Biological Forum – An International Journal **14(3): 911-915(2022)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Genetic Diversity Study among Garden Pea (*Pisum sativum* var. *hortense* L.) Genotypes

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(Received 20 June 2022, Accepted 02 August, 2022)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: Pea (*Pisum sativum* var. *hortense* L.), is leguminous vegetable crop belongs to the family leguminosae with a diploid chromosome number 2n=14 and it is grown as a garden and field crop throughout the temperate regions of the world. China is the major pea producing country followed by India and USA. Although, it is cultivated in different regions of the country, but the average pod yield is quite low in Bihar when compared with National average (7.5 t/ha). The plant breeders are always interested to know the genetic divergence among the varieties available due to reasons that crosses involving genetically diverse parents are likely to produce high heterotic effect and they produce wide spectrum of variability. Hence the investigation was carried out to identify high yielding genotypes for Bihar condition. A total of 28 garden pea (*Pisum sativum* var. *hortense* L.) genotypes were evaluated to study the genetic diversity for the characters under study. The genotypes were grown in plots using Randomized Complete Block Design (RCBD) at Experimental farm of the Department of Horticulture (Vegetable and Floriculture), Bihar Agricultural College, BAU, Sabour, Bhagalpur, Bihar during 2018-19. The analysis of variance shown that mean sums of squares due to genotypes were significant for all the parameters. The multivariate analysis revealed that genotypes were arranged in 9 clusters with maximum number of genotypes in cluster I (15). Protein content contributed maximum towards total genetic divergence. The inter-cluster distance ranged from 118.51-3590.62. The highest intra-cluster distance was exhibited by cluster I (324.27). The maximum inter-cluster genetic divergence was recorded between II and IX (3590.62). Crosses involving genotypes of cluster II (Badshah-10, Taj-C3, IC-109696, ADU-12, Same-04 and Arkel) and IX (Nirali) would expect maximum heterosis and desirable recombinants in the segregating generations of garden pea. Genotypes 'Peas TSX-10', 'Punjab-89', 'Badshah-10', 'Haze-02' and 'VM-10' were observed to be promising on the basis of pod characters and yield.

Keywords: Diversity, garden pea, yield, heterosis, genetic divergence.

INTRODUCTION

Garden pea (*Pisum sativum var. hortense* L.), belongs to family leguminosae (Fabaceae), and is extensively grown and popular vegetable crop. It is the second most important food legume worldwide after *Phaseolus vulgaris* (Taran *et al*., 2005). It is a rich source of protein, amino acids and carbohydrates. Peas are highly nutritive and are rich source of digestible proteins (7%), along with carbohydrates and minerals. It is used as a fresh vegetable or in soup, canned, processed or dehydrated. Worldwide garden pea occupies an area of 2.66 million hectares, production of 20.67 million tonnes with a productivity of 7.75 t/ha. In India, area of 0.053 million hectares, production 5.345 million tonnes with a productivity of 10.08 t/ha. In Bihar, it occupies an area 10,510 ha with a production of 66,360 tonnes and the productivity is 6.31 t/ha (Anonymous, 2017). Although, it is cultivated in different regions of the country and is one of the preferred winter vegetables, but the average green pod yield is quite low in Bihar (6.31t/ha) when compared with National (10.08t/ha) and world average (7.5 t/ha). Hence the investigation was carried out to identify high yielding genotypes for Bihar condition. The variability between different cultivars of a crop species is known as genetic diversity. Variability differs from diversity in such a way that variability shows observable phenotypic differences whereas diversity may or may not having observable phenotypic differences, latter may or may not have such an expression. The method of surveying hereditary difference is the D^2 measurement proposed by Mahalanobis (1936). In this method, forces of differentiation at two levels (intra and inter cluster levels) are screened out, and thus play an effective part in the selection of genetically divergent parents for utilization in any hybridization programme (Singh 1983). Keeping these facts in view, the present investigation was carried out with the objective to analyse genetic diversity among the genotypes of garden pea.

MATERIALS AND METHODS

The experimental material for the present study comprised of 28 genotypes of vegetable pea (*Pisum sativum* var. *hortense* L.). These genotypes were evaluated during *rabi* season at the Experimental farm of the Department of Horticulture (Vegetable and Floriculture), Bihar Agricultural College, BAU, Sabour, Bhagalpur, Bihar during 2018-19. The experiment was laid out in complete randomized block design with three replications. The pea seeds were sown at a spacing of 30 cm x 10 cm during the first week of October. Recommended package of practices were followed for healthy growth of the crop. The observations were recorded on randomly taken five plants of each genotype in each replication followed by computing their means for the horticultural and quality traits. The data were statistically analysed as per the standard procedure for analysis of variance (Panse and Sukhatme 1954). Using D^2 values, different genotypes were grouped into various clusters following Tocher's method as suggested by Rao (1952).

