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GENETIC DIVERSITY AND CHARACTER ASSOCIATION STUDIES IN GARDEN PEA (*PISUM SATIVUM* L.) GENOTYPES UNDER VINDHYANCHAL PLATEAU OF M.P., INDIA

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ABSTRACT

The experiment was conducted with 22 germplasm and laid out in randomized block design with three replications. The path revealed that days to 50% flowering, days maturity, plant height at harvest, No. of primary branches at harvest, No. of nodes at harvest, root nodules at 60 days, chlorophyll content (SPAD), days to picking 1, days to picking 2, No. of pods per plant, pods length (cm) pod yield (g/plant), shelling (%), pod length (cm), No. of primary branches at 40 days, number of seed, average pod weight (g), No. of seeds per pod had high positive direct effect on pod yield (q/ha) in all the environment under consideration, where as No. of leaves per plant at harvest, dry of 100 seed (g) and shelling (%) showed negative direct effect on pod yield (q/ha) in EI and EII of garden pea genotypes. The contribution of individual traits towards the total divergence was found maximum for pod yield q/ha, No. of leaves at 60 days, days to picking 2, pod length (cm), No. of seeds per pod and dry of 100 seed (g) in E-I and E-II. On the basis of D^2 values, 22 genotypes were grouped into 4 clusters. The cluster III showed maximum intra cluster D^2 value ($D^2 = 23.20$) followed by cluster I ($D^2 = 20.56$) and cluster II ($D^2 = 19.97$), whereas cluster IV showed zero value for intra cluster distance. The highest inter cluster divergence was observed between genotypes of cluster II and IV (70.57), followed by cluster III and cluster IV (57.66), cluster II and cluster III (55.19), cluster I and cluster II (52.44), cluster I and cluster III (36.85). The cluster distance was lowest between clusters I (20.56) and cluster IV (36.56).

Key words : Analysis of variance, Germplasm, Path coefficient, Genetic diversity, Correlation coefficient, Ideotype, Chlorophyll content.

Introduction

Garden pea (*Pisum sativum* L.) is an important vegetable and pulse crop grown throughout the world. It belongs to the family Leguminosae and has chromosome number of $2n = (2x) = 14$. It is one of the major, highly valued and extensively cultivated legume crops throughout the world. Globally, it is grown in approximately 5.5 million hectares per year and ranks as the third most important grain legume crop after soybean and common bean (Rana

et al., 2017). Garden pea also holds a prominent place among vegetables due to its high nutritive value, particularly proteins and other health-building substances like carbohydrates, vitamin A, vitamin C, calcium and phosphorus (Sharma, 2010). It contains a good proportion of essential amino acids particularly lysine (Ghobary, 2010) and is the cheapest source of protein in diet. It is mainly cultivated for its fresh green seeds (garden pea), tender green pods (snow peas), dried seeds (pulse) and

foliage (Duke, 1981). The seeds and immature pods of green peas contain the most vitamins. The pea is a good predecessor to other crops as it enriches the soil with the nodule bacteria which live in its roots and it fixes nitrogen which live in its roots and it fixes nitrogen which becomes available to other plants (Rudnicki and, 2002). Yield is a quantitative character and is associated with component characters. Hence, yield and its contributing traits are affected by the environment. Correlation coefficient analysis measures the mutual relationship between various characters and determines the component characters on which selection can be made for improvement in yield. Assessing the direct and indirect effects of each component towards yield through path coefficient analysis would help in identifying the reliable characters contributing to yield. A genetic divergence is also an important approach to assess the variability patterns of specific traits in whole germplasm and to select desirable parents for improvement of a specific trait through hybridization where selection is not responsive. Grouping of genotypes based on D^2 analysis will be useful in choosing suitable parental lines for heterosis breeding which in turn help the farmers to choose elite varieties. A reliable technique to estimate the genetic divergence available in a population is D^2 statistics proposed by (Mahalanobis, 1936).

