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RESEARCH PAPER

Assessment of genetic diversity based on morpho-phenological and productivity traits in field pea (*Pisum sativum* L.)

A. GURUPRASAD, M. D. PATIL AND I. S. KATAGERI

Department of Biotechnology, College of Agriculture, Vijayapur
University of Agricultural Sciences, Dharwad - 580 005, Karnataka, India
E-mail: guruprasadchinnu@gmail.com

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Abstract: In the present study, one hundred sixty field pea genotypes received from National Bureau of Plant Genetic Resources (NBPGR), New Delhi, Indian Institute of Pulse Research (IIPR), Kanpur and local collections were evaluated for assessing genetic divergence for exploitation in a breeding programme aimed at improving productivity. The genetic divergence was deciphered using Mahalanobis D^2 statistics. The intra cluster D^2 value ranged from 0.00 to 40.52 while inter cluster D^2 value ranged from 25.22 to 102.38 indicated that the genetic material used in the study is highly divergent. The maximum intra cluster distance was recorded for Cluster I (40.52) while Cluster VIII (0.00) showed no intra-cluster distance values revealing homogenous nature of the genotype within the cluster. Initiation of first flowering had maximum (28.41%) contribution towards diversity followed by fifty per cent flowering (18.47%), while SPAD readings at 75 DAS followed by 45 DAS (0.27% and 0.29% respectively) had least contribution. Based on the cluster means it was noticed that the genotypes superior for yield and most of the other yield attributing traits are grouped in Cluster III, the genetically more divergent lines were grouped in Cluster VII and VIII as indicated by inter-cluster distance value (102.38). Selecting lines of these clusters probably provide promising recombinants and better segregants for future breeding programme.

Key words: Diversity, Genetic, Inter cluster distance

Introduction

Pea (*Pisum sativum* L.) is one of the oldest crop grown in world, approximately 9000 years ago along with cereals like wheat and barley (McPhee, 2003). Pea has a wide range of agricultural and horticultural uses. The green seeds are used as fresh, frozen or canned vegetables and the mature dry seeds are used as dhal. It is grown on a wide range of soil types ranging from light sandy to heavy clayey soils. In recent years the value of peas for fodder purposes has increased (its green matter contains 14 to 24 % proteins, average 16%) as well as its value as a vegetable crop (green peas are the high protein-containing vegetable with a protein content of 6-7 % on the fresh weight basis). The most important tasks for pea breeding are development of high yielding varieties with stable productivity, sufficiently good resistance to diseases and unfavourable environmental conditions, different maturing types, high rate of organic matter accumulation during the initial phases of growth, sufficiently high intensity of photosynthesis, increases in protein content. To develop a new variety there is need of the magnitude of genetic variability in the base material and the vast of variability for desired characters. A good knowledge on genetic diversity or genetic similarity could be helpful in long term selection gain in plants (Kumar *et al*., 2012).

The early recorded diversity study on pea was done by Mendel (1865), which changed the way we think about inheritance and his laws made him as father of genetics. Evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm. Better knowledge on genetic diversity or genetic similarity could help to sustain long term selection gain (Choudhury *et al*., 2006).

The genetically diverse parents are always able to produce high heterotic effects and great frequency of desirable segregants in further generation as already reported by earlier workers (Kumar *et al.,* 1994). D^2 statistic is a useful tool to measure genetic divergence among genotypes in any crop developed by Mahalanobis (1936). However, in the present study, an attempt has been made to identify genetic divergent lines in 160 genotypes, so as to select the potential parents for breeding programme to attain the anticipated improvement in grain yield of field pea.

Material and methods

A field experiment was conducted during *Rabi* 2019 at I block, Regional Agricultural Research Station (RARS) Vijayapur, which is situated in Northern dry zone of Karnataka between 16°46' N latitude and 75°45' E longitude with an altitude of 595 meters above mean sea level (MSL). The experiment was laid out in augmented block complete design with one hundred sixty accessions (treatments) received from National Bureau of Plant Genetic Resources (NBPGR), New Delhi, Indian Institute of Pulsed Research (IIPR), Kanpur and local collections. Observations were recorded on five randomly selected competitive plants for eleven quantitative characters *viz.,* Initiation of first flower, Days to 50 per cent flowering, Number of primary branches per plant, Plant height (cm), Number of pods per plant, Number of seeds per pod, Days to maturity, Hundred seed weight (g), Seed yield per plant (g), Seed protein (%) along with SPAD chlorophyll meter readings (SCMR) at 45 days and 75 days interval after sowing. Along with analysis of variance, genetic divergence was estimated using Mahalanobis (1936) D^2 statistics and clustering was done according to Tocher's method as described by Rao (1952).

