

GENETIC DIVERSITY IN RELATION TO GRAIN YIELD AND NEUROTOXIN IN GRASSPEA (*Lathyrus* sp.) GENETIC RESOURCES

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Genetic divergence as measured by D^2 technique was studied for grain yield, its components and neurotoxin content in 65 genotypes of grasspea. The genotypes were grouped into six clusters and the maximum intra-cluster distance was observed in cluster III comprising 16 genotypes. Clusters I and II followed by I and IV were identified as genetically divergent. Considering the cluster means and cluster distances, RLS 6, Pusa 24, BioL- 212, LS 157-14 and BioR-202 of cluster IV (for 100-seed weight); RLS 3, BioR-231, RLS 12, Bio I-222, P94-3 of cluster V (for low ODAP and earliness); RLS 9630, RLS 617, RLS 9625, RLS 9622, RLS 9603, RLS 7 of cluster III (for number of pods plant⁻¹) are expected to give promising and desirable recombinants of high yield with low neurotoxin content.

Key words : *Lathyrus*, grasspea, cluster analysis, genetic diversity, neurotoxin, grain yield

The long neglected grasspea crop has been an important food, feed and fodder legume crop of dryland agriculture. The drought tolerance and the low cost of production make an insurance and dependable crop of poor families, especially during famine conditions when the production of other crops is impossible due to excessive drought. Thus, its ability to provide an economic yield under most adverse conditions has made it a popular crop in subsistence farming. The objectives in grasspea improvement programme are to improve its yield potential, adaptability to different biotic and abiotic stresses and nutritional quality through reduction in its neurotoxin content causing neurolathyrism in human beings (Adiga *et al.*, 1963; Murthy *et al.*, 1964).

Therefore, future efforts in the improvement of grasspea should be geared to : (i) Hybridization for low or toxin free varieties (ii) Development of early, high yielding varieties. In the present study 65 genotypes including low ODAP

somaclonal variants, breeding lines and germplasm accessions were evaluated. (i) to determine the magnitude of variability among the genotypes for yield, its components and ODAP content. (ii) to determine the grouping pattern of genotypes into different clusters and (iii) to identify genetically diverse and agronomically desirable genotypes for exploitation in a breeding programme aimed at improving grain yield potential of grasspea and reducing the toxin content present in its seeds.

MATERIALS AND METHODS

The material for the study comprised 52 germplasm accessions, 6 breeding lines, 4 somaclonal variants and 3 checks viz., Pusa 24, BioL-212 and Local cultivar of grasspea genotypes. These were evaluated in randomized complete block design with three replications at Research Farm, Indira Gandhi Agricultural University, Raipur. Each entry represented single row of 2m length with a spacing of 30 cm between rows

and 10 cm between plants in a row. A recommended package of practices was adopted to grow a normal crop. Observations on metric traits were recorded on five randomly selected plants of each accession per replication (Table 1). ODAP content in dry seeds was estimated using colorimetric method as suggested by Rao *et al.* (1978). The data were subjected to the Mahalanobis D^2 statistic (1936) to measure the genetic divergence. The varieties were grouped into a number of clusters by Tocher's method as described by Rao (1952).

Table 1. Parameters of genetic variability

Character	Mean	Range		GCV %	PCV %	h^2 BS %	GA
		Min	Mix				
Days to 50% flowering	56.42	50.33	62.67	4.30	4.96	75.30	4.34
Days to maturity	107.89	98.67	119.67	5.36	5.65	90.20	11.32
Plant height (cm)	43.34	33.00	54.87	9.88	11.69	71.30	7.45
No. of pods plant ⁻¹	19.74	10.53	33.20	23.52	27.77	71.70	8.10
No of seeds pod ⁻¹	2.81	2.30	3.47	7.82	10.89	51.50	0.32
100-seed weight (g)	8.11	6.17	11.87	11.54	14.01	67.90	1.59
Grain yield plant ⁻¹	0.86	0.35	1.54	25.97	33.77	59.10	0.36
ODAP%	0.37	0.07	0.66	44.19	45.44	94.60	0.33

RESULTS AND DISCUSSION

The results of the present study exhibited low to high variability for all the eight characters under study. Considerable genetic divergence was also present among the genotypes indicating adequate scope for selection of superior and diverse genotypes.

The data presented in Table 1 showed the estimates of PCV and GCV were high for ODAP content, grain yield plant⁻¹, number of pods plant⁻¹, and 100-seed weight. Wide range of variation was observed for ODAP content ranging

from 0.07 to 0.66 per cent grain yield plant⁻¹ (0.35 to 1.54 g), number of pods plant⁻¹ (1053 to 33.20) and seed size (6.17 to 11.87 g/100 seeds). This reveals that there is ample scope of selection of superior genotypes for grain yield and low neurotoxin. Large variation in seed ODAP ranging from 0.1 to 1.0 per cent has also been reported in landraces by Jain *et al.* (1972) and Pandey *et al.* (1997). High heritability with high genetic advance for days to maturity, number of pods plant⁻¹, plant height and days to 50 per cent flowering indicated that selection may be effective for these traits. High heritability coupled with low genetic advance for ODAP content and grain yield clearly indicated that more attention should be paid while exercising selection for these traits.

Based on the relative magnitude of D^2 values, 65 genotypes were grouped into six clusters (Table 2). Maximum number of 22 cultivars were accommodated in cluster VI followed by 16 in cluster III, 8 in cluster V, 7 in cluster II and 6 each in cluster I and IV. The average intra-cluster distance between the members of cluster III was maximum followed in descending order by cluster IV, V, VI, II and I (Table 3), suggesting that genotypes in cluster III were relatively more diverse than the genotypes in the above clusters. The minimum intra-cluster distance exhibited by cluster I indicated limited genetic diversity among the constituent genotypes.