RESULT AND DISCUSSION

The analysis of variance shown that mean sum of squares due to genotypes were significant for all the growth parameters, yield contributing traits, and quality characters, indicating the presence of sufficient genetic variability in the genotypes.

On the basis of D^2 values, 28 genotypes of garden pea were arranged into nine clusters following Tocher's procedure (Rao, 1952) and also represented in dendrogram (Fig. 1). Among different clusters, cluster I was the largest one. Singh and Mishra (2008); Katkani *et al.* (2022) also reported cluster I as the largest one. Out of the 9 clusters of 28 genotypes, cluster I comprised of maximum 15 genotypes (VM-10, Peas TSX-10, EC-507771, Pusa Prabhat, IC-552770, Muze-02, EC-412882, Azad P3, IC-269571, AP-3, VM-12, P-3771, Muze-01, P-3824 and Buxe-03) followed by cluster II with 6 genotypes (Badshah-10, Taj-C3, IC-109696, ADU-12, Same-04 and Arkel) and the remaining clusters namely III (EC-598559), IV (Punjab -89), V (NBR-Ruchi), VI (EC-269571), VII (VM-11), VIII (Haze-02), IX (Nirali) were monogenotypic *i.e.*, containing one genotype (Table 1). Different clustering patterns in garden pea were also obtained by earlier workers Siddika *et al.* (2014), Georgieva *et al.* (2016); Katkani *et al.* (2022); Singh and Mishra (2008); Ahmed *et al.* (2021).

The average intra-cluster distance ranged from 0 to 324.27 with the highest in cluster I (324.27) followed by cluster II (239.4). The clusters III, IV, V, VI, VII, VIII and IX were constituted by a single genotype each and hence, their intra-cluster distance was zero. The inter-cluster distance ranged from 118.51-3590.62. The maximum inter-cluster genetic divergence was observed between clusters II and IX (3590.62) followed by clusters III and clusters IX (2542.12), clusters II and VII (2193.85) and clusters II and VI (1902.16) (Table 2). This clearly suggests the presence of sufficient amount of genetic diversity among the garden pea genotypes. Since the intra-cluster distance was low, the chances of getting good recombinants by hybridization between parents within cluster would be low. Therefore, it is necessary to attempt hybridization between genotypes falling under different clusters based on inter-cluster distance. A wide range of inter-cluster genetic distance among the different clusters of pea genotypes have also been reported by Singh *et al.* (2008); Georgieva *et al.* (2016); Khan *et al.* (2017); Muthuselvi and Shanthi (2013); Kumar and Kumar (2016) also reported. Maximum number of transgressive segregants could be obtained in a hybridization programme involving genotypes of cluster II and IX as parents.

Cluster means for different traits showed substantial differences among the clusters for each trait (Table 3). The cluster IV superior for lower node number at which at which first flower appeared, seeds per pod and shelling (%). Cluster V found superior for early maturity manifested by days to first picking and also for pod length and high TSS. Cluster VI Showed maximum mean values for number of primary branches. Cluster VII exhibited highest mean values for five traits namely days to first flower, days to 50% flowering, minimum internodal length, ascorbic acid and total sugar, whereas cluster VIII for maximum plant height, pods per plant and pod yield per plant. Cluster IX showed maximum mean values for nodes per plant and protein. These findings are in accordance with Brahmaiah *et al.* (2014). The contribution of individual characters to divergence has been worked out in terms of number of times it appeared first (Table 4). Protein (38.62%) contributed maximum towards genetic divergence followed by ascorbic acid (38.10%), total sugar (12.17%) and no. of primary branches (3.97%). Variable contribution of different plant growth and yield characters to genetic distance have also been reported by Georgieva *et al.* (2016); Gupta *et al.* (2017) in garden pea.

Table 1: Cluster compositions in garden pea following multivariate analysis.

