

Original Research Article

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Study of Genetic Divergence in Pea (*Pisum sativum* L.) based on Agro-Morphic Traits

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ABSTRACT

The investigation was carried out with 20 genotypes of pea (*Pisum sativum* L.) at Horticulture Research Centre (HRC) of SVPUAT, Meerut, UP during 2016-17 to study the genetic diversity among the genotypes. The experiment was laid down in randomized block design (RBD) with 03 replications. The experiment having 10 observations on the basis of 5 randomly selected plants from each replication. D² analysis grouped into four clusters showing the existence of considerable amount of variation among the genotypes. Maximum pod yield 73.20 q/ha was found in PB-89 genotype. Cluster pattern revealed that, cluster III had largest number of genotypes (10) followed by cluster II (5 genotypes), cluster IV (3 genotypes) and cluster I had only (2 genotypes). Highest intra cluster distance were found cluster II (D² =1.983) whereas, highest inter cluster distance was observed between cluster III and I (D² = 6.627). The cluster means revealed the best cluster for various growth and flowering traits, depending upon the aim of breeding, hence the potential line can be selected from different clusters as parents.

Keywords

Genetic divergence,
Agro-morphic traits,
Horticulture

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Introduction

Vegetables are truly known as functional food and contain those ingredients that add bodily functional food in addition being nutritious and are also known as protective food. They are rich source of vitamins, carbohydrates, proteins etc. Vegetables are commonly used as culinary purposes.

Pea (*Pisum sativum* L.) is a very unique nutritious vegetable and used in Indian kitchen. Pea has unique distinction on account of their utility as pulse as well as vegetable. Green pea is generally used as vegetable.

It is a highly nutritious vegetable and contains digestible protein 7.2g, carbohydrates 15.8g, fat 0.1 g, vitamins like vitamin C 9 mg, vitamin A 139 IU and minerals like calcium 20.0 mg phosphorus 139 mg, iron 1.5 mg (Choudhary, 1990). Besides these, pea adds additional plant nutrient like nitrogen in soil by nitrogen fixation by useful bacteria i.e., rhizobium. Pea belongs to the family *Leguminosae* (*Fabaceae*) and having chromosome number 2n = 14. It is an annual herbaceous plant and commonly known as leguminous vegetable crop. Pea is an important plant in human and animal nutrition

because of it has high protein content 23-33%. Green peas are eaten cooked as a vegetable and are marketed fresh, canned or frozen. Peas are rich in health benefiting phyto-nutrients, minerals, vitamins and anti-oxidants.

The breeder need to isolate the suitable genotypes on the basis of genetic divergence for the hybridization purpose, Mahalanobis D^2 statistics techniques based on multivariate analysis of quantitative among the group. It also pin-points suitable genotype for their utilization in hybridization programmes.

In order to produce transgressive segregants and genetically different parents must to be selected for recombination breeding in self-pollinated crops. The characterization of genetic diversity in crop species has long been based on morphological attributes, however, morphological variation is often found to be of limited use because the expression of morphological attributes may be affected by environmental conditions, thereby constraining the analysis of genetic variation (Nisar *et al.*, 2008). On the basis of morphological data, genetic diversity assessments needs a high precision of field experiments through recommended design and analysis so that the germplasm may be exploited to develop better genotypes for the upcoming scenario (Sajjad *et al.*, 2011). Knowledge of genetic diversity is a useful tool in gene bank management and in planning experiments, as it facilitates efficient sampling and utilization of germplasm by identifying and/or eliminating duplicates in the gene stock and helps in the establishment of core collections (Ghafoor *et al.*, 2005).

Materials and Methods

A total of 20 genotypes of pea collected for divergence study (Table 3). The present investigations were carried out in 2016-17 at

Research Farm of HRC, SVPUAT, Meerut in RBD method with three replications. Each plot comprised one row of 1.8 m length spaced 45 cm with plant to plant and row to row is 10 cm. All the recommended cultural practices were followed under irrigated conditions as and when needed. The observations were recorded on five random competitive plants per replication for each genotype of ten important characters *i.e.* days to 50% flowering, plant height (cm), number of first fruiting node, length of first fruiting node (cm), number of pods per plant, length of pod (cm), width of pod (cm), number of seeds per pod, pod yield per plant (g), pod yield (q/ha). The Mahalanobis D^2 (1936) statistical method was used to quantify genetic diversity among the genotypes. The D^2 values were used to classify the entire germplasm into distinct clusters, which was done following to Tocher's method [Rao (1952)].

