 at spacing of 30 cm between rows. Standard agronomic package of practices were adopted to raise a good crop. The crop was harvested in 3-4 pickings and finished on March 2016. The extent of genetic divergence was calculated by using $D^2$ statistics [8]. The $D^2$ values were obtained as the corresponding uncorrelated values of any two uncorrelated genotypes [9]. Intra and inter cluster distances were calculated by formula given by [10].

## RESULTS AND DISCUSSION

*Clustering pattern*

$D^2$ statistic is a useful tool to measure genetic divergence among genotypes in any crop developed by [8]. Twenty-four entries were collected from different sources and analyzing to find out genetic diversity. The $D^2$ values between any two genotypes were calculated as the sum of squares of the difference between the uncorrelated mean values of eleven characters used for final grouping of the genotypes. Twenty-four genotypes were grouped into five clusters following Tocher's method [9]. The distribution pattern of entries and clustering is given in (Fig 1). Cluster I includes 15 genotypes, forming the largest cluster followed by cluster II (6); cluster III, IV, V comprised of sole genotype, respectively. The pattern of group constellation indicated that genotypes were randomly formed into different clusters irrespective of their geographical distribution. Clustering of genotypes could become possible by [11-13] due to existence of genetic variability in pea.

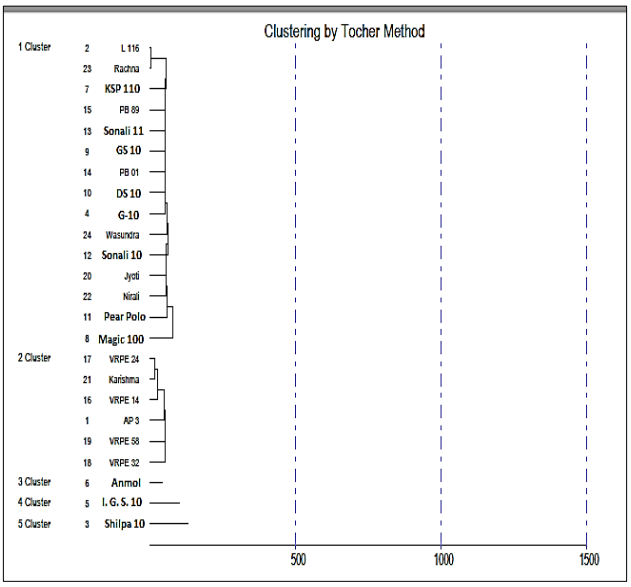


Fig 1 Clustering pattern of 24 genotypes of garden pea

*Contribution of characters towards genetic divergence*

Each character contributed in different proportion to total genetic diversity. The per cent contribution of all the characters is presented in (Table 1, Fig 2). Out of 11 characters studied, pod yield (q/ha) contributed maximum towards diversity by 31.16% which followed by plant height (cm) (23.91%), dry matter (%) (14.86%) and harvesting span (10.51%), days to 50% flowering (9.78%), number of pods per plant (2.90%), number of seeds per pod (2.90%), days to marketable maturity (2.17%), protein content (1.81%). Number of branches/ plant and first fruiting node did not contribute to the diversity (Table 1, Fig 2). Considerable contribution of plant height, green pod yield per plant and protein content was found to the total genetic divergence [14]. Our findings are in agreement with [15] reported maximum contribution of pod yield towards genetic diversity of crop. Contribution of characters like days to flowering and number of pods/plant was reported by [16]; number of seeds per pod [17].

