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Genetic divergence study in pea

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Abstract
The thirty genotypes/varieties of pea were studied out during *Rabi* 2018-19 at Instructional-cum-Research Farm of Horticulture Section, Rajarshee Chhatrapati Shahu Maharaj College of Agriculture, Kolhapur. The experiment was laid in a Randomized Complete Block Design with two replications for plant height at maturity, days to 50 percent flowering, average no. of branches per plant, weight of dry matter, number of pods per plant, length of pod, width of pod, number of seeds per pod, seed yield per plant, shelling percentage, TSS, moisture content, tenderness, total mineral content and pod yield per plant. Analysis of variance showed significant differences among all the genotypes under study. The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters indicating the effect of environment on these characters.

Keywords: Pea, genetic variability, divergence, d^2 analysis, cluster means

Introduction

Pea (*Pisum sativum* L.) belongs to family leguminosae having chromosome number $2n=2x=14$. It is a self-pollinated crop. Pea is important legume vegetable grown in India as a winter vegetable in the plains of north and as a summer vegetable in the hills of India. Pea is originated in South West Asia. It is one of the most important vegetable as well as pulse crop in India.

It is highly nutritious vegetable grown throughout the world. It contains more proteins, carbohydrates, vitamins, and minerals like calcium and phosphorus. Pea is an excellent source of protein (27.8%), carbohydrates (42.65%), vitamins, minerals, dietary fibers, and antioxidant compounds. Pea can supply the required nutrients to various age groups owing to their high protein content and favourable composition of amino acids & low trypsin inhibitor levels (Aysh, 2014) [2].

Pea is cultivated in about 554 thousand hectare area in the world among the rabi pulse crop. Field pea is potentially the highest yielder. Uttar Pradesh ranks first in area 221 thousand hectare and production 2511.38 thousand metric tonnes. Madhya Pradesh stands second position in area 94.99 thousand hectare followed by Punjab 37.62 thousand hectare respectively. Highest productivity is recorded in Jharkhand 22.07 metric tonnes per hectare followed by Tamil Nadu 15.90 metric tonnes per hectare and Jammu and Kashmir 12.93 metric tonnes per hectare. (Anon, 2018) [1].

The plant is a short lived, herbaceous, annual which climbs by leaflet tendrils. The cultivars may be dwarf, semi dwarf or tall. The root system is not strongly developed except tap root. The stem is slender, usually single and upright in growth. The leaves are pinnate with upto 3 pairs of leaflet. The rachis terminates in a simple and branched tendril. There are large stipules at the base of leaf. The plant may be single stemmed or many axillary stems may be originate at the cotyledonary node or any superior node, specially if the apical growing point is destroyed, leaflets of a pair are opposite or slightly alternate. The inflorescence is raceme arising from the axils of leaf. The flowers are soliatary axillary or upto 3 flowers per receme; bracts very small, calyx oblique, lobes unequal, corolla white, pink or purple; keel short, incurved, obtuse, stamens diadelphous, filaments broad, anthers uniform. Pods swollen or compressed, straight or curved on short stalk. Seeds are angular or globose, smooth or wrinkled, green, grey or brown. (Hari Har Ram, 2006) [8].

Materials and Methods

A total of 30 genotypes/varieties of pea collected for divergence study. The present investigations were carried out in 2018-19 at Instructional-cum-Research Farm of Horticulture

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Section, Rajarshee Chhatrapati Shahu Maharaj College of Agriculture, Kolhapur in RBD method with two replications. Each plot comprised one row of 1.5 m length spaced 15 cm with plant to plant and row to row was 30 cm. All the recommended standard cultural practices were followed under irrigated conditions as and when needed. The observations were recorded on five random competitive plants per replication for each genotype of fifteen important characters i.e. plant height at maturity, days to 50 percent flowering, average no. of branches per plant, weight of dry matter, number of pods per plant, length of pod, width of pod, number of seeds per pod, seed yield per plant, shelling percentage, TSS, moisture content, tenderness, total mineral content and pod yield per plant. The Mahalanobis D^2 (1936) statistical method was used to quantify genetic diversity among the genotypes. The D^2 values were used to classify the entire germplasm into distinct clusters, which was done following to Tocher's method [Rao (1952)] [15].

