Original Research Article

Assessment of genetic divergence in pea (*Pisum sativum* L.) genotypes in Western U.P

Abstract

The present investigation was carried out with 20 genotypes of pea (*Pisum sativum* L.) at Horticulture Research Centre (HRC) of SVPUAT, Meerut, UP during 2021-22 to identify the nature and magnitude of genetic divergence among genotypes based on phenotypical traits using the multivariate analysis. 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. D^2 analysis grouped all 20 varieties into five clusters revealing the presence of considerable amount of variation among genotypes. Cluster pattern revealed that, cluster I and II had highest number of 5 genotypes succeeded by cluster III had 4 genotypes, cluster IV and cluster V contain 3 genotypes each. Maximum intra cluster distance were recorded in cluster I (D^2 =2.264) indicating maximum difference among the genotypes within cluster and minimum intra cluster distance was recorded in cluster V (D^2=1.481), whereas, Maximum inter cluster distance (D^2=5.211) was observed between cluster II and IV and minimum were observed (D^2=2.373) was observed between cluster III and V. The cluster means revealed the cluster IV was best cluster for various characters like plant hight, number of pods per plant, pod length, days to maturity and pod yield, providing upon the aim of breeding, hence the potential genotype can be opted from different clusters as parents.

Keywords: Pea, Genotypes, Phenotypical Analysis, Cluster, Breeding, Diversity

Introduction

Vegetable is increasingly becoming important as produce domestic and export markets. Although most of them are good sources of minerals, vitamins and protein necessary for the needs of minerals, vitamins and the like, they have great potential to improve nutrition and therefore the health of consumers (Wills *et al.,* 1998).

Pea (*Pisum sativum* L.) is an important legume vegetable grown throughout the world. It is a native of Mediterranean region with Near East and Ethiopia as secondary centres (Blixt, 1970). Pea (*Pisum sativum* L.) (2n = 14). is a self-pollinated crop and belongs to family Leguminosae. It is a cool season crop most extensively grown in the temperate region throughout the world. Peas are used alone and mixed with other vegetables. It is developed principally as a winter vegetable in the fields of North Indian conditions and as a late spring vegetable in the bumpy area (Thamburaj 2005). 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). Being a short duration crop it is highly utilized for crop rotation and it is capable to enhance the soil structure and provides breaks for the disease control (Martin *et al*., 2008). In order to supply 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 supported morphological attributes, however, morphological variation is usually found to be of limited use because the expression of morphological attributes could also be littered with environmental conditions, thereby constraining the analysis of genetic variation (Nisar *et al*., 2008). On the idea of morphological data, genetic diversity assessments needs a high precision of field experiments through recommended design and analysis in order that the germplasm is also exploited to develop better genotypes for the upcoming scenario (Sajjad *et al*., 2011). In the present study is an attempt to obtain information on the genetic diversity in twenty genotypes of pea and asses their utility in developing hetrotic combination for commercial purpose.

Method and Materials

The present investigations were carried out at Horticulture Research Centre, SVPUAT, Meerut in RBD method with three replications during Rabi season of 2021-22 by taking 20 diverse genotypes of pea (Table 1). The observations were recorded on five random competitive plants per replication for each genotype of ten important characters viz. days to germination, days to 50% flowering, plant height (cm), number of pods per plant, seed per pod, length of pod (cm), width of pod (cm), days to maturity, pod yield per plant (g) and pod yield (q/ha). The Mahalanobis D^2 (1936) statical 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).

Result and Discussion

The analysis of variance for 20 genotypes of pea disclosed significant difference for all the 10 characters, which represented the presence of wide spectrum of variability among the genotypes represented in Table2. On the basis of Mahalanobis D^2 values, all the twenty genotypes of pea under study were grouped in to 5 clusters showed in Table 3. The Clustering pattern of pea genotypes were grouped into five clusters. Maximum number of genotypes 5 distributed in cluster I and II each. Cluster I have genotypes namely Kashi Mukti, Kashi Nandani, Arkel, AP-3 and Kashi Ageti. Cluster II also have 05 varieties namely Pant Matar-2, Kashi Samradhi, Mithi Phali, PC-531 and Kashi Uday followed by Cluster III have Four varieties name viz. Arka Ajit, Pusa Pragati, Arka Kartik, and VL-3. Cluster IV have three varieties namely Kashi Shakti, Kashi Samrath and Bonneville and cluster V was also had three varieties name viz. Arka Sampoorna, Arka Priya and Solan Nirog.

The average intra and inter cluster D^2 value and average intra and inter cluster distance value are presented in Table-4. The maximum inter cluster D^2 (5.211) was observed between cluster II and IV, whereas minimum inter cluster distance (2.373) was observed between cluster III and V. The intra cluster distance was recorded maximum (2.264) in cluster I succeeded by cluster II (2.233), cluster IV (2.129) and cluster III (1.605) and minimum (1.481) in cluster V. The maximum inter cluster D^2 values indicated that genotypes of cluster II and VI were not closely related, whereas the genotypes of cluster III and V were found closely related due to minimum inter cluster D^2 values. Therefore, it is evident from the modest fluctuation of D^2 values that the genotypes of the cluster do not considerably differ in terms of their relative genetic distance. Hence, these genetically diverse genotypes can be used as promising parents for hybridization. Based on the significant difference in cluster means for various features, diversity among the genotypes was also calculated. Nearly all of the ten characters showed distinct mean values for various clusters, which reflects their genetic divergence. The cluster mean table 5 shows that the genotypes in cluster II showed maximum mean value for width of pod (cm), whereas genotypes of cluster IV revealed maximum mean value for 50% flowering, plant height (cm), number of nodes per plant, length of pod, days to maturity pod yield per plant (gm), pod and pod yield (q/ha) and genotypes of cluster V showed maximum mean value for days to germination and seeds per pod. Relative appraisal of group implies showed that for working on unambiguous characters, the genotypes may be chosen from the cluster having high mean incentive for that specific character. This comparison indicates that clusters IV and V had better cluster means for most of the characters, therefore, these clusters might be considered better for selecting genotypes as divergent parents. The similar results were found by Tara *et al.* (2006), Vipin *et al* (2008a), Vipin *et al.* (2008b), Singh and Mishra (2008), Shrivastava *et al.* (2012), Supe *et al.* (2013) and Kumar *et al.* (2015), and Kumar and Kumar (2016).

