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Cluster analyses for various Agro-morphological traits in Fieldpea (*Pisum sativum* L.) Genotypes

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ABSTRACT: Fieldpea (*Pisum sativum* L.), a multi-functional, highly nutritious winter-season pulse crop. It has tremendous potential to offer health benefits, especially with the heightened emphasis on nutrition. In any breeding programme, choosing parental genotypes that might produce better heterotic combinations requires an understanding of the genetic variety present among genotypes of crop. So, with this objective present investigation were carried out among thirty nine fieldpea genotypes. Experiment consisting of 39 genotypes (12 parents and their 27 crosses) were held in randomized block design with three replication at Pulses Research Area, Department of Genetics and Plant Breeding, CCS, Haryana Agricultural University, Hisar during *rabi* 2020-21. As due to continuous selection pressure for specific traits like yield, the varieties have become more vulnerable to biotic and abiotic stresses, which has jeopardized their potential for long-term sustained genetic improvement. So, there is need to isolate the superior inbreds and hybrids that can be used as a further breeding programme. Results revealed that thirteen agro-morphological traits delineated 39 genotypes into four major clusters. Furthermore, higher inter-cluster distance was observed than intra-cluster distance. The maximum intra-cluster distance was observed in cluster I (75.60) and the maximum inter cluster distance was observed between cluster Ⅰ and cluster IV (94.97). Cluster II and cluster I has high mean value for most of the traits. So, In order to create superior hybrids, the genotypes in cluster II can be crossed with genotypes of cluster I.

Keywords: Agro-morphological traits, *Pisum sativum* L., superior inbreds, genotypes.

INTRODUCTION

Field pea (*Pisum sativum* L.), a winter season legume, is a nutritionally rich pulse ensuring nutritional security of poor population in developing countries. They are widely grown around the world as food, feed and fodder (Parihar *et al.*, 2020 a, b), providing excellent source of various vitamins, nutrients and essential amino acids. Peas have diploid chromosome number of 2n = 2x= 14 (Yarnell, 1962). Since its domestication, field pea has been utilized in variety of ways for human consumption such as, its tender green pods and seeds are used as vegetables (Duke, 1981), while the mature dry seeds are used in either whole, split or flour form (Bastida Garcia *et al.*, 2011). It is an important economic and nutritional crop that is commonly referred to as "poor man's meat" due to its high protein (25.10%), fiber (13.40%), vitamin and mineral content, and prebiotic carbohydrate (61.80%) content while being affordable to lower-income consumer (Sharma *et al.*, 2023). Field pea is used in various culinary and confectionaries as main ingredient like, in dal, soup, stew, snacks, vegetables, and flour (Dahl *et al*., 2012; Singh *et al.*, 2018; Mahajan *et al.*, 2018). Pea offers various health benefits to human body such as managing Type 2 diabetes and body weight, regulating proper cardiovascular and gastrointestinal functions and reducing blood cholesterol levels. Due to its fast growth and inherent ability of fixing atmospheric nitrogen, it is also used in crop rotation, as cover crop and as green manure (Rohilla *et al.*, 2022). In addition, hay from pea crop serves as a nutritional fodder for animals (Bastida Garcia *et al*., 2011). In terms of production worldwide, Canada, Russian Federation, China, India, and United States of America are the leading countries (Parihar *et al*., 2020 a,b). However, field pea is prone to various biotic and abiotic stresses that severely affect the sustainable production of this legume.

In the course of domestication of crops, major genes have been lost with the loss of their wild relatives and related species. This reduced level of pre-existing variation has hampered field pea breeding programmes to great extent. Genetic diversity is the primary requirement for any crop improvement program, whether through natural selection or targeted plant breeding (Gupta *et al.*, 2022). A prior knowledge of genetic diversity is crucial in developing stress tolerant and high yielding varieties as it helps in identifying potential better performing genotypes suitable for particular environment (Sunayana *et al.*, 2017). The proper investigation of genetic diversity helps in efficient sampling, maintenance, evaluation and proper utilization of germplasm by identifying and eliminating duplicates present in the gene bank or field experiment

materials (Smith and Smith 1989; Ghafoor *et al.*, 2005). Moreover, there are more chances of recovering transgressive sergeants in segregating generations. Under such circumstances, research for analyses of genetic diversity present in field pea genotypes became prominently important for all kind of breeding procedures.

