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Assessment of genetic diversity in advanced breeding lines derived from intraspecific crosses of garden pea (*Pisum sativum* L.)

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ABSTRACT

An intraspecific hybrid breeding program involving six crosses, Palam Sumool (PS) × Palam Priya, PS × Pb-89, PS × Azad P-1, PS × Palam Triloki and VRPMR10 × Sugar Giant, Green Pearl × DPP-9411 was initiated in 2006 onwards followed by pedigree selection, resulted in isolation of 45 genotypes with desirable attributes. These progenies along with five recommended varieties were evaluated during 2014-15 to assess degree of divergence. A considerable genetic diversity was observed among genotypes, dispersed in 18 diverse clusters. Of these, 17 were monogenotypic while cluster I had maximum genotypes. Internodal length contributed maximum towards total genetic divergence followed by nodes per plant, protein content and average pod weight. Superior performing genotypes *viz.,* 'DPP-2011-SP-7', 'DPP-2011-SP-17', and 'DPP-2011-SP-24' from cluster I and 'DPP-2011-SP-6', 'DPP-2011-SP-22' 'DPPMR-09-1', 'DPPMR-09-2', 'DPP-2011-SN-5' and 'Palam Triloki' from monogenotypic clusters offer promise for their direct use as varieties and as potential parents in future breeding programmes.

Key words: Garden pea, Genotypes, Genetic divergence, Pedigree, *Pisum sativum.*

INTRODUCTION

Garden pea (*Pisum sativum* L.) a diploid (2n=2x=14) cultivated species of genus Pisum, family Leguminosae, is one of the principal vegetable crops which is cultivated for its green pods in the temperate and sub-tropical areas of the world. Four centres of origin based on genetic diversity proposed by Vavilov (1926) were Central Asia, the Near East, Abyssinia (Ethiopia) and the Mediterranean. However, the exclusive origin and primary source of diversity of the crop is not well known (Davies, 1976). It is one of the world's oldest crops, as it was first cultivated with cereals like barley and wheat, 7000 years ago (McPhee, 2003).The Hindu Kusch region in India, which includes southern slopes of Himalayan mountain range, is one of its secondary centres of diversity (Ambrose, 2008).

It provides an exceptionally varied nutrient profile of health building substances namely, vitamins, minerals and also lysine -a limiting essential amino acid in cereals (Sharma *et al.,* 2014). The protein content of pea varies from (23-33%) (Cousin *et al.,* 1985; Jaiswal *et al.,* 2013). It is used as vegetable, pulse and processed as pickle, canned, frozen or dehydrated to increase availability during off-season (Guleria *et al.,* 2009). Moreover, pea contributes to yield of the succeeding crop in rotation by improving nitrogen status of the soil (Rowland *et al.,* 1994). It is an important food legume grown throughout India especially in northwestern Himalayan region. Owing to diverse agro-climatic conditions in Himachal Pradesh, the crop is grown year round as an off-season cash crop during summer in the high altitude areas and during winter in low and mid hills. The green pods available during the summer months find ready market in the plains bringing high remuneration to the growers. The consumers also have a special preference for pea from hilly regions due to its characteristic flavor, good quality and sweetness (Kumar *et al.,* 2015).

Systematic study and evaluation of germplasm is of great importance for current and future agronomic and genetic improvement of the crop (Nalla *et al.,* 2014). Pea improvement is based mainly on exploiting the natural sources of germplasm by means of selection or hybridization followed by selection (Zohary and Hopf, 2000). Selection is most basic and traditional method for improvement of traits showing additive and additive × additive type of gene action, but for improvement of those traits with non-additive type of gene action and didn't respond to selection, there is a need for partitioning of non-additive component of genetic variance further into additive and non additive variance by hybridization or crossing of parents having desirable attributes and which is achieved through genetic divergence studies (Kumar and Kumar, 2015).

Despite continuous breeding efforts, the average yield of pea is low due to its narrow genetic base and limited variability used in the development of recommended varieties (Kumar *et al.,* 2004) on account of farmers preference for

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cultivars with few specific traits such as lush green pods. Also, genetic drift in this extensively grown age old few cultivars and development of new pathogen races also lead to low/stagnant yield. Heterogeneous local population of the genus forms an important source of genetic variation (Zeven, 1998). Genetic diversity analysis assists in interpreting the genetic background and breeding value of the germplasm. Determination of genetic diversity of any given crop species is a suitable precursor for improvement of the crop because it generates baseline data to guide selection of parental lines and design of a breeding scheme.

Amongst various tools to assess genetic diversity, D^2 statistic is a powerful tool for estimating genetic diversity among different genotypes and to identify the parents for hybridization to obtain desirable recombinants. The assessment of genetic divergence helps in reducing the number of breeding lines from the large germplasm and the progenies derived from diverse parents are expected to show a broad spectrum of genetic variability and provide better scope to isolate superior recombinants. Selection of genotypes from divergent clusters and components having more than one positive traits for hybridization programme may lead to improvement in yield and quality of pea (Singh *et al.*, 2017). Keeping this in view, study was undertaken to gather information on genetic divergence of 50 genotypes of garden pea developed through hybridization. The information shall enable the breeders to make informed decisions about suitable parents while planning breeding programme for high yield along with desirable horticultural traits.