Materials and Methods

The experiment was carried out in Randomized Block Design with three replications and experiment was conducted in the year 2021-22. The experiment was conducted with 22 germplasm. Data were recorded on days to 50% flowering, days to maturity, plant height (cm) at 20, 40, 60 days and at harvest, No. primary branches at 20, 40, 60 days and at harvest, No. of leaves per plant at 20, 40, 60 days and at harvest, No. of nodes at 20, 40, 60 days and at harvest, chlorophyll content, days to picking 1, days to picking 2, No. of pods per plant, pod length (cm), average pod weight (g), number of seeds per pod, dry of 100 seed (g), shelling (%), pod yield (g/plant) and pod yield q/ha. The mean values were subjected to statistical analysis to work out ANOVA for all the characters, as suggested by Panse and Sukhatme (1957). The path-coefficient was estimated using simultaneous equation and the equation showed a basic relationship between correlation coefficient and path-coefficient.

$$A = B \times C$$

The solution for the vector “C” may be obtained by multiplying both side by inverse of “B” matrix *i.e.*, $B^{-1} A = C$. After calculation of values of path-coefficient *i.e.*, “C” vector, it is possible to obtain path values for residual

(R). Residual effect was calculated using formula referred from Singh and Chaudhary (2005).

$$R = \sqrt{1 - \sum d_i^2} \times r_{ij}$$

Where,

d_i = direct effect of the i^{th} character

r_{ij} = correlation coefficient of i^{th} character with j^{th} character

Direct and indirect effects of different characters on flower yield were calculated at genotypic and phenotypic level. The Mahalanobis's D^2 statistics (1928) was used for assessing the genetic divergence between populations. The generalized distance between any two populations is defined as $D^2P = b_1d_1 + b_2d_2 + \dots + b_p d_p$

A resource for group distance based on multiple characters with $X_1, X_2, X_3, \dots, X_p$ as the multiple measurements available on each individual as $x^1_1, x^2_2, \dots, x^1_p, x^2_p$, respectively is the difference in the means of two populations. The ‘P’ values are to be estimated that the ratio of variance between the populations to the variance within the populations is maximized. Taking variance and covariance under consideration, the D^2 value may be estimated by this formula.

$$D^2 = \sum w_{ij} \sum (x^1_i - x^2_j) (x^1_i - x^2_j)$$

Where, W_{ij} is the inverse of estimated variance and covariance matrix.

The Average intra cluster distance of formula was used for measuring the intra cluster distance as $\sum Di^2/n$

Where,

$\sum Di^2/n$ is the sum of distance between all possible contributions of the population included in the cluster.

The average inter cluster distance was used the First of all, the distance clusters were measured. The clusters were taken one by one and their distances from other cluster were calculated.

Results and Discussion

Studies on Path coefficient analysis

Data in Table 1 presents the path revealed that days to 50% flowering, days maturity, plant height at harvest, no. primary of branches at harvest, no. of nodes at harvest, Root nodules at 60 days, Chlorophyll content (SPAD), Days to picking 1, Days to picking 2, no. of pods per plant, pods length (cm) Pod yield (g/plant), Shelling %, Pod length (cm), no. primary branches at 40 days, number of seed, average pod weight (g) no. of seeds per pod had high positive direct effect on pod yield (q/ha) in all the environment under consideration, where as no. of leaves per plant at harvest, dry of 100 seed (g) and shelling %

Table 1 : Path coefficient analysis for yield and its component characters in garden pea.

