# Genetic Divergence in Pea (*Pisum sativum* L.)

**RS Rathi\* and RPS Dhaka**

*Department of Agriculture Botany, KPG Simbhaoli, Ghaziabad, Meerut University (U.P) India*
*\*National Bureau of Plant Genetic Resources, Pusa, New Delhi-110 012*

Genetic divergence of 35 genotypes of pea (*Pisum sativum* L.) was assessed using Mahalanobis's $D^2$ statistics. These genotypes could be grouped in seven clusters. Grouping of genotypes in different clusters was not related to their geographic origin. Estimates of *intra*-cluster distance ranged from 0.0-8.49. It was maximum in cluster III and minimum in cluster IV. The maximum *inter*-cluster values 7.26 and 24.14 were obtained between cluster VI and VII. The maximum diversity was observed between cluster II and VI which suggested that the genotypes of these two clusters are genetically very close. The over all picture indicated that the cluster I, II, III, IV and VI were quite divergent from the rest of the clusters also from one another. Selecting genotypes from such divergent groups for breeding programme/hybridization is likely to yield high heterotic response and release better segregants in subsequent generations.

**Key Words: Exotic, Genetic divergence, Indigenous, *Pisum sativum***

Pea (*Pisum sativum* L.) is a very important crop for multipurpose use and can be grown very well in semi-arid to temperate regions. Considering the importance of this crop, the knowledge of the nature and degree of divergence at *inter-* and *intra-* allelic level is very useful in characterization of genotypes and selecting desirable parents for breading programme. The present research work was conducted on indigenous and exotic genotypes, including some released varieties, to determine the genetic divergence.

## Materials and Methods

The experimental material consisted with 35 diverse genotypes comprising indigenous and exotic material of pea. Two rows of 3m length in a replication were planted for each genotype. The experiments were laid out in randomized block design with three replications during 1996-98 season. The plants were spaced at 45-15 cm. Research trial was conducted at research Farm of Kisan Post Graduate College, Simbhaoli, Ghaziabad, Uttar Pardesh. Observations were recorded for five randomly selected plants in each genotype per replication. Eight environments were created by manipulating the dates of sowing and fertilizer doses as 10-15 November (20:40, 10:40) and 25-30 December (20:40, 10:40) respectively. The Mahalanobis's $D^2$ statistics was used to measure the genetic divergence as suggested by Rao (1952). Using V statistics which in turn utilizes Wilk's Criteria, a simultaneous test of differences between mean value of a number of correlated variables is done (Rao, 1948).

## Results and Discussions

The analysis of variance revealed significant difference among 35 genotypes for all the 13 characters studies during both the years. Based on $D^2$ value, the 35 genotypes could be grouped in to seven clusters. The cluster pattern of these genotypes is depicted in Table 2. Cluster V included maximum of 12 genotype followed by cluster II that included 11 genotypes. The cluster VII has only one genotype (IC-11191) while cluster II included two genotypes. Cluster IV and VI included three genotypes each while cluster II had only two genotypes.

Cluster mean are presented in Table 3 for all 13 characteristics. The highest seed yield per plant (11.48) was recorded in cluster III while lowest seed yield was recorded for cluster VI that included only one genotype (IC-11191). Highest test weight (17.81) was observed in cluster VI followed by (16.74) with cluster V. The cluster III consisted of early flowering with 69.71 day where as cluster VII with early maturity 91.17, the maximum (12.69) cluster mean for number of pods per plant was calculated in cluster V, but the maximum pod length (6.92) was noted in cluster III which includes only two genotypes viz. Boneville and Arkel. The highest dry matter yield (34.82) was recorded in cluster V that consisted maximum number of 12 genotypes. The cluster VI that included only one genotype (IC-11191) showed the lowest values except days to flower, plant height and number of seeds per pod (Table 1).

The *intra-* and *inter* cluster divergence ($D^2$) values are presented in Table 2. The maximum cluster distance was observed between cluster VI and VII ($D^2$=24.14) followed by cluster IV and VI ($D^2$=20.21) and lowest distance was noted between cluster II and IV ($D^2$=7.26). The *intra-* cluster values ranged from 0.00-8.49 (cluster

