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Cluster analysis in field pea (*Pisum sativum* L.)

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Abstract

113 field pea genotypes including three checks viz., Rachna, Ambica and HFP 4 were grouped in 11 distinct and non-overlapping clusters using Non-hierarchical Euclidean cluster analysis, which substantiated presence of considerable diversity in the germplasm collections studied in the experiment. Cluster VI had highest number of genotypes, followed by cluster IV, IX and XI. Lowest number of genotypes was recorded in cluster VIII. The eleven clusters in divergence analysis contained genotypes of heterogeneous origin thereby indicating no parallelism between genetic and geographic diversity. Cluster pairs exhibiting very high inter-cluster distance were observed between clusters V and X and cluster III and X. The highest intra cluster distance was observed in cluster II followed by cluster I and cluster VII, while, the lowest values were recorded in case of cluster X. The results of Non-hierarchical Euclidean cluster analysis obtained under present study are also in agreement with the result of (Sureja and Sharma, 2001 and Yadav et. al., 2009). Maximum contribution in manifestation of total genetic divergence was made by plant height followed by biological yield/plant. The minimum contribution was shown by number of primary branches/plant, grain yield/plant and 100 seed weight. Cluster analysis showed that there was a considerable difference in intra-cluster group means for all the ten characters.

Keywords: Field pea, Non-hierarchical Euclidian cluster analysis, genetic divergence

Introduction

Field pea is a self-pollinated leguminous crop, mainly grown in *rabi* season and are relished as vegetable for their fresh pods. Other than this, field pea pods can be frozen and canned assisting in its use all around the year. Due to high protein content (23-33%) of field pea it can be used as both animal feed and for human consumption; proposed by workers, Santalla *et al.* (2001) [5] and Tyagi *et al.* (2012) [9]. Field pea is an important pulse crop in India but still its productivity is low, and this calls for an urgent need to evolve high yielding varieties having high protein content, resistance to biotic and abiotic stresses coupled with suitability for different agro-climatic conditions and cropping systems. With aforementioned context as the base of the experiment, diversity analysis was carried out in 113 field pea genotypes. In process of finding diversity in the experimental material, genetic divergence analysis using D² Statistics Mahalanobis P.C. (1936) [3] or non-hierarchical Euclidean cluster analysis was done to explore the genetic variability present in field pea germplasm. Cluster analysis classifies the genotypes into homogenous group per cluster with little diversity within cluster, while diversity between two clusters is usually high. Cluster thus formed can be utilized in hybridization programme depending upon breeding objective. Selection of suitable divergent parents for hybridization facilitates in obtaining desirable segregants in the segregating generations (Moll and Robinson, 1962) [4].

Material and methods

113 field pea genotypes including three checks viz., Rachna, Ambica, and HFP 4 were planted in Augmented Block Design and studied through Non-hierarchical Euclidean cluster analysis. Required cultural practices were pursued to support optimum crop growth. The experimental plot was divided into 11 blocks of equal size and each block had 13 plots in which 10 plots were used for accommodating the test genotypes which were not replicated while remaining 3 plots were allocated to checks *i.e.* Rachna, Ambica, and HFP 4 which were randomized and replicated as well. Each plot had a of 4 m length, having inter and intra row spacing of 30 cm and 5 cm, respectively. The analysis of variance for different characters in "Augmented Block Design" was done according to (Federer, 1956) [2]. Five competitive plants were randomly selected for recording observations on all the 10 metric traits of each genotype including three checks; except for days to 50 per cent flowering and days to maturity, which were recorded on the plot basis.

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Experimental results

The cluster mean for ten characters are given in Table 3, which showed considerable differences between the cluster mean for different traits. The genotypes of cluster I characterized by high mean performance for number of seeds/pod (6.881) and low mean performance for number of pods/plant (14.307) and biological yield/plant (44.732). The genotypes in cluster II had the lowest mean value (15.309) for 100 seed weight. The genotypes of cluster III characterized by high mean performance for plant height (168.980) and days to 50% flowering (74.842). The genotypes falling in cluster V took maximum mean value for biological yield/plant (81.414) and minimum mean value for harvest index (22.299). The cluster VI was characterized by the lowest mean value for plant height (52.831). Cluster VII had high mean values for days to maturity (126.691) and lowest mean values for primary branches/plant (1.175), number of seeds/pod (4.211) and grain yield/plant (15.642). Cluster VIII had high mean value for primary branches/plant (3.021). Cluster IX exhibited highest mean value for 100 seed weight (22.22). The genotypes of cluster X has showed highest mean value for number of pods/plant (22.023), grain yield/plant (23.909) and biological yield/plant (55.242) and it showed lowest mean values for days to 50% flowering (63.434) and days to maturity (117.091). The clusters IV and XI had average mean performance for all the characters.