S. no.	Characters	Days to 50% flowering	Days to maturity	Plant height at harvest	No. of primary branches at harvest	No. of leaves at harvest	Root nodules at 60 days	Chloro-phyll content	Days to picking 1	Days to picking 2	No. of pods per plant	Pod length (cm)	Average pod weight (g)	Number of seeds per pod	Dry of 100 seed (g)	Shelling %	Pod yield (g/plant)	Pod yield q/ha
1	Days to 50% flowering	0.9670	0.7266	0.0577	0.0056	0.2883	-0.0519	0.2915	0.7246	0.8764	0.3079	0.1496	0.2493	0.0722	-0.0680	0.1580	0.2199	0.3686
2	Days to maturity	0.2977	0.3962	0.0601	-0.0560	0.1190	-0.0163	0.2561	0.1647	0.2564	0.1553	0.0862	0.1346	0.0033	-0.1505	-0.3918	0.1547	0.5539
3	Plant height at harvest	0.3479	0.8848	0.8303	0.7993	-0.0384	0.4084	0.2112	-0.6893	0.0349	0.2539	-0.5540	-0.2948	-0.8908	-0.2233	-0.0251	0.7226	0.2280
4	No. primary of branches at harvest	0.0012	0.0693	-0.4033	-0.4900	-0.0555	-0.4914	-0.0209	0.0738	0.0436	-0.1137	0.0403	-0.1023	-0.0538	0.0634	-0.2777	-0.2081	0.2602
5	No. of leaves at harvest	0.4411	0.4444	-0.0097	0.1677	0.4795	-0.1194	-0.0187	0.6445	0.4969	0.0352	-0.0223	0.1301	0.1015	-0.0165	0.0083	0.1653	-0.1463
6	No. of nodes at harvest	0.1040	0.0801	0.0470	0.0604	0.1577	0.0428	0.0653	0.0845	0.1032	0.1491	0.0039	0.1054	-0.0311	-0.0699	0.1511	0.0688	0.1580
7	Root nodules at 60 days	-0.0779	-0.0595	0.0965	0.4545	-0.1170	0.4502	0.4075	-0.2544	-0.0473	0.3740	0.1453	0.4446	0.1998	0.1580	-0.7490	0.5965	0.2570
8	Chlorophyll content	-0.4793	-0.0276	-0.6030	-0.0678	0.0201	-0.4467	-0.5899	-0.2777	-0.6387	-0.5281	-0.3510	-0.2325	0.0900	0.2210	0.6710	-0.4177	0.5569
9	Days to picking 1	-0.9366	-0.5196	0.1478	0.1882	-0.5444	0.2193	-0.2183	-0.2499	-0.1592	-0.2823	-0.6246	-0.3817	-0.4895	-0.3091	0.2517	-0.3706	0.2335
10	Days to picking 2	0.6015	0.4294	0.0040	-0.0591	0.2229	-0.0216	0.2666	0.6155	0.6637	0.2288	0.3316	0.3439	0.2198	0.0680	-0.2664	0.2923	0.4510
11	No. of pods per plant	0.0473	0.0583	0.0575	0.0345	0.0035	0.0383	0.0494	0.0336	0.0513	0.1487	0.0459	0.0717	0.0444	-0.0539	-0.1232	0.0628	0.2198
12	Pod length (cm)	0.2532	0.3559	-0.1555	-0.1346	-0.0247	0.1639	0.3613	0.8178	0.8176	0.5051	0.6366	0.4348	0.2503	0.2953	0.4549	0.4104	0.4412
13	Average pod weight (g)	-0.3640	-0.4797	0.0714	-0.2948	-0.1242	-0.4328	-0.2065	-0.4312	-0.7316	-0.6811	-0.2378	-0.4119	-0.9656	-0.2631	-0.1658	-0.3627	0.2878
14	Number of seeds per pod	-0.0770	-0.0085	0.1575	-0.1132	-0.0707	-0.1420	0.0583	-0.4037	-0.3414	-0.3076	-0.7875	-0.7050	-0.0308	-0.1261	-0.2115	-0.7983	0.1950
15	Dry of 100 seed (g)	0.0358	0.1935	0.0195	0.0660	0.0057	-0.0555	0.0708	-0.1260	-0.0522	0.1847	-0.0919	-0.0949	-0.0623	-0.5094	0.1728	0.0486	-0.5215
16	Shelling %	0.2112	-0.6893	-0.5540	0.7226	-0.0153	0.9268	0.1388	-0.0383	0.0097	0.2124	0.3341	-0.3845	-0.5371	-0.5444	0.7937	-0.2865	-0.0466
17	Pod yield (g/plant)	0.0982	0.1687	0.0535	0.1835	0.0483	0.1777	0.1135	0.1281	0.1903	0.1823	0.3722	0.4169	0.3345	-0.0412	0.0466	0.4320	0.5826