MATERIALS AND METHODS

The experimental material for present study comprised of 45 lines (Table 1) derived from hybridization programme, initiated in 2006 onwards in six intervarietal crosses namely, Palam Sumool (PS) × Palam Priya, PS × Pb-89, PS × Azad P-1, PS × Palam Triloki and VRPMR10 × Sugar Giant, Green Pearl × DPP-9411 followed by pedigree selection along with five recommended varieties *viz.*, Punjab 89, Palam Priya, Palam Sumool, Azad P-1 and Palam Triloki. These 50 genotypes (Table 2) were evaluated at the Research Farm of the Department of Vegetable Science and Floriculture, CSK HPKV, Palampur during winter 2014-15 in randomized complete block design with three replications. The soil of experimental field was clay loam with pH 5.7. Seeds were directly sown in the field in the month of November 2014 in two rows each of 4m length at inter and intra-row spacing of 45 cm and 10 cm, respectively. The seeds were sown at a depth of 3-4 cm. The standard cultural practices were followed to raise the crop.

The observations were recorded on randomly selected 10 plants of each genotype over the replications for 16 traits, *viz.*, first flower node, days to flowering, days to first picking, number of branches, internodal length (cm), nodes per plant, plant height (cm) at final harvest, pod length (cm), seeds per pod, shelling (%), pods per plant, pod yield per plant (g) and average pod weight (g).Besides, quality parameters such as total soluble solids (^{o}brix) using hand refractometer, ascorbic acid (mg/100g fresh weight basis) as described by Ranganna (1979) and protein content (%) following method of Jackson (1973) were also estimated. For shelling (%) data were recorded on 25 randomly taken pods from each genotype in each replication at the time of second harvest.

Wilk's criterion was used to test the significance of difference in mean values for all the 16 characters. The sum of squares and sum of products of error and error + variety variance – covariance matrix were used for this purpose. The estimation of 'V' (Wilk's criterion) was done by using the following relationship:

$$V = W/S$$

where, 'V'- Wilk's criterion, W- Determinant of error matrix and S- Determinant of error + variety matrix.

Using 'V' statistic which, in turn, utilizes Wilk's criteria, simultaneous test of difference mean values of a number of correlated variables/characters at 'pq' df (where, p = Number of characters and q = Number of genotypes-1) was done as suggested by Rao (1952). The data were subjected to multivariate analysis utilizing Mahalanobis D^2 statistic as suggested by Mahalanobis (1936) and Rao (1952) using statistical software WINDOSTAT 8.0 developed by Indostat Services. Genotypes were grouped into various clusters following Tocher's method as suggested by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed that mean squares due to genotypes were significant (Table 3) for all the traits. Thus, it highlighted the presence of sufficient genetic variability among the genotypes. The significance of 'V'

Table 1: Pedigree of 45 genotypes derived from intervarietal crosses.

Parentage	No of lines derived	Source
Palam Sumool × Palam Priya	21	Both parents from CSKHPKV, Palampur
Palam Sumool × Pb-89	18	Pb-89 from PAU, Ludhiana
Palam Sumool × Azad P-1	3	Azad P-1 from CSAUA&T, Kanpur
Palam Sumool × Palam Triloki	1	Both parents from CSKHPKV, Palampur
VRPMR10 × Sugar Giant	1	VRPMR-10 from IIVR, Varanasi and Sugar Giant from CSKHPKV, Palampur
Green Pearl × DPP-9411	1	Green Pearl from Pvt. Sector and DPP-9411 from CSKHPKV, Palampur

Table 2: Genotypes used in the study and their sources.