Table 1 Contribution of characters towards genetic divergence

| Source | Times ranked 1st | Contribution (%) |
|---|---|---|
| Days to 50% flowering | 27 | 9.78 |
| Plant height (cm) | 66 | 23.91 |
| No. of branches per plant | 0 | 0.00 |
| First fruiting node | 0 | 0.00 |
| Number of pods per plant | 8 | 2.90 |
| Number of seeds per pod | 8 | 2.90 |
| Days to marketable maturi | 6 | 2.17 |
| Harvesting span (days) | 29 | 10.51 |
| Dry matter (%) | 41 | 14.86 |
| Protein content (%) | 5 | 1.81 |
| Pod yield (q/ha) | 86 | 31.16 |

*Intra and Inter-cluster distances*

The intra-cluster distances ranged (0 – 168.79) indicates that collection of germplasm was highly divergent. Maximum intra-cluster distance was recorded in cluster I followed by cluster II (Table 2, Fig 3). Cluster III, IV and V exhibited zero intra-cluster distance since each cluster had sole genotypes. The inter-cluster distances ranged from 299.96 to 1430.70. Maximum inter-cluster distance (1430.70) was recorded between cluster III and cluster V which followed by in between cluster II and V (1255.51). Statistical distances represent the index of genetic diversity among the clusters. Overall comparison of genetic divergence revealed greater inter-cluster distances than intra-cluster distances among clusters. This indicated that genotypes were closely related in same cluster and distant related between clusters. Because of maximum inter-cluster distances between cluster III (i.e., Anmol) and cluster V (Shilpa-10), crossing would result to develop highly heterotic hybrid as suggested by [12]. The genotypes of cluster II may also be used as parents in hybridization programme to develop desirable segregants. Similar statement was given by [14-15].

Table 2 Inter and intra cluster distances: Tocher Method

| | Cluster-I | Cluster-II | Cluster-III | Cluster-IV | Cluster-V |
|---|---|---|---|---|---|
| Cluster | 168.790 | 341.345 | 324.653 | 467.128 | 708.111 |
| Cluster | 341.345 | 150.374 | 299.959 | 805.168 | 1255.508 |
| Cluster | 324.653 | 299.959 | 0.000 | 512.141 | 1430.697 |
| Cluster | 467.128 | 805.168 | 512.141 | 0.000 | 787.317 |
| Cluster | 708.111 | 1255.508 | 1430.697 | 787.317 | 0.000 |

