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Multivariate Analysis of Quantitative Traits in Field Pea (*Pisum sativum* var. *arvense*)

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ABSTRACT

Background: Field pea is one of the important cool season grain legume crops cultivated in India. In this investigation, experimental material *i.e.* eighty germplasm lines of field pea with four checks (IPF 4-9, Adarsh, Ambika and IPFD 10-12) were evaluated to determine the estimates of genetic diversity in the test genotypes.

Methods: The data were recorded on thirteen quantitative characters for the study of genetic diversity. The mean data of each characters were subjected to cluster analysis by using D^2 Mahalanobis clustering method. The principle component analysis (PCA) for measuring genetic divergence was done by XLSTAT and R 4.0 statistical package.

Result: Eighty-four germplasms including checks were categorized into five distinct clusters, indicates the occurrence of high genetic diversity in the evaluated set of germplasm. Between cluster III and IV highest inter-cluster distance was observed, indicates the maximum diversity among genotypes of these clusters. Considerable differences were observed for cluster mean among different distinct clusters for all the thirteen characters. The hybridization programme involving genotypes from cluster III and cluster IV may be used to isolate suitable segregants. Principal component analysis grouped different traits under study into thirteen principal components (PCs) in which only five PCs with eigen value >1 accounted 70.97% of total variation present in genotypes. The traits falling to these five PCs may be given due importance in field pea improvement programmes.

Key words: Field pea, Genetic divergence, Principal component analysis.

INTRODUCTION

Field pea (*Pisum sativum* var. *arvense*) is an herbaceous, annual, autogamous crop having chromosomes (2n=14), belongs to genus *Pisum* of family *Fabaceae* (*Leguminosae*). It is grown in higher altitude in tropical areas with temperature varies between 7-30°C. Pea is mainly valued for nutritional content of their seeds. Nutritionally, pea is rich source of protein ranging from 21-25% with higher concentration of lysine and tryptophan amino acids (Bhat *et al.*, 2013 and Gregory *et al.,* 2016) and have low level of cysteine and methionine amino acids (Ceyhan and Avci, 2005). The ripe, mature, dried seeds of field pea used as pulse (split seeds) or as flour and as whole in the form of chhola chat. In addition to their nutritional value, they have capability to improve fertility of soil by establishing the symbiotic association between the root nodules of plants and nitrogen fixation bacteria. Therefore, cultivation of pulses elevates the productivity of soil in terms of yield potential of subsequent crops by 20-40 per cent has been recorded (Pande and Joshi, 1995). In India, the area and production of field pea was around 6.06 lakh hectares and 8.11 lakh tonnes with annual productivity of 1338 kg/ha (FAOSTAT, 2019).

As per the vision of IIPR, Kanpur, the population of India is continuously increasing and it will likely to reach 1.68 billion by 2030. The demand of pulses for year 2030 is forecast to reach 32 million tonnes with an anticipated yearly needed growth rate of 4.2%. In total output of pulses, a quantum hike is required to increase the availability per capita and to meet the challenges of rising population. Therefore, high yielding variety of field pea with good qualities of seed are needed. For this purpose, selection of genetically diverse parental genotype to be used in hybridization programme is based on the assumption that “Crosses involving divergent parents offer greater possibility of obtaining desirable segregants in the segregating generations”. Several researchers addressed the need of a diverse parent to obtain superior genotypes in the segregating generations (Kumar and Kumar, 2016; Singh *et al.,* 2017 and Prasad *et al.*, 2018). Therefore, efforts should be made to increase the wider use of existing diversity from germplasm collection.

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MATERIALS AND METHODS

Eighty diverse genotypes of field pea with four check varieties (IPF 4-9, Adarsh, Ambika and IPFD 10-12)

comprised experimental material, collected from ICAR-IIPR, Kanpur; CSAUAT, Kanpur and CCSHAU, Hisar. The experimental material evaluated in Augmented Block Design during *rabi*, 2019-20 at Research Block of BUAT, Banda. The whole experimental site divided into eight blocks and each block had fourteen plots. In each block, ten plots accommodate test genotypes (not replicated), whereas remaining four plots were allocated to checks. Each plot consists of single row of genotypes with 5m length and spacing of 30x10 cm. The observations were recorded for 13 quantitative traits *viz*., days to 50% flowering (DF), days to maturity (DM), plant height (PH), number of branches plant^{-1} (NB), number of nodes plant^{-1} (NN), number of effective nodes plant^{-1} (NEN), number of effective pods plant^{-1} (NEP), number of seeds plant^{-1} (SP), pod length (PL), 100-seed weight (SW), seed yield plant^{-1} (SY), biological yield plant^{-1} (BY) and harvest index (HI). The mean data of each characters were subjected to cluster analysis by using D^2 Mahalanobis clustering method. The principle component analysis (PCA) for measuring genetic divergence was done by XLSTAT and R 4.0 statistical package.