Code	Genotype	Source	Code	Genotype	Source	Code	Genotype	Source
1	PalamPriya	CSK HPKV, Palampur	18	DPP-2011-SP-22	CSK HPKV, Palampur	35	DPP-2011-SN-16	CSK HPKV, Palampur
2	Pb 89	PAU, Ludhiana	19	DPP-2011-SP-23	CSK HPKV, Palampur	36	DPP-2012-SN-1	CSK HPKV, Palampur
3	Azad P-1	CSAUA&T, Kanpur	20	DPP-2011-SP-24	CSK HPKV, Palampur	37	DPP-2012-SN-2	CSK HPKV, Palampur
4	PalamSumool	CSK HPKV, Palampur	21	DPP-2011-SP-25	CSK HPKV, Palampur	38	DPP-2012-SN-4	CSK HPKV, Palampur
5	PalamTriloki	CSK HPKV, Palampur	22	DPP-2011-SP-28	CSK HPKV, Palampur	39	DPP-2012-SN-7	CSK HPKV, Palampur
6	DPP-2011-SP-3	CSK HPKV, Palampur	23	DPP-2011-SP-29	CSK HPKV, Palampur	40	DPP-2012-SN-8	CSK HPKV, Palampur
7	DPP-2011-SP-6	CSK HPKV, Palampur	24	DPP-2011-SP-32	CSK HPKV, Palampur	41	DPP-2012-SN-9	CSK HPKV, Palampur
8	DPP-2011-SP-7	CSK HPKV, Palampur	25	DPP-2011-SP-33	CSK HPKV, Palampur	42	DPP-2012-SN-10	CSK HPKV, Palampur
9	DPP-2011-SP-8	CSK HPKV, Palampur	26	DPP-2011-SP-38	CSK HPKV, Palampur	43	DPP-2012-SN-11	CSK HPKV, Palampur
10	DPP-2011-SP-10	CSK HPKV, Palampur	27	DPP-2011-SN-1	CSK HPKV, Palampur	44	DPP-2012-SN-12	CSK HPKV, Palampur
11	DPP-2011-SP-11	CSK HPKV, Palampur	28	DPP-2011-SN-4	CSK HPKV, Palampur	45	DPP-2012-SA-1	CSK HPKV, Palampur
12	DPP-2011-SP-14	CSK HPKV, Palampur	29	DPP-2011-SN-5	CSK HPKV, Palampur	46	DPP-2012-SA-3	CSK HPKV, Palampur
13	DPP-2011-SP-15	CSK HPKV, Palampur	30	DPP-2011-SN-6	CSK HPKV, Palampur	47	DPP-2012-SA-4	CSK HPKV, Palampur
14	DPP-2011-SP-16	CSK HPKV, Palampur	31	DPP-2011-SN-8	CSK HPKV, Palampur	48	DPP-2011-ST-1	CSK HPKV, Palampur
15	DPP-2011-SP-17	CSK HPKV, Palampur	32	DPP-2011-SN-10	CSK HPKV, Palampur	49	DPPMR-09-1	CSK HPKV, Palampur
16	DPP-2011-SP-20	CSK HPKV, Palampur	33	DPP-2011-SN-13	CSK HPKV, Palampur	50	DPPMR-09-2	CSK HPKV, Palampur
17	DPP-2011-SP-21	CSK HPKV, Palampur	34	DPP-2011-SN-15	CSK HPKV, Palampur			

(statistic) value was tested by percent (%) at 784 degrees of freedom. Simultaneous test of significance based on Wilk's criterion and D^2 values obtained for each pair of population were observed to be significant which indicated the presence of sufficient genetic diversity among germplasm lines studied in present investigation. Hence, further analysis was made to estimate D^2 analysis. The multivariate analysis (D^2) illustrating genetic divergence, arranged 50 genotypes into eighteen clusters (Table 4) where in seventeen clusters were monogenotypic (solitary) and remaining one was polygenotypic following Tocher's procedure and also depicted through dendrograms (Fig 1) indicating thereby different clustering patterns. Different clustering patterns using different genetic material were also reported by Sharma *et al.,* (2013), Sanwal *et al.,* (2015) and Kumar and Kumar (2015) in pea.

The cluster I was the largest consisting of thirty three genotypes with 66.00 per cent constitution (Table 2). Kumar *et al.,* (2007) and Devi *et al.,* (2010) also arranged genotypes into different clusters and reported cluster I as the largest one. Clusters II, III, IV, V, VI, VII, VIII, IX, X, XI, XII, XIII, XIV, XV, XVI, XVII and XVIII contained one genotype each *viz.*, 'DPP-2012-SA-4', 'DPP-2011-SP-15', 'DPP-2011-SP-10', 'DPP-2011-SN-5', 'DPP-2012-SA-3', 'DPP-2011-SP-22', 'DPPMR-09-1', 'DPP-2011-SP-6', 'DPP-2011-SP-32', 'DPP-2011-SP-33', 'Punjab-89', 'DPP-2012-SN-8', 'Palam Priya', 'DPP-2011-SP-28', 'DPPMR-09-2', 'Palam Triloki' and 'DPP-2012-SN-7', respectively, suggesting that these genotypes diverged most from others. Sharma *et al.,* (2013) and Parihar *et al.,* (2014) also observed clusters with one genotype only and also suggested that such genotypes were more divergent from others. The clustering

Table 3: Analysis of variance for different traits in garden pea.

Characters	Mean sum of squares		
	Replication	Treatment	Error
df	2	49	98
Morphological traits			
First flower node	2.74	4.04*	0.43
Days to flowering	152.51	43.63*	5.96
Days to first picking	484.83	85.29*	8.85
Number of branches per plant	0.02	0.08*	0.01
Internodal length (cm)	0.01	1.84*	0.01
Nodes per plant	1.51	43.67*	1.58
Plant height (cm)	66.49	194.86*	34.42
Yield and yield contributing traits			
Pod length (cm)	1.70	3.07*	0.22
Seeds per pod	0.23	2.16*	0.16
Shelling (%)	2.32	62.62*	10.92
Pods per plant	5.47	7.33*	0.47
Pod yield per plant (g)	245.57	418.30*	16.64
Average pod weight (g)	0.55	1.94*	0.09
Quality traits			
Total soluble solids (°Brix)	0.03	4.47*	0.67
Ascorbic acid (mg)	1.96	19.22*	2.16
Protein content (%)	0.51	34.38*	1.58

*Significant at P≤0.05

Table 4: Cluster composition of different genotypes following multivariate analysis.