The analysis of character contribution towards genetic divergence between 113 genotypes is given in Table 4. The maximum contribution in manifestation of total genetic divergence were made by plant height (73.31%) followed by biological yield/plant (18.05%). The minimum contribution was shown by no. of primary branches/plant (0.00%), grain yield/plant (0.11%) and 100 seed weight (0.71%). By analyzing character, which had subtle contribution towards genetic divergence in 113 genotypes of field pea are given in Table 4. In the total contribution to genetic divergence, plant height played significant role followed by biological yield and harvest index; number of seeds per pod and primary branches per plant had minimum contribution towards genetic divergence. The role of number of pods/plant, biological yield/plant, harvest index were medium range in manifestation of total genetic divergence in the available germplasm. Other characters showed moderate contribution towards total genetic divergence the similar results were reported by (Dixit *et al.*, 2002) [1]. In this respect, the highest intra cluster distance observed in cluster II followed by cluster I and cluster VII, while, the lowest values recorded in case of cluster X. The maximum inter cluster distance was recorded between cluster V and X and cluster III and X, which suggested that members of these two clusters are genetically very diverse to each other. The lowest inter cluster distance was shown between cluster VI and IX, X and XI, which indicated that genotypes, present in these cluster pairs were

genetically close to each other. The cross between genotypes belonging to clusters separated by low inter-cluster distance is unlikely to through promising recombinants in segregating generations.

Table 3 contains perusal of cluster means for different characters of field pea germplasm. The genotypes of cluster I had seven genotypes which showed minimum mean value, for number of pods per plant and biological yield per plant. The five genotypes of cluster II were characterized by low mean performance for 100 seed weight. Cluster III had nine genotypes which showed maximum mean values for plant height and days to 50% flowering. Cluster IV having twenty genotypes characterized by average mean performance for all traits. Cluster V had six entries showed high mean value for biological yield per plant and low mean value for harvest index. Cluster VI had twenty genotypes characterized for low mean value plant height. Cluster VII had five genotypes characterized for high mean value for days to maturity and low mean value to number of primary branches per plant, number of seeds per pod and grain yield. Cluster VIII had five genotypes showed high mean value for number of primary branches per plant. Cluster IX with 19 genotypes showed high mean value for test weight. Cluster X with six genotypes had high mean value for number of pods per plant, grain yield and harvest index. Cluster XI with eleven genotypes showed average mean performance for all the characters.

Summary and conclusion

The importance of genetic divergence in plant breeding has been emphasized by several scientists as an effective method of assessment of genetic divergence and thus has been widely used for analysis of genetic diversity in field pea (Sureja and Sharma, 2001, Dixit *et al.*, 2002 and Singh and Singh, 2003) [8, 1, 7]. In this experiment, genetic divergence study revealed that the highest intra cluster distance was found for cluster II (14.42) which comprised five genotypes namely, HUDP-16, EC-392177, PP-101, IP-FD-2-6, P-1089 followed by cluster I (13.92) which comprised of seven genotypes namely, KPMR-602, DMR-7, EC-384890, IP-2K-107, EC-595960, VL-42, DMR-7. Similarly, lowest intra cluster distance was obtained for cluster X (7.28) as shown in Table 1. Saxesena *et al.* (2013) [6] had studied the cluster mean values for different quantitative characters with pea genotypes. The eleven clusters found in divergence analysis contained genotypes of heterogeneous origin there by indicating no parallelism between genetic and geographic diversity. The intra and inter cluster distance were calculated and are presented in Table 2. The highest intra cluster value was observed in cluster II (14.42). The maximum inter cluster distance was recorded between cluster V and X (38.81). Therefore, crosses between members of cluster separated by high inter-cluster distances are likely to throw desirable segregants.