Note: Diagonal bold values indicate the intra-cluster distance

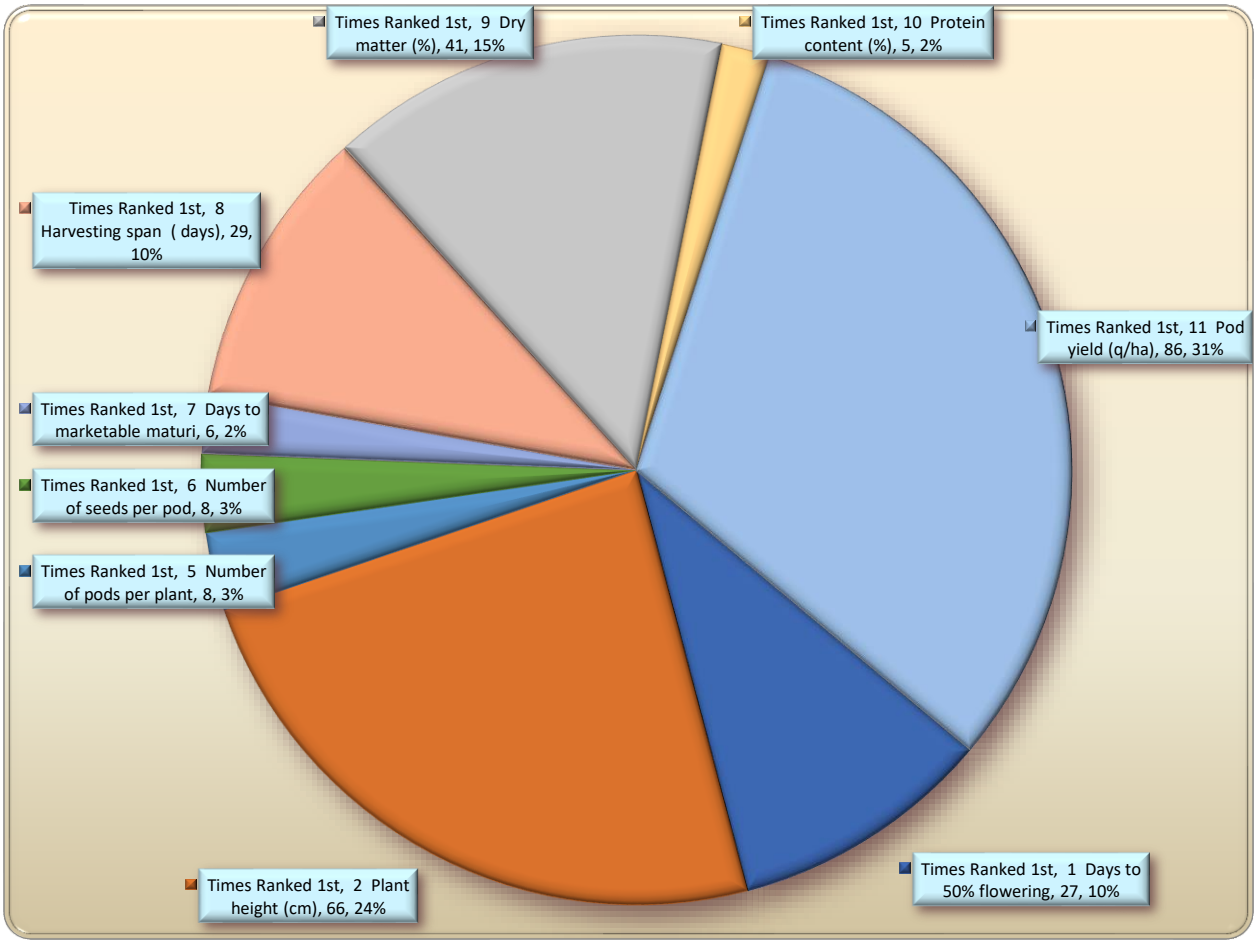


Fig 2 Contribution percent of characters towards divergence

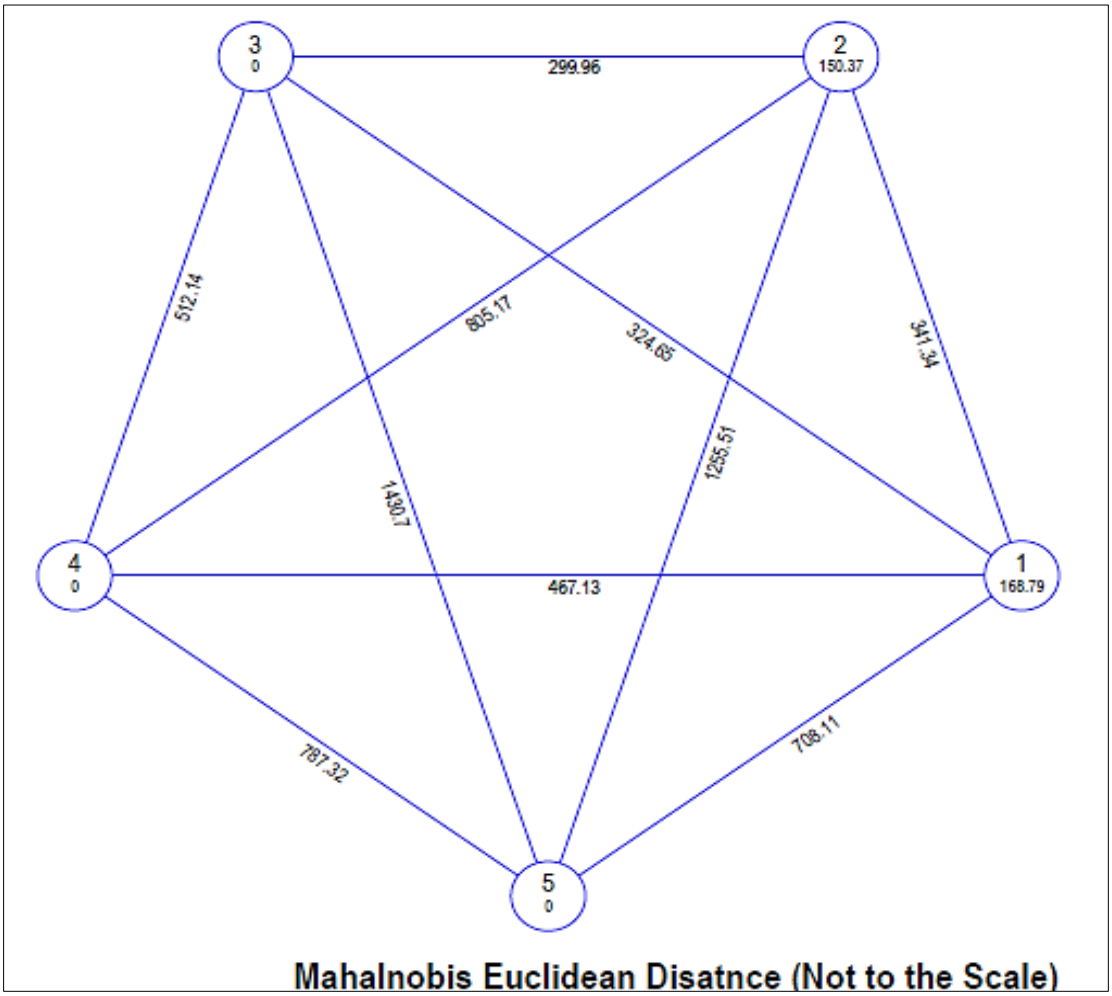


Fig 3 Dendogram showing intra and inter cluster distances

*Cluster means analysis*

Characterization of individual genotype in respect of their mean values for different characters helps breeder for discrimination of genotypes from diverse germplasm. Considerable distances in cluster mean were observed for studied characters (Table 3). Cluster II had genotypes earliest for blossoming and marketable maturity with longest harvesting span which followed by cluster III. Earliness is very important trait of vegetable crops as early variety fetches higher returns from market. Cluster II could be used in hybridization programme to develop early hybrids or segregants for incorporating in any high yielding variety. Cluster V was the highest pod yielder followed by cluster IV. This has become as a result of highest plant height, number of pods/ plant and number of seeds/pod in cluster V. Genotypes belonging to this cluster could be used as donor parent for improving green pod yield of pea. Cluster I recorded highest mean value (16.12) for number of branches/plant which showed that cluster I can produce the large number of branches. In case of first fruiting node, highest mean value (10.80) was