Residual effect: 0.5499

Table 2 : Contribution of different characters toward clustering in garden pea genotypes.

S. no.	Characters	Contribution %	S. No.	Characters	Contribution %
1	days to 50 % flowering	0.87	17	No. of nodes at 60 days	0.00
2	Days to maturity	0.00	18	No. of nodes at harvest	0.00
3	Plant height (cm) at 20 days	0.00	19	Root nodules at 60 days	0.43
4	Plant height(cm)at 40 days	1.30	20	Chlorophyll content	0.43
5	plant height (cm) at 60 days	0.43	21	Days to picking 1	3.90
6	plant height at harvest	0.01	22	Days to picking 2	11.26
7	No. primary branches at 20 days	0.00	23	Length of inter nodes (cm)	3.46
8	No. primary branches at 40 days	0.00	24	No. of pods per plant	9.52
9	No. primary branches at 60 days	0.00	25	Pod length (cm)	6.49
10	No. primary of branches at harvest	0.00	26	Average pod weight (g)	0.00
11	No. of leaves per plant at 20 days	0.00	27	number of seeds per pod	5.19
12	No. of leaves per plant at 40 days	0.00	28	dry of 100 seed (g)	7.79
13	No. of leaves at 60 days	11.04	29	Shelling %	0.65
14	No. of leaves at harvest	1.73	30	Pod yield (g/plant)	3.90
15	No. of nodes at 20 days	0.00	31	pod yield q/ha	31.60
16	No. of nodes at 40 days	0.00			

Table 3 : Inter and intra cluster D² values for different clusters.

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	20.56	52.44	36.85	36.56
Cluster II		19.97	55.19	70.57
Cluster III			23.20	57.66
Cluster IV				0.00

Studies on genetic diversity analysis

The present study was also aimed at analyzing the genetic divergence among the 22 genotypes of Garden pea to identify the superior and divergent parental genotypes for formulating the crossing program.

The characters which showed more (%) contribution towards the divergence should be considered prime during

Table 4 : Distribution of garden pea genotypes in different clusters by Tocher Method.

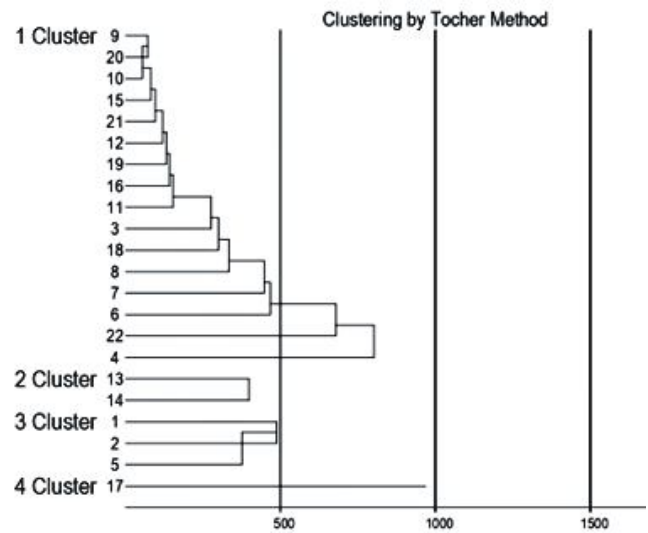
Cluster No.	Number of genotypes	Name of the Genotypes
I	16	Mater Agetha, Pusa Praghati, Kashi Nandini, sehore local Jamoniya local, Hirapur local, Sekhdakhedi local, thuna local 1, thuna local 2, Alampura local, ichhawar local, Pachama local, Doraha local, Kakad kheda local, Sadan khedi local, Fanda Local
II	2	Murdi local, Mungaoli local
III	3	Punjab 89, Mater Agetha, Arka Priya
IV	1	Raipura local