**Table 1. Cluster means and grouping patterns based on D² analysis for 13 characteristics in 35 genotypes of pea**

| Cluster No. | Name of the genotype | No. of genotypes | S. No. of genotype | Characters | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 |
| | | | | Days to flower | Days to green pod harvesting | Days to maturity | Plant height (cm) | No. of branch-es/ plant | No. of pods/ plant | Pod length (cm) | No. of pods/ node | Dry matter yield/ plant (g) | No. of grains/ pod | Seed yield/ plant | Harvest index | 100 seed weight (g) |
| I | EC 341766, EC 27168, NIC 18727 | 3 | 23,24,34 | 72.05 | 95.80 | 114.54 | 95.24 | 2.75 | 12.06 | 4.77 | 1.24 | 22.87 | 4.60 | 7.99 | 31.62 | 13.52 |
| II | DDR 13, KPF 103, HUDP-6, Arka Ajeet, DDR-12, HUDP-8, J M-1, EC 381864, EC 381865, EC 341995, KNM-4 | 11 | 1,2,3,4,6, 11,12,18, 22,25,27 | 74.93 | 99.88 | 117.79 | 72.91 | 2.58 | 10.53 | 5.93 | 1.73 | 27.35 | 4.76 | 8.85 | 33.48 | 16.59 |
| III | Boneville and Arkel | 2 | 7, 13 | 69.71 | 94.06 | 113.14 | 70.53 | 2.365 | 12.28 | 6.925 | 1.94 | 23.385 | 5.895 | 11.48 | 40.92 | 14.86 |
| IV | KJPD-59, LFP-96, HFP-4 | 3 | 8,14,16 | 82.84 | 105.06 | 122.00 | 67.01 | 2.74 | 9.88 | 5.66 | 1.82 | 24.99 | 4.35 | 7.72 | 28.48 | 15.89 |
| V | DMR-1, Rachna, NIC 23636, DMR-11, BDJ 42-174, PLP-359, EC 341787, NIC 23625, NIC 12860, NIC 11181, NIC 18735, EC 8495 | 12 | 5,9,10, 15, 19, 21, 26, 28, 29,30, 33,35 | 76.70 | 100.76 | 119.66 | 120.42 | 3.01 | 12.695 | 5.51 | 1.50 | 34.82 | 4.52 | 10.03 | 29.00 | 16.74 |
| VI | KPMR-144-1, NIC 11249, EC 381856 | 3 | 17,20,31 | 76.48 | 100.76 | 119.15 | 60.69 | 2.48 | 11.98 | 5.34 | 1.87 | 25.57 | 3.72 | 8.77 | 33.36 | 17.81 |
| VII | NIC 11191 | 1 | 32 | 74.50 | 91.17 | 111.71 | 66.75 | 3.11 | 9.11 | 3.73 | 1.19 | 14.18 | 4.51 | 3.18 | 23.94 | 6.59 |

**Table 2. *Intra* and *Inter* cluster divergence D² values among seven clusters.**

| Clusters | No. of genotypes per cluster | | | | | | |
|---|---|---|---|---|---|---|---|
| | (3) | (11) | (2) | (3) | (123) | (3) | (1) |
| | I | II | III | IV | V | VI | VII |
| I | 7.76 | 13.18 | 11.88 | 14.76 | 12.40 | 17.55 | 13.02 |
| II | | 5.73 | 8.63 | 7.26 | 8.07 | 8.06 | 19.87 |
| III | | | 8.49 | 11.75 | 11.14 | 13.29 | 18.10 |
| IV | | | | 5.74 | 10.12 | 7.45 | 20.21 |
| V | | | | | 5.79 | 10.04 | 19.47 |
| VI | | | | | | 4.87 | 24.14 |
| VII | | | | | | | 0.00 |

* Underlined figures denote *Intra*-cluster divergence values

VI and III). The minimum *intr*-cluster D² value of 0.00 was recorded in cluster VII followed by 4.87 in cluster VI. Maximum *intra*- cluster D² value of 8.49 was recorded in cluster III (Table 2).

The over all analysis showed that the cluster I, II, III, IV, VI and VII were quite divergent from the others and also from one another. Among these types of cluster, the selecting genotypes for breeding programme/hybridization produce high heterotic response and release better segregant/lines in subsequent generation. However, caution may be exercised in selecting very divergent genotypes because such crosses may not yield proportionate heterotic response since a cross between extremely divergent parents create a situation where the harmonious functioning of alleles is rather distributed and consequently the physiological function are not so efficient (Dobhal *et al*, 1985). This is further substantiated by the fact that if "m' is the mean and "s' is the standard deviation of divergence value ($D^2$) among parents whose genetic divergence fall between (m-s) and (m+s) then crosses will have better chance of producing higher frequency and magnitude of heterosis as compared to cross whose parental divergence falls outside the limits, (m-s and m+s) Arunachalam and Bandhopadhyay (1984).

Hence the clustering of genotypes, has no relationship between geographic and genetic diversity could be established. The elite lines identified on the basis of $D^2$ and *per se* performance may be crossed and handled as per diallel selective matting system, Jensen (1970), so as to utilize both additive and non-additive components that are known to exist to concentrate maximum number of desirable genes in a few lines to isolate higher yielding lines (Rana, 1989).

Testing significance of $D^2$ against V Statistics (3838.81) where V statistics is distributed as $c^2$ with 442 degree of freedom indicated highly significance of $D^2$ value.

On the bases of $D^2$, the promising genotypes/ varieties namely DDR-12, Arkel, DMR-I, NIC 11249 and KPFD-59 belonging to different clusters could be crossed in a diallel fashion in order to achieve the genetic improvement.

### References

Arunachalam V and A Bandhopadhyay (1984) Limits to genetic divergence for occurrence of heterorsis-experimental evidence from crop plants. *Indian J. Genet.* **44:** 548-54.

Dobhal VK and HH Ram (1985) Genetic Divergent in pea (*Pisum sativum* L.). *Indian J. Agri. Sci.* **55:** 67-71.

Jensen NF (1970) A diallel selective matting system for cereal breeding. *Crop. Sci.* **10:** 629-635.

Rana JC (1989) Studies on gene action and response to selection in early generation in pea (*Pisum sativum* L.). *Ph. D Thesis* HPKVV, Palampur, H.P., India.

Mahalanobis PC (1936) On the generalized distance in statistics. *Proc. Nat. Sci. India.* **2:** 49-55.

Rao CR (1948) The utilization of multiple measurement in problems of biological classification. *J. Roy. Stat. Soc.,* **10-B:** 159-2003.

Rao CR (1952) *Advanced Statistical Methods in Biometrical Research.* Johan Wiley and Sons, Inc., New York.