Cluster	No. of genotypes	Genotype (s)
numberI	33	PalamSumool, Azad P-1, DPP-2011-SP-3, DPP-2011-SP-7, DPP-2011-SP-8, DPP-2011-SP-11, DPP-2011-SP-14, DPP-2011-SP-16, DPP-2011-SP-17, DPP-2011-SP-20, DPP-2011-SP-21, DPP-2011-SP-23, DPP-2011-SP-24, DPP-2011-SP-25, DPP-2011-SP-29, DPP-2011-SP-38, DPP-2011-SN-1, DPP-2011-SN-4, DPP-2011-SN-6, DPP-2011-SN-8, DPP-2011-SN-10, DPP-2011-SN-13, DPP-2011-SN-15, DPP-2011-SN-16, DPP-2012-SN-1, DPP-2012-SN-2, DPP-2012-SN-4, DPP-2012-SN-9, DPP-2012-SN-10, DPP-2012-SN-11, DPP-2012-SN-12, DPP-2012-SA-1, DPP-2011-ST-1
II	1	DPP-2012-SA-4
III	1	DPP-2011-SP-15
IV	1	DPP-2011-SP-10
V	1	DPP-2011-SN-5
VI	1	DPP-2012-SA-3
VII	1	DPP-2011-SP-22
VIII	1	DPPM-09-1
IX	1	DPP-2011-SP-6
X	1	DPP-2011-SP-32
XI	1	DPP-2011-SP-33
XII	1	Punjab-89
XIII	1	DPP-2012-SN-8
XIV	1	Palam Priya
XV	1	DPP-2011-SP-28
XVI	1	DPPM-09-2-2
XVII	1	Palam Triloki
XVIII	1	DPP-2012-SN-7

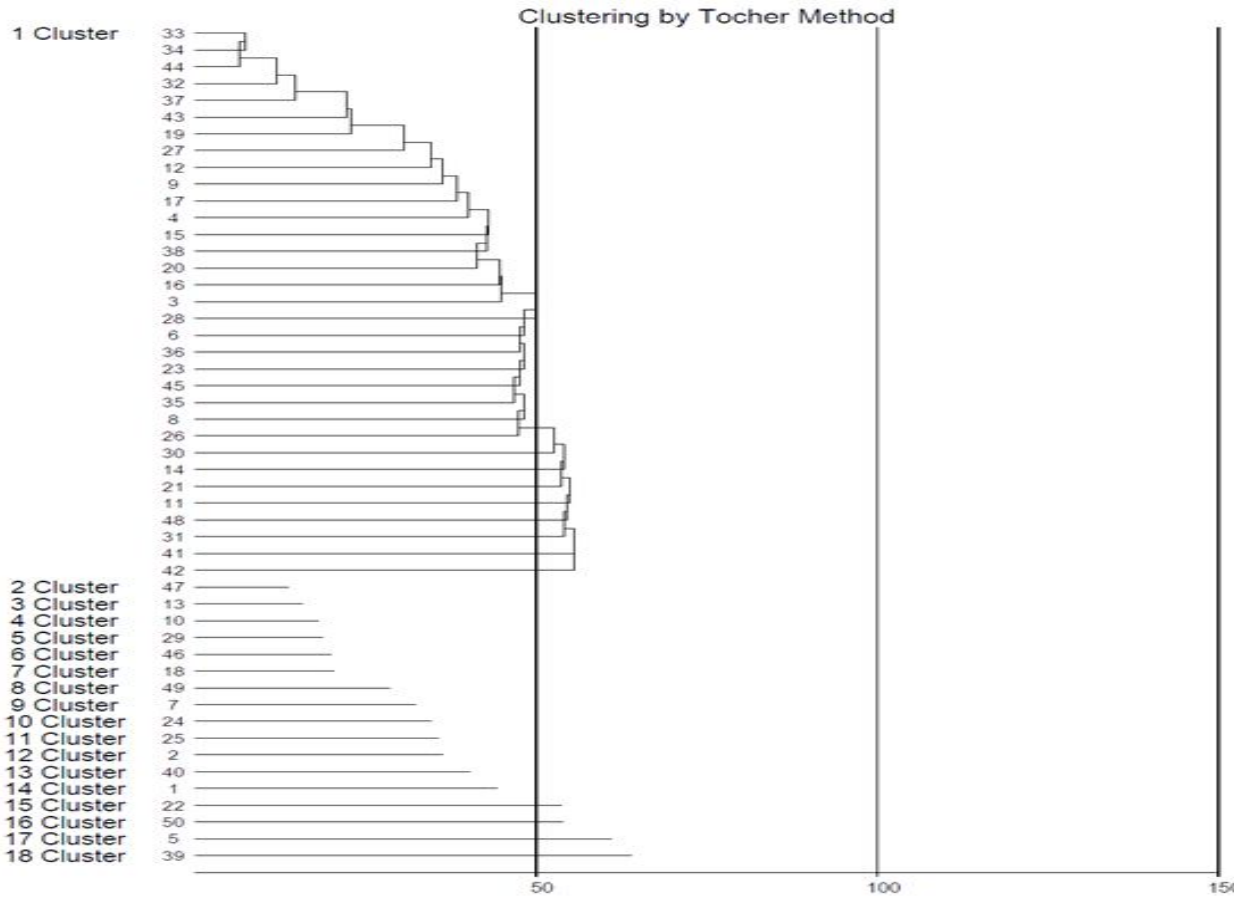

Fig 1: Dendrogram showing grouping of fifty garden pea genotypes based on D^2 statistics using Tocher's method.