Table 1: Clustering pattern of 110 Field pea genotypes on the basis of non-hierarchical Euclidean cluster analysis of ten characters

| Cluster No. | Number of genotypes | Genotypes |
|-------------|---------------------|--|
| I | 7 | KPMR-602, DMR-7, EC-384890, IP-2K-107, EC-595960, VL-42, DMR-7 |
| II | 5 | HUDP-16, EC-392177, PP-101, IP-FD-2-6, P-1089 |
| III | 9 | EC-5102P, DMR-37, EC-209228, IM-4102, EC-5102, DDR-73, EC-5117, EC-548810, NDDP-4-20 |
| IV | 20 | IP-2K-112, EC-384275, P-725, AMBIKA, RACHANA, DDR-74, EC-356166, KPMR-522, EC-1, DMR-15, PP-138, PP-5, NDP-2, HFP-9426, EC-507770, DDR-16, HUP-31, KPMR-516, IP-2K-79, PP-31 |
| V | 6 | VL-52, IPF-99-25, PANT-P-138, PANT-P-42, IPF-04-26, DMR-9102 |
| VI | 21 | IP-2K-86, HUDP-11, P-51042, HFP-8902, KPMR-389, EC-10, KPMR-687, HFP-4, HFP-8909, JM-9102, HFP-9907-B, P-489, P-1544-4, DMR-48, EC-564802, NDDP-4-27, NDP-20, HFP-511, NDP-11, IPFD-04-15, PANT-31 |

| | | |
|------|----|--|
| VII | 5 | IP-2K-117, HUDP-15, IP-2K-53, VL-44, KPMR-686 |
| VIII | 4 | VL-46, HUDP-6, HUDP-8, HUDP-28 |
| IX | 19 | VL-1, IP-2K-90, EC-538004, KPMR-400, NDP-24, EC-507771, EC-384272, EC-502159, KFP-103, PP-14, IPFD - 04-6, KPMR-528, DDR 69, IPFD-1-10, HUDP 27, KPMR 708, DMR 53, VL 45, DMR-49 |
| X | 6 | IP-2K-84, DMR 54, PANT 101, PDM-8, VRD-7, AZAD P-2 |
| XI | 11 | IP-2K-93, IPF-04-9, IP-2K-101, IP-2K-106, DDR-39, IP-2K-105, IP-2K-75, FP-10, HUP-2, IP-2K-82, IP-2K-97 |

Table 2: Estimates of average intra-and inter-cluster distances for 11 clusters in field pea genotypes

| | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI | Cluster VII | Cluster VIII | Cluster IX | Cluster X | Cluster XI |
|--------------|-----------|------------|-------------|------------|-----------|------------|-------------|--------------|------------|-----------|------------|
| Cluster I | 13.922 | 23.205 | 22.423 | 27.4 | 27.777 | 23.460 | 34.641 | 26.626 | 25.927 | 35.604 | 23.438 |
| Cluster II | | 14.427 | 22.309 | 20.463 | 22.371 | 23.272 | 25.103 | 28.103 | 22.919 | 24.847 | 16.745 |
| Cluster III | | | 11.412 | 19.755 | 25.229 | 29.547 | 35.009 | 29.621 | 24.202 | 38.112 | 31.481 |
| Cluster IV | | | | 10.519 | 17.879 | 16.315 | 22.287 | 26.153 | 13.989 | 25.565 | 20.004 |
| Cluster V | | | | | 9.782 | 25.112 | 28.572 | 24.934 | 29.022 | 38.814 | 22.622 |
| Cluster VI | | | | | | 8.661 | 14.699 | 19.422 | 12.403 | 24.433 | 15.921 |
| Cluster VII | | | | | | | 10.695 | 22.345 | 22.843 | 36.520 | 22.755 |
| Cluster VIII | | | | | | | | 9.399 | 22.901 | 35.683 | 22.006 |
| Cluster IX | | | | | | | | | 8.358 | 16.390 | 16.725 |
| Cluster X | | | | | | | | | | 7.285 | 12.978 |
| Cluster XI | | | | | | | | | | | 8.100 |