Results and Discussion

The analysis of variance for 20 genotypes of pea revealed significant difference for all the 10 characters, which indicated the presence of wide spectrum of variability among the genotypes. The minimum flowering duration (32.67) was observed with the cultivar E-6 and plant height was observed with the genotypes Sel- 3. Genotype Sel- 7 is having maximum first fruiting node (14.57). The maximum length of first fruiting node was recorded in Sel-3 (47.03cm). Very optimum dose of NPK reduce the days taken to flowering up to a certain limit and vice versa. Similar results were coated by Naeem *et al.*, (2002) for chilli.

The maximum number of pods per plant was recorded in KS-210 *i.e.* 38.60. KS-149 showed maximum length of pod (10.09cm) and width of pod (1.49cm). The performance of pea with respect to germination and nodulation was influenced by the temperature,

rainfall, humidity etc. The deficiency of major nutrients stunted the plant growth, resulting the maximum days taken to flowering. The cultivar KS-156 had maximum number of seeds (9.53). Pod yield per plant and pod yield q/ha is highest in PB 89 i.e. 182.99 g

and 73.20q/ha respectively. The plants treated with different combinations of NPK and NADEP compost results in to higher length of pods. Similar results were reported by Parsad *et al.*, (2005).

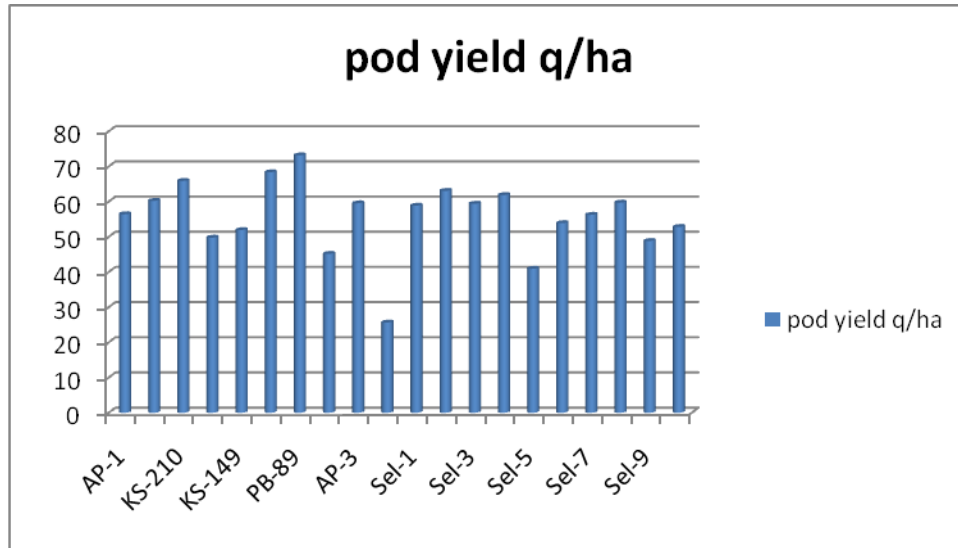


Table.1 ANOVA

| Source of Variation | DF | Days to 50% flowering | Plant height (cm) | Number of first fruiting node | Length of first fruiting node (cm) | Number of pods per plant | Length of pod (cm) | Width of pod (cm) | seeds per pod | pod yield q/ha | pod yield per plant(g) |
|---------------------|----|-----------------------|-------------------|-------------------------------|------------------------------------|--------------------------|--------------------|-------------------|---------------|----------------|------------------------|
| Replication | 2 | 4.55 | 0.66 | 0.05 | 0.68 | 0.52 | 0.20 | 0.00 | 0.01 | 0.05 | 0.01 |
| Treatment | 19 | 195.60** | 944.88** | 5.37** | 186.58* | 137.56** | 1.88** | 0.01* | 3.50** | 2050.93** | 328.16** |
| Error | 38 | 1.32 | 0.64 | 0.42 | 0.24 | 0.20 | 0.18 | 0.00 | 0.24 | 2.98 | 0.48 |

Table.2 Average of intra and inter cluster distance

| Clusters | I | II | III | IV |
|----------|--------------|--------------|--------------|--------------|
| I | 1.943 | 5.917 | 6.627 | 6.304 |
| II | | 1.983 | 2.82 | 3.86 |
| III | | | 1.976 | 2.763 |
| IV | | | | 1.621 |