Table 5: Average intra and inter-cluster distances in 18 clusters of garden pea genotypes.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII
I	**7.10**	8.83	8.09	9.78	11.57	8.76	8.16	8.71	10.23	10.12	11.06	9.41	10.61	8.91	11.03	9.53	9.94	13.61
	(2.66)	(2.97)	(2.84)	(3.13)	(3.40)	(2.96)	(2.86)	(2.95)	(3.20)	(3.18)	(3.33)	(3.07)	(3.26)	(2.98)	(3.32)	(3.09)	(3.15)	(3.69)
II		**0.00**	5.22	4.76	4.33	4.49	6.60	9.98	10.74	14.48	15.69	9.64	7.01	10.59	13.92	12.29	11.17	10.10
		(0.00)	(2.28)	(2.18)	(2.08)	(2.12)	(2.57)	(3.16)	(3.28)	(3.81)	(3.96)	(3.10)	(2.65)	(3.25)	(3.73)	(3.51)	(3.30)	(3.18)
III			**0.00**	5.24	6.83	6.16	6.34	10.39	9.94	14.50	15.54	7.61	6.50	9.43	14.74	11.36	11.35	10.79
			(0.00)	(2.29)	(2.61)	(2.48)	(2.52)	(3.22)	(3.15)	(3.81)	(3.94)	(2.76)	(2.55)	(3.07)	(3.84)	(3.37)	(3.37)	(3.28)
IV				**0.00**	5.12	5.91	5.77	11.29	10.43	15.67	17.34	9.79	7.83	11.57	15.52	14.06	11.22	11.17
				(0.00)	(2.26)	(2.43)	(2.40)	(3.36)	(3.23)	(3.96)	(4.16)	(3.13)	(2.80)	(3.40)	(3.94)	(3.75)	(3.35)	(3.34)
V					**0.00**	6.84	8.16	13.47	12.80	17.91	19.16	11.22	7.23	13.70	17.14	15.52	13.17	9.64
					(0.00)	(2.62)	(2.86)	(3.67)	(3.58)	(4.23)	(4.38)	(3.35)	(2.69)	(3.70)	(4.14)	(3.94)	(3.63)	(3.10)
VI						**0.00**	6.15	10.32	8.71	13.89	15.55	10.44	6.86	9.27	12.49	10.97	11.07	11.58
						(0.00)	(2.48)	(3.21)	(2.95)	(3.73)	(3.94)	(3.23)	(2.62)	(3.04)	(3.53)	(3.31)	(3.33)	(3.40)
VII							**0.00**	10.97	5.68	13.38	15.10	9.29	7.93	11.21	13.12	12.36	9.95	10.40
							(0.00)	(3.31)	(2.38)	(3.66)	(3.89)	(3.05)	(2.82)	(3.35)	(3.62)	(3.52)	(3.15)	(3.22)
VIII								**0.00**	12.60	8.87	10.74	10.27	14.45	6.79	11.20	9.80	9.02	17.78
								(0.00)	(3.55)	(2.98)	(3.28)	(3.20)	(3.80)	(2.61)	(3.35)	(3.13)	(3.00)	(4.22)
IX									**0.00**	13.37	15.57	12.61	10.46	11.82	12.07	12.04	12.45	12.66
									(0.00)	(3.66)	(3.95)	(3.55)	(3.23)	(3.44)	(3.47)	(3.47)	(3.53)	(3.56)
X										**0.00**	5.98	15.44	16.33	9.82	7.33	9.87	12.11	19.19
										(0.00)	(2.45)	(3.93)	(4.04)	(3.13)	(2.71)	(3.14)	(3.48)	(4.38)
XI											**0.00**	15.01	17.91	12.01	9.22	9.34	13.48	19.79
											(0.00)	(3.87)	(4.23)	(3.47)	(3.04)	(3.06)	(3.67)	(4.45)
XII												**0.00**	12.41	11.38	16.57	12.11	10.10	15.26
												(0.00)	(3.52)	(3.37)	(4.07)	(3.48)	(3.18)	(3.91)
XIII													**0.00**	12.53	15.21	13.04	15.21	7.99
													(0.00)	(3.54)	(3.90)	(3.61)	(3.90)	(2.83)
XIV														**0.00**	10.60	7.91	10.73	17.74
														(0.00)	(3.26)	(2.81)	(3.28)	(4.21)
XV															**0.00**	8.58	13.44	17.37
															(0.00)	(2.93)	(3.67)	(4.17)
XVI																**0.00**	13.73	16.75
																(0.00)	(3.71)	(4.09)
XVII																	**0.00**	18.29
																	(0.00)	(4.28)
XVIII																		**0.00**
																		(0.00)

Values in bold figures are intra-cluster distances; Values in parenthesis are $\sqrt{D^2}$= D value.

pattern revealed that the genotypes of same geographical distribution fall into different clusters which indicated the influence of genetic constitution of the genotypes in the clustering pattern. This suggests that genetic diversity is not always related to geographical diversity (Kumar *et al.*, 2006; Kumar *et al.*, 2007; Kumar and Kumar, 2015).