showed negative direct effect on pod yield (q/ha) in E-I and E-II of garden pea genotypes. Thus the direct selection of lines based on these traits would be rewarding for yield improvement. These findings are in accordance with the results of Kumar *et al.* (2015) and Lal *et al.* (2018) for pod yield (g/plant), days to 50% flowering, Singh *et al.* (2019) for days to maturity, days to picking 2, Srivastava *et al.* (2012) for average pod weight (g), pod length (cm), Kumawat *et al.* (2018) for shelling %, root nodules at 60 days, Bijalwan *et al.* (2018) for chlorophyll content, days to picking 1, for no. primary of branches at harvest and pod yield (g/plant) (Katoch *et al.*, 2016).

selection. Contribution of individual traits towards the total divergence was found maximum for pod yield q/ha, No. of leaves at 60 days, days to picking 2, pod length (cm), No. of seeds per pod and dry of 100 seed (g) in E-I and E-II. These traits were responsible for expressing maximum diversity between the clusters. Remaining traits showed low percent of contribution towards divergence in all the environment will not be considered in divergence study. Mahalanobis (D²) statistics is a powerful tool widely used by breeders in quantifying the degree of divergence at genotypic level (Table 2). Genetic diversity within a species provides broad sense genetic base and wide adaptability to a population. It also acts as a general guide

Table 5 : Cluster mean for yield and its component traits of garden pea genotype.

Cluster/ Characters	Days to 50% flowering	Days to maturity	Plant height (cm) at 20 days	Plant height (cm) at 40 days	Plant height (cm) at 60 days	Plant height at harvest	No. of primary branches at 20 days	No. of primary branches at 40 days	No. of primary branches at 60 days	No. of primary branches at harvest	Average pod weight (g)	Number of seeds per pod	Dry weight of 100seed (g)	Shelling %	Pod yield (g/plant)	Pod yield q/ha	No. of nodes at 20 days	No. of nodes at 40 days
Cluster I	49.63	105.00	14.92	38.84	68.43	70.65	1.50	3.46	5.52	7.41	6.86	7.63	16.54	44.8	50.40	54.40	5.17	10.21
Cluster II	48.20	102.67	15.05	38.59	68.34	70.30	1.43	3.43	5.40	7.30	6.95	7.67	16.46	37.9	50.64	57.81	4.37	9.07
Cluster III	56.20	112.78	14.74	38.91	68.84	71.11	1.53	3.47	5.53	7.38	7.19	8.11	16.37	51.7	51.79	60.79	6.04	10.42
Cluster IV	47.93	103.67	11.51	30.30	55.81	60.35	1.00	2.80	4.80	6.67	6.95	8.00	16.43	50.64	50.17	53.75	4.93	10.40

**Fig. 1:** Distribution of garden pea genotypes in different clusters by Tocher method.

in the choice of parents for developing hybrid. Diverse genetic background among parental line provides allelic variations necessary to create favorable new gene combination and the probability of producing unique genotypes increases in proportion to the number of genes for days to first pod picking, Habtamu and Million (2013) for No. of leaves per plant at 40 days, No. of leaves at 60 days, No. of leaves at harvest, No. of nodes at 20 days, No. of nodes at 40 days, No. of nodes at 60 days, No. of nodes at harvest, root nodules at 60 days. The characters which showed more (%) contribution towards the divergence should be considered prime during selection. Contribution of individual traits towards the total divergence was found maximum for pod yield q/ha, Pod yield (g/plant) No. of leaves at 60 days, days to picking 2, pod length (cm), No. of seeds per pod and dry of 100 seed (g). These traits were responsible for expressing maximum diversity between the clusters. Remaining traits showed low percent of contribution towards divergence will not be considered in divergence study.