recorded in cluster III which closely followed by cluster V (10.20) and lowest mean value (7.39) in cluster II. Cluster IV produced highest dry matter (30.57%) and protein content (28.93%). Such variations in cluster means were also reported by [18].

Table 3 Cluster means: Tocher Method

| Traits | Cluster-I | Cluster-II | Cluster-III | Cluster-IV | Cluster-V |
|---|---|---|---|---|---|
| Days to 50% flowering | 65.11 | 38.00 | 50.00 | 67.00 | 64.00 |
| Plant height (cm) | 70.92 | 51.11 | 80.18 | 70.24 | 80.34 |
| No. of branches per plant | 16.12 | 15.31 | 14.80 | 13.30 | 14.20 |
| First fruiting node | 9.90 | 7.39 | 10.80 | 9.70 | 10.20 |
| Number of pods per plant | 9.75 | 9.94 | 8.75 | 12.40 | 14.53 |
| Number of seeds per pod | 6.02 | 5.86 | 3.47 | 5.33 | 7.43 |
| Days to marketable maturity | 80.40 | 61.17 | 72.00 | 81.00 | 78.00 |
| Harvesting span (days) | 35.87 | 40.00 | 40.00 | 18.00 | 22.00 |
| Dry matter (%) | 18.84 | 17.18 | 21.90 | 30.57 | 18.51 |
| Protein content (%) | 26.55 | 27.94 | 23.57 | 28.93 | 27.30 |
| Pod yield (q/ha) | 46.85 | 38.81 | 27.32 | 80.52 | 150.47 |

## CONCLUSION

On the basis of findings of multivariate analysis; the genotypes AP-3, VRPE-14, VRPE-24, VRPE-32, VRPE-58 and Karishma could be selected for developing early maturing variety. Further, crossing of these genotypes with Anmol and Shilpa-10 would combine the early maturity and high yields in population.