The intra-cluster distance varied from 0 to 2.66, respectively. The intra-cluster distance was highest in cluster I, and the remaining monogenotypic clusters had zero distance (Table 5). Sharma *et al.*, (2009) and Sharma *et al.*, (2013) also observed maximum intra- cluster variation among genotypes. Since the intra-cluster distance was low, the chances of developing good segregants by hybridization among parents within cluster would be low. Therefore, it is logical to attempt crosses between genotypes falling in different clusters based on inter-cluster distance. The inter-cluster distance ranged from 4.33 (2.08) to 19.79 (4.45). The highest inter-cluster level genetic divergence was recorded between clusters XI and XVIII followed by X and XVIII, V and IX, VII and VIII, V and X, XI and XIII, VIII and XVIII and XIV and XVIII. This clearly indicated that the genotypes included in the clusters with high inter-cluster distance showed sufficient genetic diversity and selection of parents from these diverse clusters would be useful in hybridization programme for improving yield and other desirable horticultural traits. The crosses involving the diverse genotypes would be expected to manifest maximum heterosis and are more likely to evolve desirable recombinants in segregating generations. Based on inter-cluster distance, the earlier workers have also suggested selection of parents from diverse clusters for utilization in hybridization programme to obtain desirable transgressive segregants (Yadav *et al.*, 2009; Sharma *et al.*, 2013; Sanwal *et al.*, 2015).

The composition of cluster means for different characters showed considerable differences among the clusters for each character (Table 6). Cluster IX was observed to be important with maximum cluster means for the most valuable traits *viz.*, number of branches per plant, seeds per pod, shelling percentage, pods per plant, pod yield per plant, average pod weight and ascorbic acid while having comparable cluster mean for pod length, days to flowering and days to first picking. Cluster XVII was observed to be earliest as it represented the minimum cluster means for first flower node, days to flowering and for days to first picking. Hence, different clusters of genotypes on the basis of means revealed divergence for different characters and can be utilized as indicators for selecting diverse parents for specific trait in hybridization programmes (Habtamu and Million, 2013; Sharma *et al.*, 2013; Sanwal *et al.*, 2015).

It is worthy to note that in calculating cluster mean, the superiority of a particular genotype with respect to a given character could get diluted by other genotypes that

Table 6: Cluster means for different characters in garden pea.

ClustersTraits	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	Mean	Max.	Min.
First flower node	13.82	14.67	14.87	13.13	13.13	14.13	12.93	15.53	13.53	13.53	16.60	13.27	14.53	14.20	13.20	17.33	9.73	13.73	13.99	17.33	9.73
Days to flowering	90.59	91.00	91.67	87.33	88.33	89.00	87.33	93.67	88.00	95.33	96.00	89.67	93.00	96.33	90.33	98.00	73.33	93.67	90.70	98.00	73.33
Days to first picking	129.85	132.00	124.00	126.33	127.00	134.00	123.00	138.67	126.00	136.33	131.67	123.33	134.33	136.67	137.33	135.67	111.00	133.00	130.01	138.67	111.00
Number of branches	1.46	1.43	1.57	1.43	1.33	1.17	1.67	1.47	1.80	1.50	1.47	1.70	1.67	1.50	1.33	1.67	1.43	1.53	1.51	1.80	1.17
Internodal length (cm)	6.16	7.35	7.07	7.48	8.04	7.27	6.93	5.66	6.59	4.86	4.55	6.35	7.73	5.75	5.53	5.61	5.83	8.18	6.50	8.18	4.55
Nodes per plant	27.31	25.67	29.00	24.40	25.07	20.93	25.40	25.33	23.20	20.03	27.00	37.90	25.93	22.67	18.33	28.20	24.17	29.80	25.57	37.90	18.33
Plant height (cm)	66.61	86.86	72.78	74.80	73.30	82.21	64.93	65.64	66.55	54.33	60.64	58.00	78.11	71.41	78.23	65.07	55.55	83.60	69.92	86.86	54.33
Pod length (cm)	11.26	10.81	10.05	11.35	10.91	11.10	12.19	8.70	11.78	11.33	11.77	10.22	12.55	7.97	11.71	10.68	8.31	13.83	10.92	13.83	7.97
Seeds per pod	6.83	6.93	6.77	7.77	6.53	7.50	8.07	6.40	8.27	5.97	5.57	8.00	6.90	5.53	5.03	5.33	7.30	6.20	6.72	8.27	5.03
Shelling (%)	41.21	44.61	40.10	36.74	45.00	45.13	48.75	45.67	50.00	39.44	38.38	47.06	37.27	40.74	34.67	33.64	43.89	42.70	41.94	50.00	33.64
Pods per plant	7.09	5.97	9.20	9.80	6.47	7.03	9.43	6.03	9.83	4.67	4.67	9.80	6.60	7.07	3.60	5.33	6.93	6.73	7.01	9.83	3.60
Pod yield per plant (g)	44.66	35.07	54.76	53.51	36.50	46.37	65.63	28.80	82.75	27.97	31.37	55.62	48.06	36.52	28.06	39.35	37.36	58.50	45.05	82.75	27.97
Average pod weight (g)	6.26	5.87	5.95	5.44	5.65	6.62	6.96	4.77	8.71	6.02	6.29	5.69	7.27	5.16	7.82	7.39	5.38	8.69	6.44	8.71	4.77
Total soluble solids (^{o}Brix)	16.09	17.27	16.33	17.47	17.27	16.40	17.07	20.00	18.00	16.07	16.13	17.60	14.07	16.47	19.67	19.33	16.60	16.93	17.15	20.00	14.07
Ascorbic acid (mg)	24.06	20.83	24.17	22.50	18.50	19.33	23.33	25.83	26.97	26.67	20.83	20.00	22.50	21.00	23.33	19.50	20.83	25.83	22.56	26.97	18.50
Protein content (%)	19.91	22.50	17.25	20.13	21.50	17.06	21.59	22.53	20.68	22.38	25.92	18.25	14.63	14.44	24.30	16.58	23.65	27.16	20.58	27.16	14.44