Table 3: Cluster means for different characters in field pea germplasm

| Characters | Plant height (cm) | Days to 50% flowering | Days to maturity | Primary branches/ plant | Pods/ plant | Seeds/ pod | 100 seed weight (g) | Grain yield/plant (g) | Biological yield/ plant (g) | Harvest index (%) |
|--------------|-------------------|-----------------------|------------------|-------------------------|-------------|------------|---------------------|-----------------------|-----------------------------|-------------------|
| Cluster I | 140.819 | 72.498 | 122.519 | 2.016 | 14.307 | 6.881 | 18.100 | 19.004 | 44.732 | 42.550 |
| Cluster II | 111.194 | 69.079 | 122.091 | 1.361 | 19.979 | 6.211 | 15.309 | 21.042 | 64.303 | 38.461 |
| Cluster III | 168.980** | 74.842 | 126.646 | 2.455 | 19.534 | 6.495 | 19.205 | 23.835 | 65.229 | 37.923 |
| Cluster IV | 82.239 | 73.106 | 123.618 | 1.683 | 18.957 | 5.509 | 22.188 | 23.615 | 68.885 | 34.287 |
| Cluster V | 87.589 | 67.212 | 121.924 | 2.188 | 16.790 | 6.002 | 20.242 | 18.854 | 81.414 | 22.299 |
| Cluster VI | 52.831* | 72.440 | 124.859 | 1.437 | 16.746 | 5.000 | 21.188 | 19.030 | 46.431 | 41.311 |
| Cluster VII | 76.518 | 73.879 | 126.691 | 1.175 | 19.839 | 4.211 | 18.776 | 15.642 | 52.570 | 31.756 |
| Cluster VIII | 64.077 | 71.462 | 122.341 | 3.021 | 18.262 | 4.724 | 17.492 | 16.659 | 45.220 | 36.943 |
| Cluster IX | 58.050 | 72.946 | 123.424 | 1.721 | 19.495 | 5.382 | 22.225 | 23.518 | 48.303 | 48.439 |
| Cluster X | 72.707 | 63.434 | 117.091 | 1.277 | 22.023 | 5.669 | 21.475 | 23.909 | 44.970 | 55.242 |
| Cluster XI | 80.933 | 64.788 | 117.727 | 1.406 | 18.888 | 5.515 | 19.333 | 19.242 | 49.606 | 42.482 |

Table 4: Contribution of different characters with respect to genetic divergence

| Source | Times Ranked 1st | Contribution % |
|---------------------------|------------------|----------------|
| 1 Plant Height (cm) | 4639 | 73.31 |
| 2 50% flowering | 93 | 1.47 |
| 3 Days to Maturity | 45 | 0.71 |
| 4 Primary Branches/ Plant | 0.01 | 0.00 |
| 5 Pods/ Plant | 15 | 0.24 |
| 6 Seeds/ Pod | 0.01 | 0.00 |
| 7 100 Seed Weight | 10 | 0.16 |
| 8 Grain Yield(g) | 7 | 0.11 |
| 9 Biological Yield(g) | 114.2 | 18.05 |
| 10 harvest Index | 377 | 5.96 |

References

- Dixit GP, Singh IP, Khare AP. Genetic divergence study in field pea. *Legume Res.* 2002; 25(3):199-201.
- Federer WT. Augmented designs, "Hawaiian Planters", *Record.* 1956; 14:208-742.
- Mahalanobis PC. On generalized distance in statistics. *Proc. Natl. Inst. Sci.* 1936; 2:49-55.
- Moll RH, Robinson RF. Heterosis and genetic diversity in variety crosses of maize. *Crop Sci.* 1962; 2:197-209.
- Santalla M, Amurrio JM, de Ron AM. Food and feed potential breeding value of green, dry and vegetal pea germplasm, *Can. J Plant Sci.* 2001; 81:601-610.
- Saxesena RR, Lal GM, Yadav PS, Vishwakarma MK. Diversity analysis and identification of promising lines for hybridization in field pea (*Pisum sativum* L.). *The Bioscan.* 2013; 8(4):1437-1440.
- Singh G, Singh SP. Genetic divergence in pea (*Pisum sativum* L.). *Legume Res.* 2003; 26(2):131-133.
- Sureja AK, Sharma RR. Genetic divergence in garden pea (*Pisum sativum* L.) Sub. Sp. Hortense Ash and Graebn). *Vegetable Sci.* 2001; 28(1):63-64.
- Tyagi N, Singh AK, Rai VP, Kumar S, Srivastava CP. Genetic variability studies for lodging resistance and yield attribute in pea (*Pisum sativum* L.). *J Food Legumes.* 2012; 25(3):179-182.
- Yadav R, Srivastava RK, Singh R. Studies on genetic divergence in field pea (*Pisum sativum* L.). *Legume Res.* 2009; 32(2):121-124.