Various statistical approaches are used to analyse the genetic divergence present in a population; however, the multivariate D^2 analysis (Mahalanobis, 1936) can easily sort out divergent genotypes from the genetic material. This analysis can classify the germplasm collection into more or less homogenous groups and therefore, it is useful in reducing the size of germplasm collection to be evaluated. The understanding of genetic divergence allows a breeder to select divergent genotypes for breeding strategies and exploit available heterosis effectively. Hence, the present study is formulated to analyse the extent of genetic diveregence present in field pea genotypes using D^2analysis.

MATERIALS AND METHOD

The present investigation was carried out in experimental area of pulses section, department of Genetics and Plant Breeding, CCS, Haryana Agricultural University, Hisar during *rabi* 2020-21. Experiment consisting of 39 genotypes (12 parents and their 27 crosses) were held in randomized block design with three replication. The list of genotypes used in study was given below in Table 1. Each plot consist of a single row of 4m length with 45 × 15cm spacing. The experimental site was situated at 29.10° N latitude and 75.46° E longitude, at an elevation of 215.2 m above mean sea level. Extreme high and low temperatures, dryness, and scanty rainfalls characterized the sea level. It lies on the outer margin of the southwest (SW) monsoon region and has a tropical dry climate.

The morphological traits including number of primary and secondary branches plant^{-1}, nodes plant^{-1}, plant height of 1st pod, plant height, pods plant^{-1}, seeds pod^{-1}, 100-seed weight, biological, seed yield and harvest index were recorded on five competitive randomly selected plants while on days to flowering and maturity, the observations were recorded on the plot basis. Dendograms are graphical outputs produced by hierarchical clusters. Ward's approach, which finds multiple variables and then splits them into distinct groups and subgroups, is used in cluster analysis. The best and most popular approach has been suggested to be Ward's method, often known as UPGMA (unweighted paired group method using arithmetic averages). Data were analyzed using the R software version 4.1.2.

Table 1: List of Genotypes Used in Study.