Max-Maximum; Min-Minimum

are grouped in the same cluster but are inferior or intermediate for the character in question (Million, 2012). Hence, apart from selecting genotypes from the clusters which have higher inter-cluster distance for hybridization, one can also think of selecting parents based on the extent of divergence with respect to a character of interest (Nigussie and Becker, 2002; Gemechu *et al.,* 2005; Fikreselassie *et al.,* 2012).

The contribution of individual characters to divergence has been worked out in terms of number of times it appeared first (Table 7). Internodal length contributed maximum towards total genetic divergence followed by nodes per plant and average pod weight. Therefore, it could also be used as parameters based on specific trait (s) in selecting genetically diverse parents for hybridization to create variability in the population. On the other hand, earlier reports revealed that early yield per plant (Gupta and Singh, 2006) and plant height (Tiwari *et al.,* 2004; Kumar *et al.,* 2007; Sanwal *et al.,* 2015) contributed maximum towards total genetic divergence.

Table 7: Contribution of various traits towards genetic divergence in garden pea.

Characters	Times ranked Ist	Contribution (%)
First flower node	13	1.06
Days to flowering	0	0.00*
Days to first picking	9	0.73
Number of branches per plant	11	0.90
Internodal length (cm)	656	53.55**
Nodes per plant	153	12.49
Plant height (cm)	3	0.24
Pod length (cm)	36	2.94
Seeds per pod	36	2.94
Shelling (%)	21	1.71
Pods per plant	33	2.69
Pod yield per plant (g)	1	0.08
Average pod weight (g)	74	6.04
Total soluble solids (°Brix)	14	1.14
Ascorbic acid (mg)	54	4.41
Protein content (%)	111	9.06

*Minimum; **Maximum

CONCLUSION

It can be concluded that selection of genotypes as superior and diverse parents for hybridization programme should be based on diverse clusters. Superior performing genotypes *viz.,* 'DPP-2011-SP-7', 'DPP-2011-SP-17', and 'DPP-2011-SP-24' from cluster I and 'DPP-2011-SP-6', 'DPP-2011-SP-22' 'DPPMR-09-1', 'DPPMR-09-2', 'DPP-2011-SN-5' and 'Palam Triloki' from monogenotypic clusters offer promise for their direct use as varieties and as potential parents in future breeding programmes.

REFERENCES

Ambrose, M. (2008). Garden pea. In: Vegetables II: Fabaceae, Liliaceae, Solanaceae and Umbelliferae. [J. Prohens and F. Nuez (eds.)], Springer Science and Business Media, New York, USA. pp 3-26.

Cousin, J.R. Massager, A. and Vingere, A. (1985). Breeding for yield in common peas. The peas Crops. [P.H. Hebblethwaite, M.C. Heath and T.C.K. Dawkins (eds.)], Butterworths. p. 115-129.

Davies, D.R. (1976). Peas. In: Evolution of Crop Plants, [N.W. Simmonds (ed.).], Longman, London. p. 172–74.

Devi, P., Pant, S.C., Rana, D.K. and Rawat, S.S. (2010). Genetic variability and selection parameters for different genotypes of pea (*Pisum sativum* L.) under valley condition of Uttarakhand. *Journal of Hill Agriculture,* **1**:56-58.

Fikreselassie, M., Habtamu, Z. and Nigussie, A. (2012). Correlation and path analysis in Ethiopian fenugreek (*Trigonellafoenum-graecum* L.) landraces. *Crown Research in Education,* **2**:132-142.

Gemechu, K., Mussa, J., Tezera, W. and Getnet, D. (2005). Extent and pattern of genetic diversity for morpho-agronomic traits in Ethiopian highland pulse landraces II. Field pea (*Pisum sativum* L.). *Genetic Resources and Crop Evolution,* **52**:541-550.

Guleria, S., Chongtham, N. and Dua, S. (2009). Genetic variability, correlation and path analysis studies in pea (*Pisum sativum* L.). *Crop Research,* **38**:179-183.

Gupta, A.J. and Singh, Y.V. (2006). Genetic divergence in garden pea (*Pisum sativum* L.). *Indian Journal of Genetics and Plant Breeding,* **66**:341-342.

Habtamu, S. and Million, F. (2013). Multivariate analysis of some Ethiopian field pea (*Pisum sativum* L.) genotypes. *International Journal of Genetics and Molecular Biology,* **5**:78-87.

Jackson, M.L. (1973). Soil Chemical Analysis. Pretince Hall Inc., Englewood, Cliffs, New Jersey, USA.

Jaiswal, N.K., Gupta, A.K., Dewangan, H. and Lavanya, G.R. (2013). Genetic variability analysis in field pea (*Pisum sativum* L.). *International Journal of Science and Research*, **4**:1-2.