Table.3 Mean performance of 20 genotypes of pea for 10 characters

| S.no. | Geno- types | Days to 50% flowering | Plant height (cm) | Number of first fruiting node | Length of first fruiting node(cm) | Number of pods per plant | Length of pod (cm) | Width of pod (cm) | seeds / pod | pod yield /plant(g) | pod yield q/ha |
|-------|-----------------|-----------------------------|-------------------------|-------------------------------------|-----------------------------------------|--------------------------------|--------------------------|----------------------|----------------|------------------------|-------------------|
| 1 | AP-1 | 52.67 | 82.45 | 11.67 | 37.25 | 34.87 | 9.35 | 1.26 | 8.60 | 141.15 | 56.46 |
| 2 | KS-156 | 46.33 | 45.36 | 12.87 | 31.42 | 32.40 | 9.35 | 1.32 | 9.53 | 150.66 | 60.27 |
| 3 | KS-210 | 55.33 | 55.37 | 14.07 | 46.07 | 38.60 | 8.63 | 1.25 | 7.73 | 164.81 | 65.93 |
| 4 | AP-4 | 50.33 | 56.00 | 13.67 | 37.26 | 31.67 | 9.41 | 1.23 | 8.73 | 124.51 | 49.80 |
| 5 | KS-149 | 55.33 | 55.51 | 13.73 | 36.77 | 28.73 | 10.09 | 1.49 | 9.20 | 129.91 | 51.96 |
| 6 | KS-205 | 54.67 | 56.31 | 13.40 | 41.12 | 36.13 | 8.72 | 1.33 | 7.33 | 170.98 | 68.39 |
| 7 | PB-89 | 52.67 | 54.39 | 11.53 | 45.55 | 37.40 | 7.17 | 1.35 | 8.33 | 182.99 | 73.20 |
| 8 | AP-2 | 62.33 | 64.73 | 12.53 | 46.75 | 26.27 | 8.44 | 1.34 | 5.80 | 112.96 | 45.18 |
| 9 | AP-3 | 35.67 | 37.34 | 11.53 | 28.49 | 32.80 | 9.33 | 1.31 | 9.27 | 148.93 | 59.57 |
| 10 | E-6 | 32.67 | 32.27 | 8.87 | 17.23 | 11.60 | 7.37 | 1.25 | 6.73 | 64.20 | 25.68 |
| 11 | Sel-1 | 48.67 | 48.19 | 13.07 | 31.71 | 32.87 | 9.21 | 1.32 | 9.20 | 147.21 | 58.89 |
| 12 | Sel-2 | 55.33 | 88.18 | 12.60 | 46.25 | 38.20 | 8.25 | 1.29 | 7.20 | 157.79 | 63.12 |
| 13 | Sel-3 | 53.67 | 96.37 | 12.93 | 47.03 | 35.07 | 9.42 | 1.32 | 6.73 | 148.59 | 59.44 |
| 14 | Sel-4 | 58.33 | 75.69 | 13.67 | 35.33 | 36.40 | 7.58 | 1.23 | 8.27 | 154.79 | 61.92 |
| 15 | Sel-5 | 38.67 | 53.98 | 10.60 | 23.99 | 17.73 | 9.16 | 1.29 | 6.80 | 102.40 | 40.96 |
| 16 | Sel-6 | 34.67 | 76.13 | 13.87 | 38.52 | 31.27 | 8.55 | 1.24 | 8.80 | 134.85 | 53.94 |
| 17 | Sel-7 | 51.67 | 68.30 | 14.53 | 38.05 | 35.27 | 8.06 | 1.25 | 7.40 | 140.73 | 56.29 |
| 18 | Sel-8 | 49.33 | 78.44 | 12.33 | 39.27 | 36.73 | 8.70 | 1.26 | 8.73 | 149.40 | 59.76 |
| 19 | Sel-9 | 50.33 | 90.41 | 13.53 | 42.01 | 29.27 | 9.04 | 1.30 | 6.73 | 122.18 | 48.87 |
| 20 | Sel-10 | 48.33 | 69.13 | 12.67 | 35.87 | 32.87 | 7.69 | 1.23 | 8.67 | 132.13 | 52.85 |
| | Mean | 49.35 | 64.23 | 12.68 | 37.30 | 31.81 | 8.68 | 1.29 | 7.99 | 139.06 | 55.62 |
| | Range | 32.67 | 32.27 | 8.87 | 17.23 | 11.60 | 7.17 | 1.23 | 5.80 | 64.20 | 25.68 |
| | | 62.33 | 96.37 | 14.53 | 47.03 | 38.60 | 10.09 | 1.49 | 9.53 | 182.99 | 73.20 |
| | SE | 0.94 | 0.65 | 0.53 | 0.40 | 0.36 | 0.35 | 0.03 | 0.40 | 1.41 | 0.56 |
| | CD at 5% | 1.99 | 1.38 | 1.12 | 0.85 | 0.77 | 0.73 | 0.07 | 0.85 | 2.98 | 1.19 |
| | Mean | 49.35 | 64.23 | 12.68 | 37.30 | 31.81 | 8.68 | 1.29 | 7.99 | 139.06 | 55.62 |