Results and discussion

The analysis of variance revealed significant differences among the genetic material used for all the characters studied (Table 1). This indicates that there is ample scope for selection of promising lines from the present gene pool aimed at enhancing genetic yield potential of field pea. All one hundred sixty genotypes were grouped into eight clusters following Tocher's methods (Table 2). Cluster I with 114 genotypes, formed the largest cluster followed by Cluster II (13) and Cluster III (10). Cluster VIII was ungrouped, comprising single genotype. The pattern of group constellation proved the existence of significant amount of variability.

The intra-cluster D^2 value ranged from 0.00 to 40.52 while inter-cluster D^2 value ranged from 25.22 to 102.38 indicating that selected advance breeding lines were highly divergent (Table 3 and Fig. 1). The maximum intra cluster distance was recorded for Cluster VII (40.52) followed by Cluster II (20.58) and Cluster VI (20.48) while Cluster VIII (0.00) showed no intra-cluster distance value as it was solitary cluster. The maximum inter-cluster D^2 value was observed between Cluster VII and VIII (102.38) followed by Cluster II and VII (92.20), Cluster VI and VII (76.72) and Cluster III and VIII (75.88) suggesting that the genotypes belonging to these clusters may be used as parents for hybridization programme to develop desirable type, because crosses between genetically divergent lines will generate heterotic segregants (Sureja and Sharma, 2001 and Yadav *et al*., 2009). As heterosis can be best exploited and chances of getting transgressive segregants are maximum when generating diverse lines are crossed (Pratap *et al*., 1992 and Lal *et al*., 2001). The maximum contribution to genetic divergence was from initiation of first flower (28.41 %) followed by fifty per cent flowering (18.47 %), seed protein (15.34 %), days to maturity (11.93) and yield per plant (6.53 %) which had the greater contribution to genetic diversity (Table 5) therefore necessary attention is required to be focused on these characters.

The cluster means of 12 characters and overall score across all the clusters are presented in the Table 4. Based on the scores of individual trait means across clusters, Cluster III found to be top ranked and was followed by Cluster II, while III rank was shared by Cluster IV and Cluster V with same score values. Similarly, rank IV, V, VI and VII were designated to Clusters I, VI, VII and VIII, respectively.

Cluster means for initiation of first flower ranged from 40.63 days (Cluster VII) to 82 days (Cluster VIII), these clusters also showed minimum and maximum cluster means for days to maturity which ranged between 101.25 days and 149.00 days, while cluster mean for fifty per cent flowering was minimum in Cluster II (55.46 days) and maximum in Cluster VIII (96.00 days). Cluster VII was found to have genotypes having high SCMR both at 45 DAS (48.08) and 75 DAS (43.84), whereas Cluster VI means for SPAD 45 (33.38) and SPAD 75 (33.12) were minimum.

The genotypes superior for yield and other yield attributing traits including plant height (87.30 cm), primary branches (2.05),

Table 1. Analysis of variance of quantitative traits studied in field pea genotypes

Source	df	IFF	FPF	DM	SPAD 45	SPAD 75	PH	PPP	PB	SPP	100 SW	YPP
Block (Eliminating Treatments)	4	10.75 ns	32.53 ns	37.25 ns	2.38 ns	4.29 ns	23.99 ns	0.79 ns	0.02 ns	0.04 ns	0.49 ns	0.24 ns
Treatment (Ignoring Blocks)	159	75.29 **	56.82 **	93.03 **	20.53 **	18.49 **	419.53 **	12.86 **	0.33 **	1.11 **	12.88 **	19.97 **
Treatment: Check	5	32.19 **	61.28 **	101.39 **	16.72 **	20.95 **	2073.63 **	23.14 **	1.11 **	1.05 **	34.76 **	127.43 **
Treatment: Test	153	76.65 **	56.75 **	91.09 **	20.74 **	18.53 **	327.24 **	11.71 **	0.31 **	1.06 **	11.43 **	9.95 **
Treatment: Test and Test vs. Check	154	73.22 **	54.82 **	87.6 **	16.72 **	20.95 **	354.62 **	23.14 **	1.11 **	1.05 **	10.95 **	127.43 **
Treatment: Test vs. Check	1	82.22 **	44.41 ns	348.01 **	6.81 ns	1.02 ns	6270.22 **	137.37 **	0.18 *	9.53 **	125.9 **	1016.71 **
Error	20	7.31	12.31	19.71	3.43	3.63	15.39	0.39	0.03	0.07	0.73	0.38

ns P > 0.05; * P <= 0.05; ** P <= 0.01

IFF = Initiation of first flower, FPF = Fifty per cent flowering, PH = Plant height, DM = Days to maturity