The relative divergence of each clusters from other clusters (inter-cluster distances) indicated greater divergence between cluster I & II ($D = 5.180$) followed by clusters I & IV ($D = 4.700$), II & V ($D = 4.507$) and IV & V ($D = 2.506$). The selection of divergent genotypes from above clusters would produce a broad spectrum of variability for yield and ODAP content which may enable further selection and improvement of these traits. The hybrids developed from the selected genotypes within the limits of

Table 2. Clustering of 65 grasspea genotypes based on D^2 statistics

Cluster	No. of genotypes included	Genotypes
I	6	RLS 9641, Pusa 24, BioL-212, RLS-6, LS 157-14, BioR-202
II	7	RLS 9604, RLS 9605, RLS 9606, RLS 9607, RLS 9610, RLS 9614, RLS 9615
III	16	RLS 9617, RLS 9619, RLS 9620, RLS 9622, RLS 9625, RLS 9628, RLS 9630, RLS 617, LS 9311-8, RLS 7, RLS 9602, RLS 9603, RLS 9611, RLS 9612, RPL 26, LS 157-12
IV	6	LS 155-6, LS 193-10, RLS 9601, RLS 9613, BioL-208, RLS 11
V	8	RLS 3, BioR-231, RLS 9, RLS 10, RLS 12, Biol-222, P 94-3, Local
VI	22	RLS 9616, RLS 9618, RLS 9621, RLS 9623, RLS 9624, RLS 9626, RLS 9627, RLS 9629, RLS 9631, RLS 9632, RLS 9633, RLS 9634, RLS 9635, RLS 9636, RLS 9637, RLS 9638, RLS 9639, RLS 9640, RLS 9642, RLS 9608, RLS 9609, RLK 273-1

compatibility of these clusters may produce high magnitude of heterosis or desirable transgressive segregants which would be rewarding in grasspea breeding programme. Quader (1985) and Vedna Kumari *et al.* (1996) also reported sufficient diversity even in a limited number of genotypes of grasspea.

The inter-cluster distance analysis revealed the maximum divergence between cluster I & II followed by cluster I & IV, II & V and IV & V (Table 3). Due emphasis in breeding programme should be given to RLS 9641, Pusa-24, BioL-212, RLS 6, LS 157-14, BioR-202 of cluster 1; RLS 9604, 9605, 9606, 9607, 9610, 9614, 9615 of cluster II; LS 155-6, LS 193-10, RLS 9601, RLS 9613, BioL-208, RLS 11 of cluster IV; RLS 3, BioR-231, RLS 9, RLS 10, RLS 12, BioL-222, P94-3 and local cultivar of cluster V.

Table 3. Mean intra-cluster (diagonal and bold) and inter-cluster distances among six characters

Cluster	I	II	III	IV	V	VI
I	1.692	5.180	3.068	4.700	2.130	3.793
II		1.774	3.480	2.925	4.507	3.043
III			2.083	3.561	2.965	2.289
IV				1.901	4.506	3.049
V					1.859	3.098
VI						1.852

Note : D values given above in the diagonal and non-diagonal

Crosses among parents having genetic divergence are likely to yield desirable combinations. Therefore, a crossing programme should be initiated between the genotypes belonging to different clusters. Two important factors to be considered are :

- (i) Choice of particular cluster from which genotypes are to be used as parents in crossing scheme, and
- (ii) Selection of particular genotypes from selected groups

The cluster mean values for all the traits are furnished in Table 4. There was a wide range of variation in the cluster mean values for most of the characters except for number of seeds pod⁻¹. The maximum and minimum mean values for characters viz., days to 50% flowering, 60.33 (ii) and 53.87 (V); days to maturity; 117.00 (II) and 100.71 (V); plant height, 50.29 (I) and 39.24 (II); number of pods plant⁻¹, 25.14 (III) and 16.66 (IV); number of seeds pod⁻¹, 3.11 (I) and 2.60 (II); 100-seed weight, 10.23 (IV) and 7.68 (V); grain yield, 1.30 (I) and 0.57 (IV); ODAP per cent, 0.54 (VI) and 0.19 (V), respectively were observed. This indicates that while planning hybridization programme cultures like RLS-3, BioR-231, RLS 12, Biol-222 and P 94-3 from cluster v hold like RLS-3, BioR-231, RLS 12, Biol-222 and P 94-3 from cluster V hold be considered for low ODAP and earliness. Similarly,

Table 4. Cluster means for different characters

C*	Genotypes included	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of pods plant ⁻¹	No. of seeds pod ⁻¹	100-seed weight (g)	Grain yield plant ⁻¹	ODAP (%)
I	6	55.61	101.72	50.29	17.67	3.11	8.23	1.30	0.26
II	7	60.33	117.00	39.24	18.05	2.60	7.89	0.66	0.23
III	16	55.65	109.50	45.72	25.14	2.95	7.72	0.84	0.36
IV	6	57.56	113.33	43.78	16.66	2.67	10.23	0.57	0.33
V	8	53.87	100.71	42.93	16.90	2.88	7.68	1.17	0.19
VI	22	56.56	106.64	41.04	18.80	2.70	8.00	0.80	0.54

C*-Cluster

RLS 9630, RLS 617, RLS 9625, RLS 9622, RLS 9603 and RLS 7 (cluster III) for number of nods plant⁻¹; RLS 6, Pua 24, BioL-212, LS 157-14 and BioR-202 (cluster I) for grain yield plant⁻¹; BioL-208, LS 193-10, RLS 9613 (cluster IV) for 100- seed weight. Thus, these genotypes hold great promise as parents to obtain promising hybrids and create further genetic variability for these characters.

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