Original Research Article

Assessmentof 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~~ has~~10~~ tenobservations ~~on the basis of~~based on~~5~~ fiverandomly selected plants from each replication. D^2 analysis grouped all 20 varieties into five clusters revealing the presence of considerable amount of variation amonggenotypes. Cluster pattern revealed that~~,~~ ~~cluster I and II had highest number of 5genotypes succeededby cluster III had 4 genotypes, cluster IV and cluster V contain~~ clusters I and II had the highest number of 5 genotypes succeeded by cluster III with 4 genotypes, cluster IV and cluster V containing~~3~~ threegenotypes each. Maximum intra cluster distances were recorded in cluster I (D^2=2.264), indicating maximum difference among the genotypes within the cluster andminimum intra cluster distance was recorded in cluster V (D^2=1.481),whereas, Maximum ~~inter~~ inter-cluster distance (D^2=5.211) was observed between cluster II and IV and the minimum ~~were~~ wasobserved (D^2=2.373) was observed between cluster III and V. The cluster means revealed thecluster IV was the best cluster for various characters like plant height, number of pods per plant, pod length, days to maturity and pod yield,providing upon the aim of breeding~~, h~~. Hence the potential genotype can ~~be opted~~opt from different clusters as parents.

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

Introduction

~~Vegetable~~ The vegetable is increasingly becoming important as producedin 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~~, consumers' health (Wills *et al.*, 1998).

Pea (*Pisum sativum* L.) is an important legume vegetable grown ~~throughout the world~~worldwide. It is a native of the 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 the family Leguminosae. It is a~~ cool~~n excellent 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-~~short-duration crop, it is highly utilized for crop rotation, and it ~~is capable to~~can 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~~To supply transgressive segregants, genetically different parents must be selected for recombination breeding in self-pollinated crops. ~~The characterization of genetic diversity in crop species has long been supported morphological attribut~~Morphological attributes have long supported the characterization of genetic diversity in crop species~~, h~~. 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 need~~s a high precision of field experiments through recommended design and analysis in order~~ a high precision of field experiments through recommended design and analysis so that the germplasm is also exploited to develop better genotypes for the upcoming scenario (Sajjad *et al.*, 2011). ~~In t~~The present study ~~is an attempt~~attempts to obtain information on the genetic diversity in twenty ~~genotypes of pea and asses their utility in developing hetrotic combination for commercial purpose~~pea genotypes and assess their utility in developing heterotic combination for commercial purposes.

Method and Materials

The present investigations were carried out at Horticulture Research Centre, SVPUAT, Meerut in the RBD method with three replications during the 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 the pod (cm), the width of the 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~~following Tocher's method (Rao (1952).

Result and Discussion

The analysis of variance for 20 genotypes ~~of pea~~ disclosed significant differences for all the ~~10~~ tencharacters, ~~which represented~~representing~~the presence of~~ a ~~wide~~ broadspectrum of variability among the genotypesrepresented in Table2.~~On the basis of~~Based onMahalanobis D^2 values, all the twenty genotypes of pea under study were grouped into 5 clusters,~~showed~~ shownin Table 3. The Clustering pattern of pea genotypes ~~were~~ wasgrouped into five clusters. ~~Maximum~~ The maximum number of genotypes ~~5~~ fivedistributed in clusters 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: Pant Matar-2, Kashi Samradhi, Mithi Phali, PC-531 and Kashi Uday, followed by Cluster III, which have Four varieties named~~ namely Pant Matar-2, Kashi Samradhi, Mithi Phali, PC 531 and Kashi Uday followed by Cluster III have Four varieties name~~ viz. ArkaAjit, Pusa Pragati, Arka Kartik, and VL-3. Cluster IV ~~have~~ hasthree varieties, namely Kashi Shakti, Kashi Samrath and Bonneville, and cluster V ~~was~~ also ~~had~~ hasthree varieties named viz. ArkaSampoorna, Arka Priya and Solan Nirog.

The average intra and ~~inter~~ inter-cluster D^2 value and average ~~intra~~ Intra and ~~inter~~ inter-cluster distance value are presented in Table~~-~~4. The maximum ~~inter~~ inter-cluster D^2 (5.211) was observed between clusters II and IV~~, whereas~~. In contrast, minimum ~~inter~~ inter-cluster distance (2.373) was observed between clusters III and V. The ~~intra~~ intra-cluster distance was recorded as 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~~ inter-cluster D^2 values indicated that ~~genotypes of cluster II and VI~~cluster II and VI genotypes were not closely related~~, whereas~~. In contrast,~~the genotypes of cluster III and V~~cluster III and V genotypes were found to be closely related due to minimum ~~inter~~ 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 different 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~~Diversity among the genotypes was also calculated based on the significant difference in cluster means for various features. Nearly all ~~of the ten characters showed distinct mean values for various clusters, which reflects~~ten characters showed distinct mean values for various clusters, reflecting their genetic divergence. The cluster mean ~~table~~Table5 shows that the genotypes in cluster II showed maximum mean value for the width of the pod (cm)~~, whereas~~. In contrast, 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 the group ~~implies~~ showed that for working on unambiguous characters, the genotypes ~~may~~mightbe chosen from the cluster having a high mean incentive for that specific character. This comparison indicates that clusters IV and V had better cluster means for most ~~of the~~ characters~~, t~~. Therefore, these clusters might be considered better for selecting genotypes as divergent parents. ~~The s~~Similar results were found by Tara *et al.* (2006), Vipin *et* ~~al~~*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~~genotypes 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 improve pea productivity.

S.No.	Genotypes	Institute
1.	Kashi Shakti	I.I.V.R,Varanasi
2.	Kashi Mukti	I.I.V.R,Varanasi
3.	KashiSamrath	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.	ArkaAjit	I.I.H.R,Bangalore
8.	Arkel	England
9.	ArkaSampoorna	I.I.H.R,Bangalore
10.	KashiSamridhi(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.	PusaPragati	I.A.R.I,NewDelhi
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 1 List of genotypes used in experiment

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

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Table 3 Clustering pattern of 20 genotypes of ~~pea~~ pea-~~on the basis of~~ based onMahalanobis 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**	ArkaAjit, Pusa Pragati, Arka Kartik,VL-3
IV	**3**	Kashi Shakti, Kashi Samrath, Bonneville

V	**3**	ArkaSampoorna, 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~~ tencharacters 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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