Results and Discussion
The analysis of variance revealed significant differences among the genotypes/varieties for all the characters studied indicating presence of considerable amount of genetic variability for all the characters. The computation from co-variance matrix gave non-hierarchical clustering based on Mahalanobis D^2 values among 30 genotypes/varieties and grouped them into five clusters. The clustering pattern of 30 genotypes of pea indicated that the genotypes/varieties included in the investigation could be grouped into five clusters. The cluster I was largest with twenty two genotypes/varieties (JP-15, T-61, Ballop Allony, GE-477, P-108, Forestrier, PLV, Phule Priya, Muller, IC-2990, Linken HP, PRP-4, PH-1, Palnu Green, IC-25-61, PRS-4, NBVP, Padali, T-163, Main Crop, P-101, Selection-35) followed by cluster II with five genotypes/varieties (PARL-4, KTP-4, Continental, VP-8902, Rachan), cluster III, IV and I having only one genotype each (G-19, IC-80-45 and PB-29A respectively). Group constellation of pea genotypes/varieties through genetic divergence has also been reported by Singh *et al.* (2002) [13] in pea, Kosev (2015) [10] in field pea, Chaudhary *et al.* (2016) [4] in pigeon pea, Gupta *et al.* (2017) [7] in pea and Bijalwan *et al.* (2018) [3] in garden pea.

The cluster II earned the highest cluster mean values for plant height at maturity (88.77 cm), average no. of branches/plant (5.94), no. of pods/plant (52.84), pod width (1.24 cm), no. of seeds/pod (5.50), seed yield/plant (31.56 g), Shelling % (57.13%), TSS (17.98^{0}B), moisture content (79.21%), and pod yield/plant (550.20 g).

Table 1: Clustering pattern of 30 pea genotypes by Tocher's method

Cluster Number	Total number of genotypes included	Genotype number
I	22	JP-15, T-61, Ballop Allony, GE-477, P-108, Forestrier, PLV, Phule Priya, Muller, IC-2990, Linken HP, PRP-4, PH-1, Palnu Green, IC-25-61, PRS-4, NBVP, Padali, T-163, Main Crop, P-101, Selection-35
II	5	PARL-4, KTP-4, Continental, VP-8902, Rachan
III	1	G-19
IV	1	IC-80-45
V	1	PB-29A

Cluster V showed earliness in relation to lowest values for days to 50% flowering (30.80 DAS) and having lowest weight of dry matter (5.06 g). Cluster IV had highest values for length of pod (11.27 cm) (Table 2). In this way, it was evident from this parameter that cluster II had highest values for maximum number of pod yield contributing characters. Variable cluster means for different plant growth and pod yield characters have also been reported by Chaudhary *et al.* (2016) [4] in pigeon pea, Georgieva *et al.* (2016) [6] and Gupta *et al.* (2017) [7] in garden pea.

Table 2: Cluster means for 15 characters of 30 pea genotypes

Sr. No.	Characters	Cluster means				
		I	II	III	IV	V
1	Plant Height at maturity	74.74	88.77	78.24	80.45	69.00
2	Days to 50% Flowering	45.61	46.54	43.90	48.40	30.80
3	Avg. no. of branches/plant	4.12	5.94	4.70	2.60	4.30
4	Weight of dry matter (g)	17.80	17.20	26.91	31.37	5.06
5	No. of pods /plant	35.48	52.84	35.50	33.60	26.80
6	Length of pod (cm)	10.50	10.38	11.10	11.27	11.14
7	Width of pod (cm)	1.07	1.24	1.05	1.08	0.74
8	No. of seeds per pod	4.33	5.50	4.10	4.60	5.10
9	Seed yield per plant	23.69	31.56	24.28	26.33	10.95
10	Shelling %	46.56	57.13	46.34	47.63	45.43
11	TSS	16.52	17.98	12.21	16.79	13.29
12	Moisture content	72.92	79.21	70.95	74.03	68.21
13	Tenderness	1.34	1.95	1.39	1.26	1.20
14	Total mineral content	12.03	12.58	12.83	9.90	9.84
15	Pod yield/plant	215.33	550.20	218.36	180.90	106.72

Inter cluster distance ($\sqrt{D^2}$) values worked out as per Mahalanobis's D^2 statistic indicated that the genotypes included in clusters V and II were genetically divergent in the view of highest inter cluster mean (5.32) followed by clusters III and II (4.61) and clusters V and IV (4.59). Minimum inter-cluster distance was observed between cluster I and cluster I (3.2). Intra-cluster distance is a measure of genetic divergence existing among the genotypes included in the same cluster.