## LITERATURE CITED

1. Ambrose MJ. 1995. From near east centre of origin the prized pea migrates throughout world. *Diversity* 11: 118-119.
2. Zohary D, Hopf M. 2000. *Domestication of Plants in the Old World*. Oxford University Press, Oxford, UK.
3. Sharareh H. 2006. Effects of various processing conditions on nutritional qualities oflegumes. *The Emerging Bean Magazine* 27.
4. Vavilov NI. 1926. Studies on the origin of cultivated plants. *Trudy Byuro Prikl Botany* 16: 139-248.
5. Singh P, Dass S, Dwivedi, VK, Kumar Y, Sangwan O. 2005. Genetic divergence studies in maize (*Zea mays* L.). *Annals of Agri Bio. Res.* 10(1): 43-46.
6. Nath V, Lal H, Rai N, Ram D. 2009. Hierarchical clustering and character association studies in cowpea. *Indian Journal of Plant Genetic Resource* 22: 22-25.
7. Chattopadhyay A, Rana NP, Seth T, Das S, Chatterjee S, Dutta S. 2014. Identification of selection indices and choosing of parents for vegetable cowpea breeding programme. *Legume Research* 37(1): 19-25.
8. Mahalanobis PC. 1936. On the generalized distance in statistics. *Proc. Natl Inst. Sc.* India 2: 49-55.
9. Rao CR. 1952. *Advanced Statistical Methods in Biometric Research*. John Wiley and Sons, New York.
10. Singh RK, Chaudhary BD. 1979. *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, New Delhi.
11. Ramzan A, Tahira Noor, Khan TN, Hina A. 2010. Correlation, cluster and regression analysis of seed yield and its contributing traits in pea *(Pisum Sativum L.*). *Journal of Agricultural Research* 52(4): 481.
12. Habtamu S, Million F. 2013. Multivariate analysis of some Ethiopian field pea (*Pisum sativum*) genotypes. *International Jr. Genet. Molecular Bio.* 5(6): 78-87.
13. Parihar AK, Dixit GP, Pathak V, Singh D. 2014. Assessment of the genetic components and trait associations in diverse set of field pea (*Pisum sativum*) genotypes. *Bangladesh Jr. Botany* 43(3): 323-330.
14. Dalsaniya SB, Poshiya VK, Savaliya JJ, Pansuriya AG, Davada BK. 2009. Genetic divergence in cowpea *(Vigna unguiculata* L.). *Legume Research* 32(4): 250-254.
15. Vavilapalli SK, Celine VA, Vahab AM. 2014. Genetic divergence analysis in vegetable cowpea (*Vigna unguiculata* subsp. *unguiculata* L..) genotypes. *Legume Geno. Genetics* 5 (2): 4-6.
16. Pandey A, Kumar A, Thongbam P, Pattanayak A. 2013. Genetic divergence, path coefficient and cluster analysis of chickpea (*Cicer arietinum*) cultivars in the mid-altitudes of Meghalaya. *Indian Jr. Agril. Sciences* 83(12): 1300-1312.
17. Nancee, Rana MK, Partap PS, Ranjan R. 2013. Study of genetic divergence on vegetable cowpea (*Vigna unguiculata* (L.) Walp.). *Vegetable Science* 40(2): 182-184.
18. Ajayi AT, Adenubi I, Adesoye. 2013. Cluster analysis technique for assessing variability in cowpea (*Vigna unguiculata* L. Walp) accessions from Nigeria. *Ratar Povrt.* 50(2): 1-7.