RESULT AND DISCUSSION

Cluster analysis was performed which grouped the 84 genotypes (including checks) into 5 diverse clusters on the basis of D^2 values. The composition of different clusters varied from 8 to 22 genotypes. The maximum number of genotypes (22) was grouped into cluster I. Minimum number of genotypes was presented in cluster V with 8 genotypes. Similarly, cluster II, III and IV exhibited 18, 21 and 15 genotypes, respectively. The discrimination of germplasm lines into so many discrete clusters indicated presence of substantial diversity in the material evaluated, which is in agreement with earlier reports of Prasad *et al.,* (2018) and Kumar *et al.,* (2019). Estimates of intra-and inter-cluster distance for four clusters are shown in (Table 1). The highest intra-cluster value was observed for cluster II (36.71) followed by cluster V (35.25), cluster IV (32.06), cluster III (28.58) and cluster I (26.53), suggesting large genetic variability within the genotypes of these clusters. The highest inter-cluster distance found between cluster III and IV (136.92) followed by cluster III and V (106.44) and cluster II and IV (92.48), showing the maximum diversity between the genotypes of these clusters. It is therefore proposed that if diverse genotypes from these groups are used in breeding programmes together with other desirable attributes, better segregants for high seed yield and yield contributing traits due to non-allelic interactions are anticipated. The minimal inter-cluster difference between cluster I and cluster II (51.21) followed by cluster I and cluster V (52.52) showed that the genotypes of these clusters were genetically least diverse and had exactly the same genetic architecture (Jeena and Singh, 2002). Such genotypes can also be used in breeding programmes to establish bi-parental crosses between the most diverse and closest groups in order to break the undesirable relation between yield and its associated traits (Haddad, 2004).

Dendrogram of eighty-four field pea genotypes was constructed by Ward clustering method (Ward, 1963) to calculate the appropriate genotypic variability existing among all studies clusters (Fig 1).

The diversity was also endorsed by the appreciable amount of difference between cluster means for different characters (Table 2). Cluster V exhibited the highest mean value for branches plant^{-1}, nodes plant^{-1}, effective nodes plant^{-1}, effective pods plant^{-1}, biological yield plant^{-1} and seed yield plant^{-1} as well as least mean values for days to 50% flowering and days to maturity. The highest mean value for days to maturity, plant height and pod length found in cluster IV and for days to 50% flowering and seeds pod^{-1} in cluster II. Cluster III had highest mean value for 100-seed weight and harvest index as well as least mean values for plant height, branches plant^{-1}, nodes plant^{-1}, effective pods plant^{-1}, biological yield plant^{-1} and seed yield plant^{-1}. None of the characters had highest mean value in cluster I. These findings revealed that different clusters were superior for different characters.

Principle component analysis (PCA)

PCA is a statistical method of multivariate analysis which reduce the set of large number of variables to set of small number of linearly uncorrelated variables, which can explain the most of variation present in the original variables (Anderson, 1972 and Morrison, 1982). The outcome of PCA revealed that only the first five principle components (PCs) displayed more than 1.00 eigen value and demonstrated a maximum variability of around 70.97% among field pea germplasm with respect to yield component traits (Table 3 and Fig 2). The traits falling to these five PCs may be given due importance in field pea improvement programmes.

The PC1 had the highest variability (25.49%) followed by PC2 (17.34%), PC3 (11.63%), PC4 (8.78%) and PC5 (7.72%). The present study was also supported by the

Table 1: Estimates of average intra- and inter-cluster distances for four clusters in field pea germplasm.