Maximum intra-cluster distance was noted for cluster II (3.36) followed by cluster I (3.2) (Table 3). A wide range of inter-cluster genetic distance among the different clusters of pea genotypes/varieties have also been reported by Singh *et al*. (2002) [13] in pea, Tiwari *et al*. (2004) [14] in pea, Kumar *et al*. (2014) [11] in French bean, Georgieva *et al*. (2016) [6] in pea.

Table 3: Average intra-inter cluster distance ($\sqrt{D^2}$) for 30 pea genotypes

Cluster	I	II	III	IV	V
I	3.2	4.14	3.79	3.82	4.33
II		3.36	4.61	4.53	5.32
III			0.00	3.67	4.39
IV				0.00	4.59
V					0.00

The contribution of different characters to total genetic divergence is important to assess relative importance of the characters to be included in genetic diversity studies. The data on this parameter as depicted in Table 4 indicated that TSS contributed maximum towards genetic divergence (17.47%) followed by shelling percentage (17.01%), weight of dry matter (14.71%), width of pod (14.48%), number of seeds per pod (11.95%), total mineral content (8.28%), pod yield per plant (5.52%), number of pods per plant (5.06%) and length of pod (2.30%).

Table 4: Contribution of different characters to total divergence in pea

Sr. No.	Source	Times ranked 1st	Contribution %
1	Plant height at maturity	0	0.00%
2	Days to 50% flowering	2	0.46%
3	Average no. of branches/plant	3	0.69%
4	Weight of dry matter	64	14.71%
5	No. of pods /plant	22	5.06%
6	Length of pod (cm)	10	2.30%
7	Width of pod (cm)	63	14.48%
8	No. of seeds per pod	52	11.95%
9	Seed yield per plant	1	0.23%
10	Shelling percentage	74	17.01%
11	TSS	76	17.47%
12	Moisture content	1	0.23%
13	Tenderness	7	1.61%
14	Total mineral content	36	8.28%
15	Pod yield per plant	24	5.52%

The contribution of other characters to total genetic divergence was lower. Therefore, above traits should necessarily be included in genetic divergence studies in garden pea. The Variable contribution of different characters to genetic divergence have also been reported by Singh *et al*. (2002) [13] in pea, Tiwari *et al*. (2004) [14] in pea, Kumar *et al*. (2014) [11] in french bean, Georgieva *et al*. (2016) [6] in garden pea. It has been proved from the earlier studies that genetically distant parents are able to exert high heterosis in the progenies (Falconer, 1960) [5]. Therefore, in the view of highest inter cluster genetic distance ($\sqrt{D^2}$) between cluster V and cluster II (5.32) and maximum cluster means for most of desirable traits for pod yield in these clusters, cross combinations *viz*., PB-29A×PARL-4, PB-29A× KTP-4, PB-29A× Continental, PB-29A×VP-8902, PB-29A×Rachan and PARL-4× PRS-4 are recommended for developing progeny with high yield and desirable traits in garden pea.

Conclusion
The genotypes/varieties were grouped into 5 clusters. Cluster I was largest followed by cluster II, cluster III, cluster IV and cluster V. The maximum inter cluster distance was found between cluster V and cluster II (5.32) and minimum value was found between cluster I and cluster I (3.2). The maximum intra-cluster distance was noted for cluster II (3.36). The character TSS contributed maximum towards divergence. So, the cross combinations *viz*., PB-29A×PARL-4, PB-29A× KTP-4, PB-29A× Continental, PB-29A×VP-8902, PB-29A×Rachan and PARL-4× PRS-4 are recommended for developing progeny with high vigour and desirable traits in garden pea.

Conflict of Interest
The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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