Cluster number	No. of genotypes	Genotypes
1	15	VM-10, Peas TSX-10, EC-507771, Pusa Prabhat, IC-552770, Muze-02, EC-412882, Azad P3, EC-269571, AP-3, VM-12, P-3771, Muze-01, P-3824, Buxe-03
2	6	Badshah-10, Taj-C3, IC-109696, ADU-12, Same-04, Arkel
3	1	EC-598559
4	1	Punjab -89
5	1	NBR-Ruchi
6	1	EC-269571
7	1	VM-11
8	1	Haze- 02
9	1	Nirali

Table 2: Average intra and inter cluster distances in garden pea.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	324.27	786.6	718.41	561.68	580.54	751.21	1083.52	755.14	1587.37
II		239.4	977.65	1434.28	1450.25	1902.16	2193.85	1794.37	3590.62
III			0	1138.31	1226.65	1376.93	1422.31	1596.33	2542.12
IV				0	118.51	150.2	211.67	537.39	688.61
V					0	251.81	264.89	630.19	729.45
VI						0	271.08	451.38	520.16
VII							0	1022.97	637.93
VIII								0	815.08
IX									0

Table 3: Cluster means for different characters in garden pea.

	I	II	III	IV	V	VI	VII	VIII	IX	Mean	Max.	Min.
Growth parameters												
Days to first flower	60.52	44.29	62.60	62.60	50.67	61.73	41.53	64.60	64.87	57.05	64.87	41.53
Days to 50% flowering	61.82	52.39	70.00	60.00	58.67	74.00	47.67	75.33	72.00	63.54	75.33	47.67
First flower node	8.08	6.50	9.40	4.77	9.20	11.00	5.53	12.60	13.27	8.93	13.27	4.77
Days to first picking	87.63	82.82	80.18	86.26	74.90	93.62	85.85	93.55	87.74	85.84	93.62	74.90
No. of primary branches	2.67	2.34	3.00	2.42	1.47	6.27	2.20	2.47	1.40	2.69	6.27	1.40
Internodal length (cm)	3.38	3.68	2.88	2.77	3.88	3.37	2.62	7.86	2.88	3.70	7.86	2.62
Nodes / plant	24.00	25.60	28.70	29.01	19.74	26.33	24.79	23.24	30.09	25.72	30.09	19.74
Plant height (cm)	64.10	76.27	72.00	67.63	58.47	73.26	58.73	150.80	87.00	78.70	150.80	58.47
Yield contributing traits												
Pod length (cm)	8.56	7.93	8.25	9.65	9.73	8.22	8.57	8.14	9.54	8.73	9.73	7.93
Seeds / pod	5.67	5.83	5.69	7.56	7.00	5.27	5.26	6.02	6.14	6.05	7.56	5.26
Shelling (%)	47.88	45.30	47.78	58.17	43.82	47.42	36.13	51.91	46.51	47.21	58.17	36.13
Pods / plant	18.60	19.10	15.68	20.56	13.26	14.42	12.09	28.71	15.07	17.50	28.71	12.09
No. of pickings	3.07	3.17	4.00	3.00	2.67	3.67	2.33	3.67	2.33	3.10	4.00	2.33
Pod yield / plant (g)	82.36	73.76	57.31	101.76	66.94	77.20	74.43	108.56	86.30	80.96	108.56	57.31
Quality characters												
TSS (°Brix)	13.99	13.36	15.60	13.70	19.20	14.97	15.60	7.50	11.50	13.94	19.20	7.50
Ascorbic acid (mg/100g)	16.91	13.52	13.80	26.56	24.04	27.88	30.04	24.26	30.09	23.01	30.04	13.52
Total sugars (%)	4.23	3.81	10.94	4.90	4.36	4.74	7.40	2.94	4.82	5.35	7.40	2.94
Protein (%)	30.83	25.90	31.17	30.19	30.82	30.91	30.87	32.43	36.01	31.01	36.01	25.90