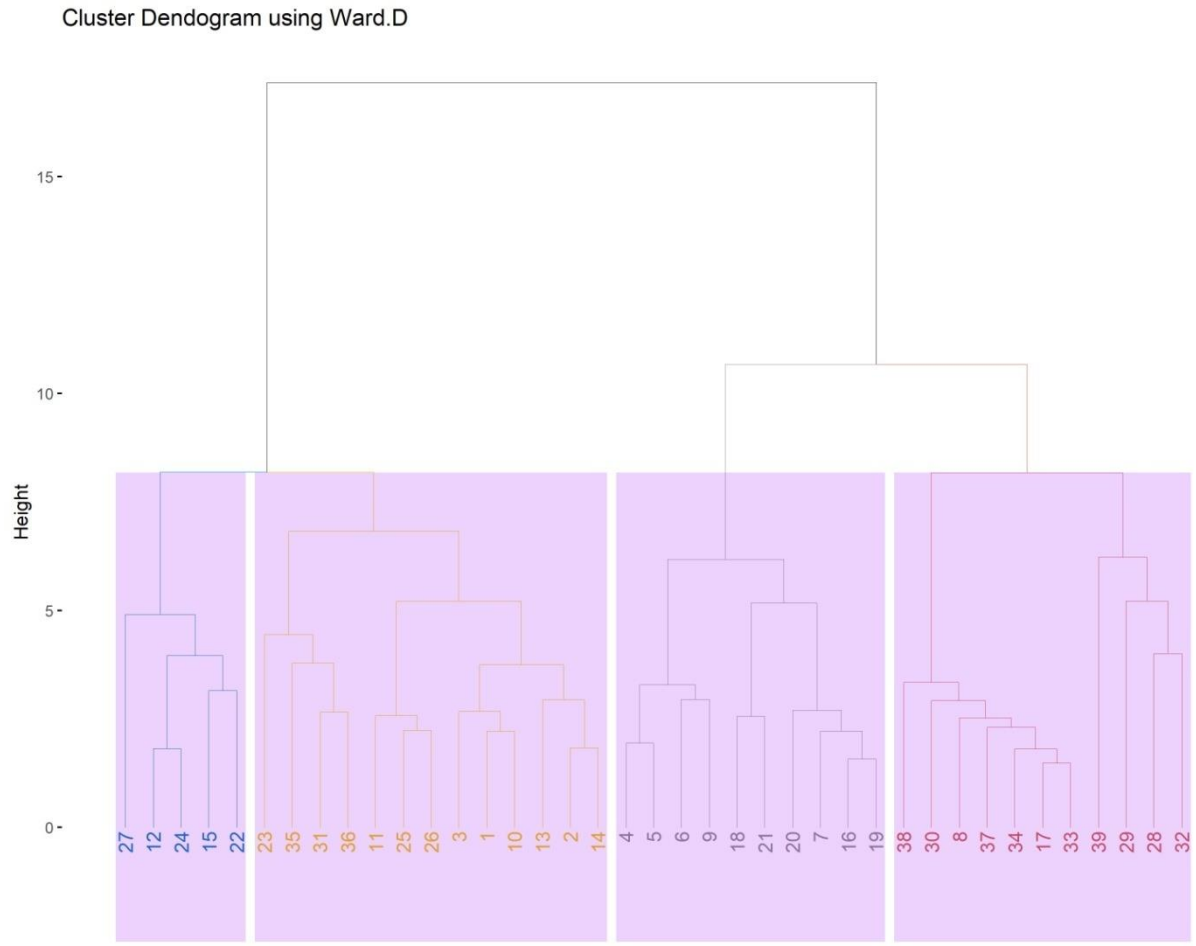
Sr. No.	Name of Genotype	Sr.No.	Name of Genotype
G1	Pant P-243 x HFP 1545	G21	Pant P-200 x GP02/1108
G2	Pant P-243 x HFP 1426	G22	RFPG 79 x HFP 1545
G3	Pant P-243 x GP02/1108	G23	RFPG 79 x HFP 1426
G4	DDR-23 x HFP 1545	G24	RFPG 79 x GP02/1108
G5	DDR-23 x HFP 1426	G25	Aman x HFP 1545
G6	DDR-23 x GP02/1108	G26	Aman x HFP 1426
G7	HFP 715 x HFP 1545	G27	Aman x GP02/1108
G8	HFP 715 x HFP 1426	G28	Pant P-243
G9	HFP 715 x GP02/1108	G29	DDR-23
G10	IPF 14-13 x HFP 1545	G30	HFP 715
G11	IPF 14-13 x HFP1426	G31	IPF 14-13
G12	IPF 14-13 x GP02/1108	G32	IPF 14-16
G13	IPF 14-16 x HFP 1545	G33	RFP 2009-02
G14	IPF 14-16 x HFP 1426	G34	Pant P-200
G15	IPF 14-16 x GP02/1108	G35	RFPG 79
G16	RFP 2009-02 x HFP 1545	G36	Aman
G17	RFP 2009-02 x HFP 1426	G37	HFP 1545
G18	RFP 2009-02 x GP02/1108	G38	HFP 1426
G19	Pant P-200 x HFP 1545	G39	GP02/1108
G20	Pant P-200 x HFP 1426		

RESULTS AND DISCUSSION

Cluster analysis in quantitative genetics allows researchers to explore the genetic diversity and structure within populations, identify genetic subgroups, and uncover the genetic basis of complex traits. It provides a valuable tool for understanding the genetic architecture of traits and can assist in selecting individuals for further breeding or genomic selection strategies. Thirteen agro-morphological traits delineated 39 genotypes into four major clusters. From Fig. 1 and Table 2, Cluster II was unquestionably the largest group, as this cluster had 13 genotypes followed by cluster IV and clusters III which had 11 and 10 genotypes respectively. Clusters I had only 5 genotypes, hence this is the smallest groups.

The dendrogram also noted the degree of similarity between the various clusters. Clusters I and IV had desirable mean values most of quantitative traits. With an inter-cluster distance of 94.97 units, Cluster II and Cluster I were the most diverse groups (Table 3), indicating that crossing and hybridization among these clusters helped harness heterosis for hybridization and selection. Clustering of fieldpea accessions together regardless of their source supports the possibility of a

common progenitor but separation by geographical or ecological isolation mechanisms (Yarnell, 1962). Similar results have been reported by Daba *et al.*, (2022); Srivastava *et al.* (2018) and Ouafi *et al.* (2016) in field pea genotypes.



(Notation of Genotypes used is given dendogram is given above in Table 1)

Fig. 1. Hierarchical clustering classified 39 fieldpea genotypes into four clusters.

Table 2: Cluster grouping of thirty nine genoptypes of fieldpea based on D^2 analysis.