Kumar, P., Partap, P.S. and Rana, M.K. (2004). Correlation studies in garden pea (*Pisum sativum* L.). *Haryana Journal of Horticultural Sciences,* **33**:243-245.

Kumar, R. and Kumar, M. (2015). Estimation of genetic divergence in garden pea (*Pisum sativum var. hortense* L.) germplasm to facilitate the selection of potential parents for hybridization programme. *Legume Research,* **39(5)**:709-712.

Kumar, R., Dhari, R. and Kumar, R. (2006). Divergence studies in pea germplasm (*Pisum sativum* L.). *National Journal of Plant Improvement,* **8**:122-124.

Kumar, R., Dhari, R., Kumar, R. and Malik, B.P.S. (2007). Assessment of morphological variability and genetic diversity in pea germplasm (*Pisum sativum* L.). *National Journal of Plant Improvement,* **9**:5-8.

Kumar, R., Kumar, M., Dogra, R.K. and Bharat, N.K. (2015). Variability and character association studies in garden pea (*Pisum sativum* var. *hortense* L.) during winter season at mid hills of Himachal Pradesh. *Legume Research,* **38**:164-168.

Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Proceedings of National Academy of Sciences,* **22**:49-55.

McPhee, K. (2003). Dry pea production and breeding: A mini-review. *Journal of Food Agriculture and Environment,* **1**:64-69.

Million, F. (2012). Variability, heritability and association of some morpho-agronomic traits in field pea (*Pisumsativum*L.) genotypes. *Pakistan Journal of Biological Sciences,* **15**: 358-366.

Nalla, M.K., Rana, M.K., Singh, S.J., Sinha, A.K., Reddy, P.K. and Mohapatra, P.P. (2014).Assessment of genetic diversity through D^2 analysis in tomato (*Solanum lycopersicon* L.). *International Journal of Innovation and Applied Studies,* **6**:431-438.

Nigussie, A. and Becker, H. (2002). Genotypic diversity and patterns of variation in a germplasm material of Ethiopian mustard (*Brassica carinata* A. Braun). *Genetic Resources and Crop Evolution,* **49**:573-582.

Parihar, A.K., Dixit, G.P., Pathak, V. and Singh, D. (2014). Genetic diversity and trait inter-relationship studies in a diverse set of field pea (*Pisum sativum* L.) genotypes. *Journal of Food Legumes,* **27**:297-301.

Ranganna, S. (1979). Manual of analysis of fruits and vegetables products. Tata McGraw Hill Book Company, New Delhi.

Rao, C.R. (1952). Advanced Statistical Methods in Biometrical Research. John Wiley and Sons Inc. New York Edn. 1.

Rowland, I., Mason, M., Pritchard, I. and French, R. (1994). Effect of field peas and wheat on the yield and protein of subsequent wheat crops grown at several rates of applied nitrogen. *Australian Journal of Experimental Agriculture,* **34**:641-46.

Sanwal, S.K., Singh, B., Singh, V. and Mann, A.(2015). Multivariate analysis and its implication in breeding of desired plant type in garden pea (*Pisum sativum*). *Indian Journal of Agricultural Sciences,* **85**:1298-1302.

Sharma, A., Bhardwaj, A., Katoch, V. and Sharma, J. (2013). Assessment of genetic diversity of garden pea (*Pisum sativum*) as perspective to isolate horticulturally desirable transgressive segregants. *Indian Journal of Agricultural Sciences,* **83**:1334-39.

Sharma, A., Sharma, M., Sharma, K.C., Singh, Y., Sharma, R.P. and Sharma G.D. (2014). Standardization of sowing date and cultivars for seed production of garden pea (P*isum sativum* var. *hortense* L.) under north western Himalayas. *Legume Research*, 37(3): 287-293**.**

Sharma, M.K., Chandel, A. and Kohli, U.K. (2009). Genetic evaluation, correlations and path analysis in garden pea (*Pisum sativum* var. *hortense* L.). *Annals of Horticulture,* **2**:33-38.

Singh, S.R., Ahmed, N., Singh, D.B., Srivastva, K.K., Singh, R.K. and Mir, A. (2017). Genetic variability determination in garden pea (*Pisum sativum* L sub sp. *hortense* Asch. and Graebn.) by using the multivariate analysis. *Legume Research,* **40(3)**:416-422.

Tiwari, S.K., Kumar, R., Singh, H.L. and Katiyar, R.P. (2004). Genetic diversity analysis in pea (*Pisum sativum* L.). *Indian Journal of Agricultural Research,* **38**:60-64.

Vavilov, N.I. (1926). Studies on the origin of cultivated plants. Bulletin of Applied Botany. *Plant Breeding,* **16**:139-248.

Yadav, R., Srivastava, R.K., Kant, R. and Singh, R. (2009). Studies on genetic divergence in field pea (*Pisum sativum* L. Poir). *Legume Research,* **32**:121-124.

Zeven, A.C. (1998). Landraces: A review of definitions and classifications *Euphytica*, **104**:127-139.

Zohary, D. and Hopf, M. (2000). *Domestication of Plants in the Old World*. 3 edition. Oxford University Press: p.316.