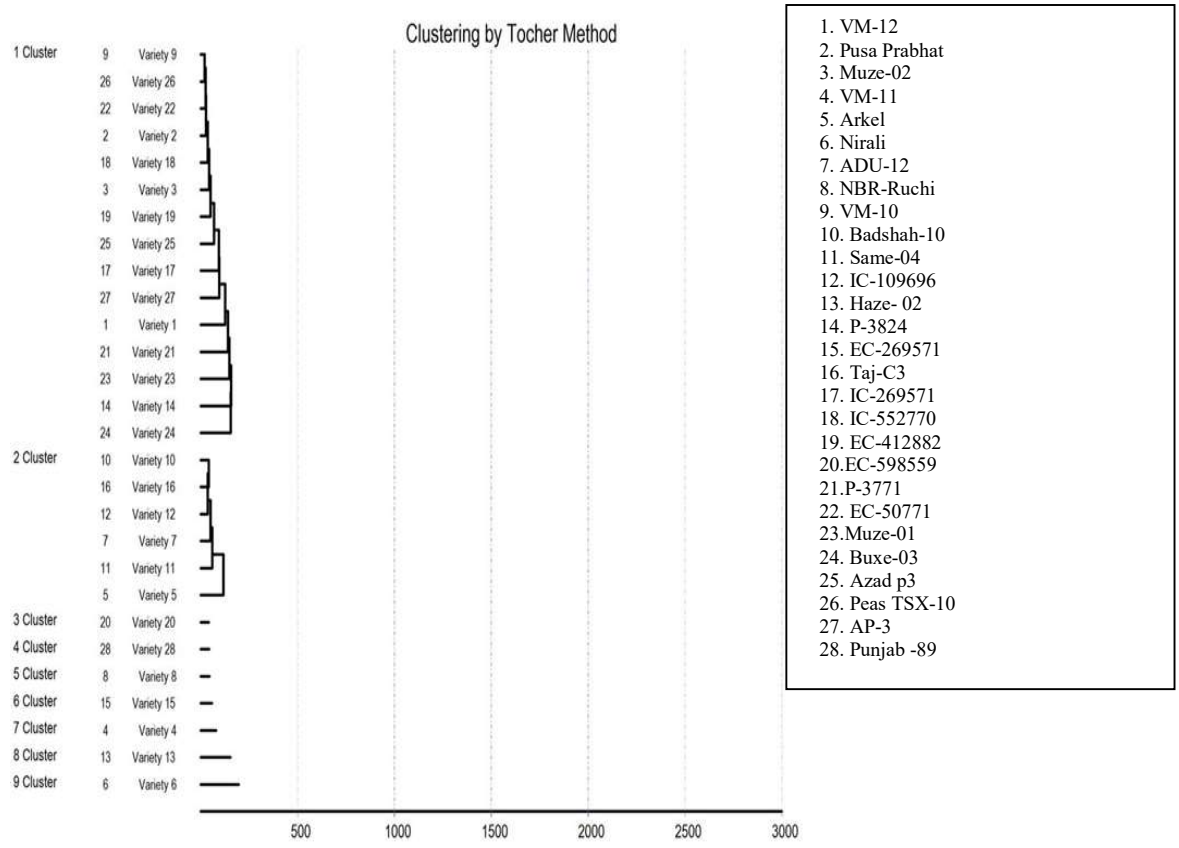

Fig. 1. Dendrogram showing grouping of 28 garden pea genotypes generated using D2 cluster analysis (Tocher's method).

Table 4: Contribution of various traits towards genetic divergence in garden pea.

Characters	Times ranked 1st	Contribution (%)
Growth parameters		
Days to first flower	0.00	0.00*
Days to 50% flowering	0.00	0.00*
First flower node	0.00	0.00*
Days to first picking	9.00	2.38
No. of primary branches	15.00	3.97
Internodal length (cm)	0.00	0.00*
Nodes per plant	0.00	0.00*
Plant height (cm)	13.00	3.44
yield contributing traits		
Pod length (cm)	1.00	0.26
Seeds per pod	0.00	0.00*
Shelling (%)	0.00	0.00*
Pods per plant	0.00	0.00*
No. of pickings	0.00	0.00*
Pod yield per plant (g)	0.00	0.00
Quality characters		
TSS (°Brix)	4.00	1.06
Ascorbic acid (mg/100g)	144.00	38.10
Total sugars (%)	46.00	12.17
Protein (%)	146.00	38.62**

CONCLUSION

The multivariate analysis revealed considerable genetic diversity present in the 28 genotypes studied. Hybridization between genotypes of cluster I such as 'VM-10', 'Peas TSX-10', 'EC-507771', 'Pusa Prabhat', 'IC-552770', 'Muze-02', 'EC-412882', 'Azad P-3', 'EC-269571', 'AP-3', 'VM-12', 'P-3771', 'Muze-01', 'P-3824', 'Buxe-03' and 'Nirali' of cluster V, could get more recombinants in the segregating generations.

FUTURE SCOPE

The genetic diversity analysis in garden pea can further be utilized in heterosis breeding, transgressive breeding and interogression of alien genes for specific traits. The use of molecular markers for diversity analysis serves as an effective tool to discriminate between lines for their use in future breeding programme.

Acknowledgement. The authors are gratefully thankful to Mr. Alok Kumar, who provided garden pea genotypes for research work.
Conflict of interest. None.

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How to cite this article: Mamatha R.M., Ramesh Kumar Sharma, Ajay Bhardwaj and Randhir Kumar (2022). Genetic Diversity Study among Garden Pea (*Pisum sativum* var. *hortense* L.) Genotypes. *Biological Forum – An International Journal*, *14*(3): 911-915.