PB = Primary branches, PPP = Pods per plant, SPP= Seeds per pod, YPP = Yield per plant, 100 SW = 100 seed weight

Table 2. Distribution of one hundred sixty field pea genotypes in different clusters

Clusters	Genotypes	Total genotypes
Cluster 1	B-22, DMR-7 (C), EC292162, EC292167, EC328778, EC329549, EC329561, EC329568, EC598536, EC598538, EC598579, EC598614, EC598635, EC598639, EC598649, EC598651, EC598667, EC598696, EC598697, EC598753, EC598770, EC598784, EC598808, EC598836, EC598851, EC598852, EC598858, EC598872, EC598882, EC959260, HUP-2 (C), IC107446, IC107498, IC109305, IC109306, IC109555, IC199303, IC208327, IC208365, IC208368, IC208370, IC208377, IC208378, IC208379, IC208380, IC208381, IC208386, IC208399, IC208931, IC209095, IC212631, IC212657, IC212688, IC218982, IC218999, IC219027, IC219029, IC219030, IC219100, IC258262, IC267151, IC267152, IC267162, IC267182, IC26756, IC268255, IC269592, IC278113, IC278813, IC278954, IC279013, IC279076, IC279082, IC279120, IC279125, IC279217, IC299013, IC299305, IC310673, IC310833, IC326395, IC328514, IC341387, IC342020, IC342025, IC342033, IC381453, IC381454, IC381455, IC396094, IC396743, IC396777, IC396802, IC398812, IC49682, IC49684, IC49689, IPF-5-19, IPFD-1-10 (C), KPMR-145, KPMR-400, KPR-103, KPS-16, KPS-17, NIPPANI LOCAL 1, NIPPANI LOCAL 2, P-2, P-725, PM-5, PM-7, RACHANA (C), TRCP-8, VL-3, YATTINGHUDDA	114
Cluster 2	EC292164, EC598546, EC598569, EC598609, EC598615, EC598654, EC598820, HFP-529, IC107452, IC98608, LOKUR COLLECTION, P-744, PM-6	13
Cluster 3	EC292174, EC598592, IC267138, IC311164, IPF-4-9 (C), IPF-99-25, IPFD-6-3 (C), KPMR - 84-1, N-10, P-3	10
Cluster 4	IC209114, IC279142, IC326345, IC347387, IM9101	5
Cluster 5	EC292174, EC598592, IC267138, IC311164, IPF-4-9 (C), IPF-99-25,	6
Cluster 6	EC329554, IC398023, IC398722	3
Cluster 7	EC33866, EC598583, IC291544, IC291553, IC342046, IC372703, IPFD-11-5, KHANAPUR 10	8
Cluster 8	EC598897	1

Table 3. Average intra and inter cluster D^2 values of field pea genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Cluster 1	15.29	25.22	27.22	27.73	24.64	36.56	36.25	50.16
Cluster 2	25.22	20.58	32.56	44.07	42.16	62.96	33.08	92.20
Cluster 3	27.22	32.56	19.89	38.79	40.45	56.04	49.93	75.88
Cluster 4	27.73	44.07	38.79	16.99	33.85	31.44	57.93	48.66
Cluster 5	24.64	42.16	40.45	33.85	19.16	34.02	49.05	31.33
Cluster 6	36.56	62.96	56.04	31.44	34.02	20.48	76.72	33.73
Cluster 7	36.25	33.08	49.93	57.93	49.05	76.72	40.52	102.38
Cluster 8	50.16	92.20	75.88	48.66	31.33	33.73	102.38	0.00

Bold values indicate intra cluster D^2 values

Table 4. The cluster means in respect of a total 12 quantitative characters and over all character wise score.

