

Genetic divergence in grass pea (*Lathyrus sativus*)*

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Grass pea (*Lathyrus sativus* L.) is an important small legume grown under dryland, marginal and hilly agro-ecological situations by poor farmers for seed as well as fodder. Being a drought-tolerant crop, it can be successfully grown as a rainfed crop during winter season. In view of this, an attempt was made to assess the genetic divergence present for seed yield, its components and seed protein content so as to identify superior varieties or strains of grass pea which can be utilized for future breeding programmes.

The experimental materials, comprised 16 diverse varieties/strains derived as somaclonal variants of variety 'Ratan' planted in randomized block design with three replications during three crop seasons, viz winter (*rabi*) 2005 to 08 at Udaipur. Each entry was grown in 6 rows each of 4 m length at the spacing of 40 cm × 10 cm between rows and plants, respectively in all the years. Recommended and uniform agronomical and plant protection measures were followed to raise the crop. Observations were recorded on 10 randomly selected plants for every genotype in each year for nine characters, viz days to flower, days to maturity, plant weight, branches/plant, pods/plant, seeds/pod, 100-seed weight and seed yield/plant and seed protein content. Seed protein content (%) was estimated by analyzing seed nitrogen following standard micro-Kjeldahl's method and the values were multiplied by 6.25 in each replication and year. The mean values obtained were statistically analyzed for each year and pooled over years. Genetic divergence was calculated for nine characters pooled over three years by using Mahalanobis D² statistics (1936). D² statistics, based upon the means and variance of the population was used to work out genetic divergence between 120 possible pairs of 16 varieties/strains of grass pea over pooled basis and based on all the nine characters.

Sixteen varieties/strains were grouped into five clusters on the basis of observed smaller D² values among varieties

*Short note

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within a cluster as compared to varieties in other clusters (Table 1). Cluster 1 contains maximum seven genotypes, followed by four in cluster II, two in cluster III and cluster IV and one in cluster V. The clustering pattern revealed that in general varieties/strains from same origin showed no tendency to be in the same cluster. Looking to the pattern of varietal distribution into different clusters in the present study, it appeared that geographical distance between the varieties had no relation with the genetic divergence as the varieties from same source had fallen into different clusters as well as the same cluster contained varieties from different source. Average inter-cluster values were maximum between cluster IV and cluster V (28.35) and minimum between cluster I and III (10.42). At intracluster level maximum value was recorded for cluster IV (9.39), followed by cluster I (8.54), cluster II (7.26) and cluster III (7.10) (Table 2). The spatial distances between clusters were arrived at by taking square root of the average D² values of intra and interclusters. Kumar

Table 1 Grass pea varieties/strains included in each cluster

Cluster	Varieties/strains (no.)	Varieties/strains
I	7	'R 15', 'R 15', 'R 31', 'R 33', 'R 02', 'L 07', 'L 212', 'L 57'
II	4	'I 22', 'R 29', 'G 158', 'L 54'
III	2	'I 30', 'G 164'
IV	2	'L 08', 'R 09'
V	1	'I 18'

Table 2 Average intra and intercluster (D²) values in 16 entries of grass pea

Cluster	I	II	III	IV	v
I	8.54	14.28	10.42	16.55	13.16
II		7.26	14.69	24.25	16.11
III			7.10	23.55	11.68
IV				9.39	28.30
V					0.00

and Dubey (2003), Dixit (2000) also reported maximum and minimum inter and intracluster distances.

SUMMARY

Sixteen of grass pea were grouped into five clusters. Cluster IV and V had maximum intercluster distance, therefore, the genotypes belonging to these clusters, namely 'L 08', 'R 09' and 'I 18' having high per se performance could be utilized in breeding programmes.

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