Conclusion:

Based on Mahalanobis D^2 analysis it can be concluded that the pea germplasm in the present study can be successfully used for planning future breeding programmes. The inter-crossing of genotypes showing the greater genetic divergence for most of the characters studied should result in superior heterotic crosses and also, generate valuable segregants in the later generations. It is expected that better performing varieties could be generated to increase productivity in field pea. Therefore, from the present study genotypes of cluster II and cluster IV based on their high values for inter cluster distance and cluster means can be hybridized as the potential parents to produce superior off-springs in the segregating generations and to improve pea productivity.

Table 1 List of genotypes used in experiment

S.No.	Genotypes	Institute
1.	Kashi Shakti	I.I.V.R, Varanasi
2.	Kashi Mukti	I.I.V.R, Varanasi
3.	Kashi Samrath	I.I.V.R, Varanasi
4.	Kashi Nandini	I.I.V.R, Varanasi
5.	Bonneville	USA
6.	Pant Matar-2	G.B.P.U.A.T, Pantnagar
7.	Arka Ajit	I.I.H.R, Bangalore
8.	Arkel	England
9.	Arka Sampoorna	I.I.H.R, Bangalore
10.	Kashi Samridhi (VRPMR-11)	I.I.V.R, Varanasi
11.	Mithi Fali	PAU, Ludhiyana
12.	Arka Priya (IIHR-1)	I.I.H.R, Bangalore
13.	Azad Pea -3	C.S.A.U.A.T , Kanpur
14.	Pusa Pragati	I.A.R.I, New Delhi
15.	PC-531	PAU, Ludhiyana
16.	Kashi Ageti	I.I.V.R, Varanasi
17.	Solan Nirog	U.H.F, Solan.
18.	Arka Kartik	I.I.H.R, Bangalore
19.	Kashi Uday	I.I.V.R, Varanasi
20.	VL-3	V.P.K.A.S, Almora

Table 2 Analysis of Variance (ANOVA) mean sum of square for ten parameters of pea.

Source of variation	d.f.	Days to Germination	Days to 50% Flowering	Plant height (cm)	Number of Pods per plant	Seeds per Pods	Length of Pod (cm)	Width of Pod (cm)	Days to Maturity	Pod yield per plant (gm)	Pod yield (q/ha)
Replication	2	0.019	1.20	2.68	0.12	0.115	0.341	0.002	0.57	0.81	0.53
Treatment	19	0.693**	242.63**	627.84**	25.83**	0.939**	0.856**	0.014**	544.89**	374.77**	598.54**
Error	38	0.040	1.43	2.15	0.10	0.056	0.033	0.001	1.12	1.32	2.23
Total	59	0.249	79.10	203.66	8.39	0.343	0.308	0.005	176.21	121.57	194.20

Table 3 Clustering pattern of 20 genotypes of pea on the basis of Mahalanobis D^2 statistics.

Clusters	No. of genotypes	Genotypes
I	**5**	Kashi Mukti, Kashi Nandani, Arkel, Azad Pea-3, Kashi Ageti
II	**5**	Pant Matar-2, Kashi Samradhi, Mithi Phali, PC-531, Kashi Uday
III	**4**	Arka Ajit, Pusa Pragati, Arka Kartik, VL-3
IV	**3**	Kashi Shakti, Kashi Samrath, Bonneville
V	**3**	Arka Sampoorna, Arka Priya, Solan Nirog

Table 4 Average Inter and intra cluster (D2) distances in twenty germplasms of pea

Clusters	I	II	III	IV	V
I	**2.264**				
II	3.607	**2.233**			
III	3.419	3.066	**1.605**		
IV	4.746	5.211	3.449	**2.129**	
V	3.403	3.204	2.373	4.071	**1.481**

Table 5 Cluster mean for 10 characters of different genotypes of pea

Clusters		Days to Germination	50% Flowering	Plant height (cm)	Number of Pods per plant	Seeds per Pods	Length of Pod	Width of Pod (cm)	Days to Maturity	Pod yield per plant (gm)	Pod yield (q/ha)
I	**Mean**	6.29	39.69	46.59	11.05	6.91	7.63	1.21	69.41	51.77	95.72
II	**Mean**	7.05	48.76	60.07	8.96	6.32	6.51	**1.26**	75.99	42.32	80.56
III	**Mean**	6.67	57.18	73.42	12.37	6.7	7.41	1.18	88.52	44.85	83.3
IV	**Mean**	7.13	**58.69**	**75.61**	**15.78**	6.98	**7.64**	1.21	**99.44**	**69.16**	**109.74**
V	**Mean**	**7.16**	46.91	73.08	8.13	**7.24**	7.53	1.17	87.47	49.75	83.01

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