Table.4 Cluster mean of 10 characters of pea

| Cluster s | | Days to 50% flowering | Plant height (cm) | Number of first fruiting node | Length of first fruiting node (cm) | Number of pods per plant | Length of pod (cm) | Width of pod (cm) | Number of seeds per pod | pod yield per plant(g) | pod yield q/ha) |
|------------|------|-----------------------|-------------------|-------------------------------|------------------------------------|--------------------------|--------------------|-------------------|-------------------------|------------------------|-----------------|
| I | Mean | 35.67 | 43.13 | 9.73 | 20.61 | 14.67 | 8.27 | 1.27 | 6.77 | 83.30 | 33.32 |
| II | Mean | 47.27 | 48.48 | 12.97 | 33.13 | 31.69 | 9.48 | 1.34 | 9.19 | 140.24 | 56.10 |
| III | Mean | 51.30 | 70.44 | 13.03 | 40.33 | 35.77 | 8.27 | 1.27 | 8.11 | 152.96 | 61.19 |
| IV | Mean | 55.44 | 83.84 | 13.00 | 45.26 | 30.20 | 8.97 | 1.32 | 6.42 | 127.91 | 51.16 |

Table.5 Clustering pattern of 20 genotypes of pea on the basis of genetic divergence

| Clusters | No of genotypes | Genotype name |
|------------|-----------------|--------------------------------------------------------------------------------------------------------|
| I | 2 | E-6, Selection-5 |
| II | 5 | KS-156,AP-4,KS-149, AP-3,Selection-1 |
| III | 10 | AP-1, KS-210, KS-205,PB-89,Selection-2, Selection-4, Selection-6, Selection-7,Seletion-8, Selection-10 |
| IV | 3 | AP-2, Selection-3, Selection-9 |

On the basis of Mahalanobis D^2 analysis, total 20 genotypes were studied and grouped into four clusters. The distribution patterns of pea genotypes into four clusters are presented in Table 5. The maximum number of genotypes 10 was found in cluster III with comprising AP-1, KS-210, KS-205, PB -89, SELECTION-2, SELECTION-4, SELECTION-6, SELECTION-7, SELECTION-8, SELECTION-10. The second highest number of genotypes (5) were claimed under cluster II namely KS-156, AP-4, KS-149, AP-3, SELCTION-1. The cluster IV comprising was found (3) genotypes namely AP-2, SELECTION-3, SELECTION-9, while cluster I containing (2) genotypes namely E-6, SELECTION-5.

The average intra and inter cluster D^2 values are presented in Table 2. The maximum inter cluster D^2 value (6.627) was recorded between cluster III and I and the minimum inter cluster D^2 value (2.763) was recorded in

cluster IV and III. The maximum intra cluster distance were found in cluster III (1.976) followed by cluster I (1.943), cluster II (1.983) and cluster IV (1.621). The maximum inter cluster D^2 values indicated that genotypes of cluster III and I were not closely related, whereas the genotypes of cluster IV and III were found closely related due to minimum inter cluster D^2 values. It is apparent therefore, the genotypes of cluster do not differ significantly with regards to their relative genetic distance as indicated from the low variation of D^2 values.

The success of breeding programmes depends upon the genetic diversity present among the parents. Divergence study suggested that crosses among genotypes like KS-156, AP-4, KS-149, AP-1, KS-210, KS-205 for getting desired segregates from breeding point of view.

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