Characters													All traits	
	IFF	FPF	SPAD 45	SPAD 75	PH	DM	PB	PPP	SPP	YP	100 SW	SP	Score	Rank
Cluster 1	58.58 (6)	66.34 (6)	44.99 (5)	37.87 (5)	61.10 (3)	113.62 (5)	1.63 (6)	7.47 (2)	2.59 (5)	4.58 (4)	14.60 (4)	19.74 (4)	55	IV
Cluster 2	45.54 (7)	55.46 (8)	45.18 (4)	38.1 (4)	53.75 (4)	102.92 (7)	1.88 (2)	7.25 (4)	3.47 (3)	5.91 (2)	18.31 (1)	19.56 (6)	52	II
Cluster 3	59.64 (5)	66.88 (5)	46.16 (3)	39.04 (3)	87.3 (1)	113.08 (6)	2.05 (1)	10.27 (1)	4.33 (1)	10.59 (1)	17.17 (2)	24.44 (3)	32	I
Cluster 4	62.80 (4)	70.00 (4)	46.79 (2)	36.69 (6)	66.43 (2)	119.6 (4)	1.45 (7)	4.85 (6)	2.00 (7)	1.77 (7)	14.78 (3)	33.93 (1)	53	III
Cluster 5	65.50 (3)	75.00 (3)	44.73 (6)	42.30 (2)	39.11 (8)	126.5 (3)	1.86 (3)	3.94 (7)	3.58 (2)	1.80 (6)	13.49 (5)	19.73 (5)	53	III
Cluster 6	69.00 (2)	80.00 (2)	33.38 (8)	32.13 (8)	42.21 (6)	127.67 (2)	1.67 (5)	6.08 (5)	2.28 (6)	1.90 (5)	10.44 (8)	28.72 (2)	59	V
Cluster 7	40.63 (8)	57.38 (7)	48.08 (1)	43.84 (1)	41.72 (7)	101.25 (8)	1.84 (4)	7.40 (3)	2.85 (4)	5.77 (3)	12.87 (7)	18.15 (8)	61	VI
Cluster 8	82 (1)	96 (1)	43.2 (7)	36.06 (7)	45.33 (5)	149 (1)	1 (8)	3 (8)	2 (7)	0.64 (8)	13.75 (6)	18.43 (7)	66	VII

Bold values in bracket indicates scores

IFF = Initiation of first flower, FPF = Fifty per cent flowering, PH = Plant height, DM = Days to maturity, PB = Primary branches PPP = Pods per plant, SPP= Seeds per pod, YPP = Yield per plant, 100 SW = 100 seed weight, SP = Seed protein

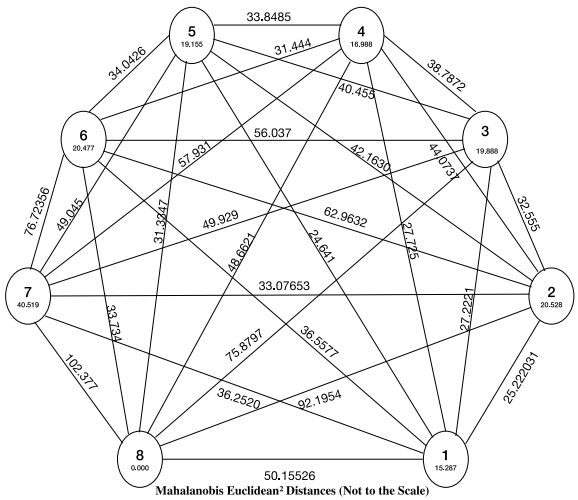

Fig. 1 Intra and inter-cluster distances for the seven groups of 160 field pea genotypes.

Table 5. Per cent contribution of characters towards genetic divergence in field pea genotypes.

Character	Contribution (%)
Initiation of first flower	28.41
Fifty per cent flowering	18.47
Seed protein	15.34
Days to Maturity	11.93
Yield per plant	6.53
100 seed weight	5.97
Seeds per pod	4.55
Plant height	3.98
Primary branches	2.27
Pods per plant	1.99
SPAD 45	0.29
SPAD 75	0.27

pods per plant (10.27), seeds per pod (4.33) and yield per plant (10.59) were found to be grouped in Cluster III, whereas genotypes with short plant height were grouped in Cluster V (36.69 cm). Cluster VIII, along with Cluster IV, had minimum mean values for primary branches (1), pods per plant (3) and seeds per pod (2), while Cluster II and VI contained bold and small seeded genotypes with mean 100 seed weight of 18.31g and 10.44g, respectively. Cluster mean for seed protein was highest for Cluster IV (33.93%), whereas it was lowest for Cluster VII (18.15%).

Based on the cluster means it was noticed that the genotypes superior for yield and most of the other yield attributing traits are grouped in Cluster III and hence, while choosing the genotypes for further use in crop breeding programme one may find useful genotypes in Cluster III. Similar studies on genetic diversity were taken up by Sureja and Sharma (2000), Singh *et al.* (2003), Tiwari *et al.* (2004), Gupta and Singh (2006), Shrivastava *et al.* (2012) and Parihar *et al.* (2014). In most of the studies, it was opined that clustering of the genotypes helps to decipher the genotypes based on genetic diversity and guides in choosing genotypes either for hybridisation to create genetic variability or to use as donors.

Conclusion

In the current study, it was noted that sufficient amount of variation was present in the germplasm lines and in them most contrasting were the first four genotypes of the Cluster VII EC33866, EC598583, IC291544 and IC291553 along with EC598897 genotype of Cluster VIII. Cluster VII had genotypes which are early and low yielding, while Cluster III had high yielding late maturing genotypes indicating cross between genotypes of the Cluster VII and III will be quite no effect in further breeding programme.

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