Cluster	Number of genotypes	Name of genotypes
I	5	Aman x GP02/1108, IPF 14-13 x GP02/1108, RFPG 79 x GP02/1108, IPF 14-16 x GP02/1108, RFPG 79 x HFP 1545
II	13	RFPG 79 x HFP 1426, RFPG 79, IPF 14-13, Aman, IPF 14-13 x HFP1426, Aman x HFP 1545, Aman x HFP 1426, P-243 x GP02/1108, Pant P-243 x HFP 1545, IPF 14-13 x HFP 1545, IPF 14-16 x HFP 1545, Pant P-243 x HFP 1426, IPF 14-16 x HFP 1426
III	10	DDR-23 x HFP 1545, DDR-23 x HFP 1426, DDR-23 x GP02/1108, HFP 715 x GP02/1108, RFP 2009-02 x GP02/1108, Pant P-200 x GP02/1108, Pant P-200 x HFP 1426, HFP 715 x HFP 1545, RFP 2009-02 x HFP 1545, Pant P-200 x HFP 1545
IV	11	HFP 1426, HFP 715, HFP 715 x HFP 1426, HFP 1545, Pant P-200, RFP 2009-02 x HFP 1426, RFP 2009-02, GP02/1108, DDR-23, Pant P-243, IPF 14-16

Table 3: Average intra (bold) and inter cluster (off diagonal) distance D2 values among four clusters in thirty nine genotypes of fieldpea.

	c1	**c2**	**c3**	**c4**
c1	**75.60**	77.20	80.58	94.97
c2		**31.61**	77.36	92.31
c3			**20.07**	57.14
c4				**66.16**

Table 4 illustrates the cluster mean values for 13 characters among 39 lines. The highest mean value for days to 50 % flowering, days to maturity, number of primary branches per plant, height of 1st pod, plant height and biological yield per plant were displayed by Cluster II, which had 13 genotypes. Cluster I, on the other hand, had the highest mean value for the characteristics such as number of secondary branches per plant, 100-seed weight, number of pods per plant, seed yield per plant and harvest index. However, Cluster III and Cluster IV had highest mean value for remaining triats number of seeds per pod and number of nods per plant, respectively. So, in order to create superior hybrids, the genotypes in cluster II can be crossed with genotypes of cluster I. The overall findings of the present study showed that, in any population improvement programme, choosing suitable parents based on genetic divergence analysis would be more beneficial than choosing parents based on geographic proximity. Similar finding of cluster analysis were observed by Kumar *et al.* (2022); Srivastava *et al*. (2018); Habtamu and Million (2013) and Ouafi *et al.* (2016) in field pea.

Table 4: Means for clusters based on agro-morphological traits.

Cluster	DF	DM	NPB	NSB	NN	Ht. of 1st pod	PH	100-SW	NPP	NSP	BY	SYP	HI
C1	73.46	122.35	2.7	1.74	13.8	37.934	74.22	16.09	28.58	4.8	34.36	16.64	48.95
C2	79.44	127.52	2.72	1.52	13.27	50.51	95.81	15.69	27.25	4.69	34.87	15.47	44.64
C3	75.96	124.03	2.47	0.74	11.94	27.45	44.36	15.65	20.87	5.39	23	11.33	48.74
C4	73.08	121.41	2.2	1	14.08	33.58	59.5	15.25	18.16	4.21	19.69	7.79	40.8

DF-Days to 50% flowering; DM-Days to maturity; NPB-Number of primary branches per plant; NSB- Number of secondary branches per plant; NN-Number of nodes per plant; Ht. of 1st pod-height; Height of first pod; PH-Plant height; 100-SW-100-seed weight; NPP-Number of pods per plant; NSP-Number of seeds per pod; BY-Biological yield per plant; SYP-Seed yield per plant; HI- Harvest index.

CONCLUSION

In the current study, 39 genotypes were investigated for diversity in order to find compatible and distinctive genotypes for pearl millet breeding programmes. There was substantial genetic variation among the genotypes for most traits, connoting the urgency of exploiting a high degree of genetic variation through selection. Different genotypes of cluster II would be crossed with genotypes of cluster I in order to improve seed yield. These genotypes would also be used as inbred lines for future hybrid development programmes. The results of the present study would help to identify heterotic clusters and superior parents for structuring breeding strategies to develop improved field pea cultivars. Cluster analysis in field pea crops provides a valuable tool for understanding the genetic diversity and structure within populations, aiding in the development of improved cultivars with desirable traits. It enables breeders to make informed decisions by identifying germplasm groups and selecting suitable parents for crossing, ultimately contributing to the enhancement of field pea varieties.

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Conflict of interest. The authors declare that the research was conducted in the absence of any commercial or financial relationships. The authors declare no conflict of interest.

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