Based on the genetic distance garden pea genotypes were grouped differently. Genotypes were grouped into 4 clusters of garden pea genotypes. On the basis of D^2 values, 22 genotypes were grouped into 4 clusters. Cluster III showed maximum intra cluster D^2 value ($D^2 = 23.20$) followed by cluster I ($D^2 = 20.56$) and cluster II ($D^2 = 19.97$), whereas cluster IV showed zero value for intra cluster distance. The highest inter cluster divergence was observed between genotypes of cluster II and IV (70.57), followed by cluster III and cluster IV (57.66), cluster II and cluster III (55.19), cluster I and cluster II (52.44), cluster I and cluster III (36.85). Cluster distance was lowest between clusters I (20.56) and cluster IV (36.56).

Clustering pattern of genotypes confirmed the quantum of diversity present in the material under study (Table 3 and Fig. 1). Genotypes *viz.*, Raipura local, I were grouped independently in different clusters. From these nongenotypic clusters, genotypes differ mainly in phenological traits *viz.*, No. of leaves at 60 days, No. of nodes at 40 days, pod length (cm), average pod weight (g) and Pod yield q/ha. Early maturing genotypes of this study may be utilized in breeding program for introgression of earliness in different cultivars. Short duration cultivars fit in crop rotation and tolerant to pest due to escape/avoid its attack in plant reproductive phase due to less days taken for its maturity.

Intra cluster distance was recorded maximum for cluster III followed by cluster I and cluster II, whereas cluster IV showed zero value. Ascending order of magnitude in intra cluster divergence indicated the existence of more diversity between genotypes involved in these clusters. These findings indicated the presence of high variability in genetic makeup of genotypes included in these clusters. High heterotic combinations may be obtained when genotypes of these distinctly placed clusters considered in hybridization program. One cluster was mono genotypic in nature. These results were indicating existence of some homology between closely situated clusters. The highest inter cluster divergence was observed between genotypes of cluster II and IV, cluster III and cluster IV, cluster II and cluster III, cluster I and cluster II, cluster I and cluster III. Cluster distance was lowest between cluster I and cluster IV. These results are in accordance with Rahman *et al.* (2013), Archi *et al.* (2017), Kanwar *et al.* (2020). These results showed that crossing between the genotypes of the clusters separated by maximum inter-cluster distance can give desirable transgressive segregates. The genetic distance had a definite role to play in efficient selection of parents for hybridization program. On the basis of these traits superior genotypes are selected and used in hybridization program as a donor parent. Intercrossing of genotypes involved in these clusters could be practiced for inducing variability in the respective characters and their rationale improvement for increasing seed yield. six genotypes of garden pea *viz.*, Murdi local, Mungaoli local, Punjab 89, Mater Agetha, Arka Priya and Raipura local (Table 4). Hence, hybridization between these lines may lead chance to the formation of transgressive segregates and these genotypes may be used in garden pea improvement program.

Conclusion

These results showed that crossing between the genotypes of the clusters separated by maximum inter-

cluster distance can give desirable transgressive segregates. The genetic distance had a definite role to play in efficient selection of parents for hybridization program. On the basis of these traits superior genotypes are selected and used in hybridization program as a donor parent. Intercrossing of genotypes involved in these clusters could be practiced for inducing variability in the respective characters and their rationale improvement for increasing seed yield. six genotypes of garden pea *viz.*, Murdi local, Mungaoli local, Punjab 89, Mater Agetha, Arka Priya and Raipura local. Hence, hybridization between these lines may lead chance to the formation of transgressive segregates and these genotypes may be used in garden pea improvement program.

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