Cluster number	Intra-cluster	Inter-cluster distance				
	distance	I	II	III	IV	V
I	26.53		51.21	91.56	52.33	52.52
II	36.71	51.21		58.60	92.48	64.27
III	28.58	91.56	58.60		136.92	106.44
IV	32.06	52.33	92.48	136.92		69.24
V	35.25	52.52	64.27	106.44	69.24	

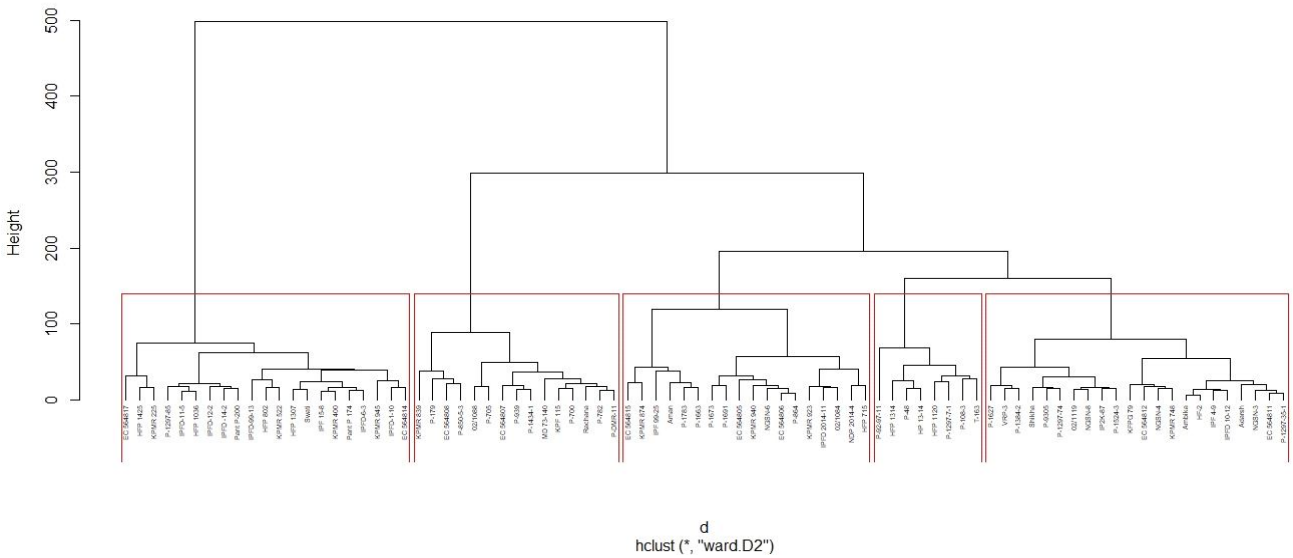

Fig 1: Dendrogram showing relationship between eighty-four genotypes of field pea.

Table 2: Cluster mean values for different characters in field pea germplasm.

Cluster number	No. of genotypes	DF	DM	PH	NB	NN	NEN	NEP	SP	PL	SW	BY	HI	SY
I	22	72.94	113.30	160.26	3.15	15.73	5.66	20.61	4.17	5.60	13.70	35.47	30.56	10.76
II	18	73.87	112.90	118.84	3.82	15.24	5.84	24.00	5.25	5.88	14.58	40.65	30.28	13.21
III	21	71.92	113.23	72.59	2.80	13.85	6.04	15.74	4.45	5.85	16.42	25.93	32.06	8.44
IV	15	72.26	113.37	206.24	3.09	16.54	6.50	25.80	4.42	6.16	13.73	39.62	26.83	10.62
V	8	67.94	111.87	157.47	3.94	16.70	7.27	43.30	4.47	5.89	14.61	73.87	32.05	23.32

Table 3: Eigen value and variability (%) for different characters in field pea genotypes.

Traits	Eigenvectors				
	PC1	PC2	PC3	PC4	PC5
Eigen value	3.314	2.254	1.512	1.142	1.003
Variability (%)	25.490	17.341	11.634	8.785	7.717
Cumulative %	25.490	42.830	54.465	63.250	70.967

previous work done by Hanci and Cebeci (2018). Eigen values helps to decide that how many variables to retain. The sum of the eigen values is generally equal to the number of variables (Sharma, 1998).

First principle component (PC1) showed variation of 25.49% in which seed yield plant^{-1}, effective pods plant^{-1}, biological yield plant^{-1}, seeds pod^{-1}, effective nodes plant^{-1}, harvest index, branches plant^{-1}, plant height, pod length, nodes plant^{-1} and 100-seed weight were major positive contributors, while days to 50% flowering and days to maturity had negative weights. Similar pattern using PC analysis in field pea for such traits was reported by Parihar *et al.,* (2014). The characters contributed to the variation in the PC1, forms a larger percentage in the variation among all genotypes. The traits found positive in PC2 were 100-seed weight, harvest index, pod length, seeds pod^{-1}, days to maturity, seed yield plant^{-1}, days to 50% flowering and effective nodes plant^{-1}. While, plant height, branches plant^{-1}, nodes plant^{-1}, biological yield plant^{-1} and effective pods plant^{-1} had the highest negative weights for PC2. Another additional variation of 11.63% and 8.78% had sown by the third, fourth respectively. These findings were consistent with the analysis by Hanci and Cebeci (2018), who reported variation of 9.93% and 8.23% for third and fourth components, respectively. The PC3 was described only by days to 50% flowering, days to maturity, plant height, branches plant^{-1}, nodes plant^{-1}, effective pods plant^{-1}, seeds pod^{-1}, pod length and biological yield plant^{-1} with positive factor loadings, meanwhile the remaining traits in that PC obtained negative loadings. PC4 was compiled with plant height, nodes plant^{-1}, effective nodes plant^{-1}, seeds pod^{-1} and pod length with their positive loading and negative loading factors were discovered for remaining traits in this PC. The PC5 was explained by variance due to

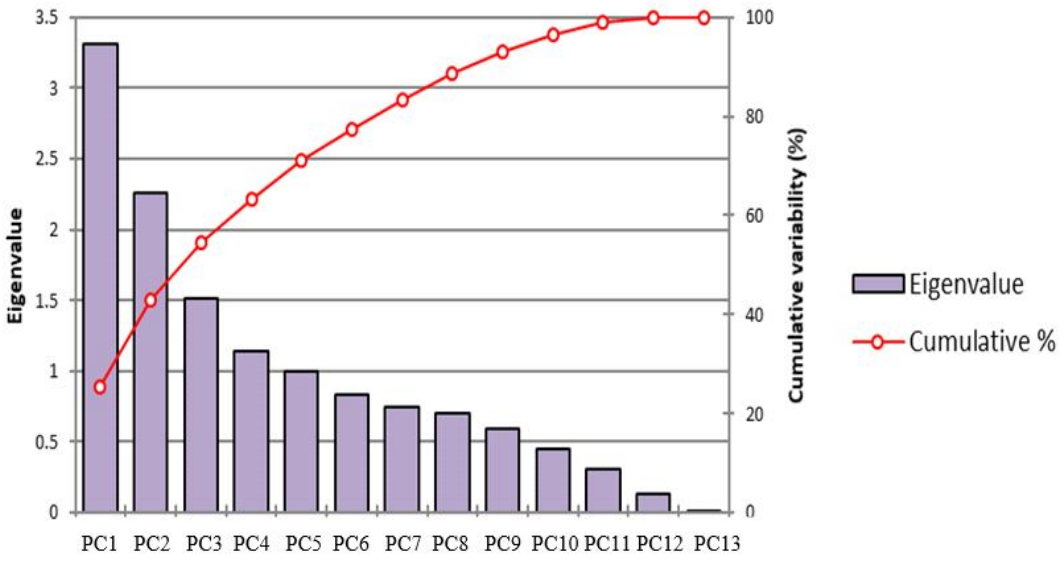

Fig 2: Scree plot showing variation for different PC values.

days to 50% flowering, days to maturity, plant height, effective nodes plant^{-1}, effective pods plant^{-1}, biological yield plant^{-1}, harvest index and seed yield plant^{-1} having positive factors loading, while branches plant^{-1}, nodes plant^{-1}, seeds pod^{-1}, pod length and 100-seed weight occur negative loadings. These conclusions are in correspondence with that of Habtamu and Million (2013), Parihar *et al.*, (2014) and Umar *et al.,* (2014). The value of positive and negative loading reveals positive and negative association patterns between the PCs and the variables. Therefore, the characters listed above, which load strongly positive or negative, have contributed most to diversity and have been the ones that have most categorized the clusters.

CONCLUSION

For identifying desirable recombinant in segregating generations, crosses between cluster members with a high cluster mean for significant characters combined with high inter-cluster distances between them are expected to be more satisfactory. Genotypes from cluster III and from cluster IV could be under-taken to isolate desirable segregants. The PCA analysis revealed significant variation among the traits with five major PCs around 70.97% variation of total variation. Further, it may be concluded that progenies resulting from diverse crosses are thus supposed to display a large range of genetic variability and a wider scope to isolate transgressive segregants in the advanced generation.

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