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GENETIC DIVERSITY IN RELATION TO ODAP CONTENT IN GRASSPEA

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ABSTRACT

The experiment was conducted to study the nature and extent of genetic diversity and its relationship with ODAP content. The materials comprising of 16 low and 16 high seed ODAP group populations were grown in two separate field trials. Observations were recorded on days to 50% flowering, flowers/plant, flowering to maturity duration, plant height, branches/plant, pods/plant, pod length, seeds/pod, 100-seed weight, biomass/plant and seed yield. The data were subjected to multivariate D^2 as well as canonical analyses. The results showed existence of considerable genetic diversity in both group of genotypes.

Key words: *Lathyrus sativus*, genetic diversity, ODAP content, multivariate analysis.

The consumption of khesari dal (*L. sativus*) in large quantities for long periods has been reported to cause an irreversible paralysis of lower limbs in human beings which is attributed to the presence of a nonprotein free amino acid, β-N-oxalyl-L-α-β-diaminopropionic acid (ODAP) in its seeds [1].

The natural germplasm of grasspea has shown large variation in seed ODAP content varying from less than 0.1% to more than 1.0% as seen from the analysis of seed ODAP in landraces [2]. Thus, the determination of the nature and extent of the genetic diversity and its relationship with seed ODAP content formed the major objective of this study. It is expected that this information may have a bearing on breeding methodology to be followed for its genetic amelioration.

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MATERIALS AND METHODS

The unselected germplasm collections from farmers field maintained at I.A.R.I., New Delhi were screened for seed ODAP content during 1988. Genotypes having significiantly lower ODAP in their seeds as compared to the seeds of the identified low-toxin variety P-24 were placed in the low-ODAP group while those having significantly high toxin than P-24 were placed in the high-ODAP group. The experimental material comprising 16 random lines from each group was sown in separate field trials in randomised complete block layout with three replications. Each plot had six 5-m long rows spaced at 50 cm with plant-to-plant distance of 25 cm. The samples of five random plants were taken at flowering and maturity stages in each replication to record data. The observations on yield/plot as well as yield traits were recorded. The mean values of five random plants/replications and yield from each plot were subjected to appropriate analysis.

RESULTS AND DISCUSSION

The 16 lines in the low-ODAP group were placed in seven clusters, four of which contained only a single line. Cluster VII of P 27 A showed very high divergence from all the remaining clusters in this group. This suggests that P 27 A has a distinct genetic background in comparison to other lines. It was characterised by bold seed and low ODAP content (0.11%).

In the high-ODAP group, six clusters were formed. Cluster I comprised five natural mutants of landrace P 27 suggesting that in spite of variation in respect of some of the morphological traits from the original line, they have maintained a close affinity among themselves.

Thus, the present study showed considerable genetic diversity even with relatively small samples of 16 low-ODAP and 16 high-ODAP lines. In contrast, Srivastava [3] observed much less divergence in a study of 30 grasspea lines. This suggests that the earlier study did not cover much of the gene pool available in grasspea.

To examine the role of ODAP content in the genetic diversification of grasspea in natural evolution, the present material which represented almost unselected landraces was subjected to multivariate analysis pooling the data from low- and high-ODAP groups. The 32 lines could be placed in 11 clusters (Table 1). This revealed that irrespective of high or low ODAP status of the lines, they grouped together in a cluster. For instance, in cluster I which contained 12 lines, five were from low group and seven were from high group. Similarly, in cluster II, out of eight lines, seven were from low and one from high ODAP group. Line P 41-2, with a high seed ODAP content clustered with P 33A, a line with a low seed ODAP content.

The intergroup values of D^2 between the low and high-ODAP groups (75.3) was lower than the intragroup distance (83.9) within high-ODAP group alone. The intragroup D^2 for the low-ODAP (35.6) was much less. The overall intragroup distance (67.8) in the pooled data (Table 2) was lower than the intergroup D^2 values between the two groups, and the intragroup distance within the high-ODAP group. This suggested that seed ODAP was in no way involved in the genetic diversification of *Lathyrus sativus* L. lines in natural evolution.

Table 1. Cluster composition of low- and high-ODAP genotypes of *Lathyrus sativus* L.

Cluster	Number of cultures	ODAP group	Strains
I	12	Low High	P 40 A, P 32 B, P 505B, P 59, P 28B, P 36B, P 27-1, P 27-2, P 27-3, P 27-4, P 27-5, P 46D
II	8	Low	P 27A, P 45, P 33B, P 1276B, P 505C, P24B, P49
		High	LSD 1
III	3	High	LSD 3, P 27-6, P 41-1
IV	2	Low	P 33A
		High	P 41-2
V	1	Low	P 505A
VI	1	High	P 505H
VII	1	Low	P59A
VIII	1	Low	P 28A
IX	1	High	P36C
X	1	High	P50B
XI	1	High	EC 51

Note. Low-ODAP (0.11–0.20%); high-ODAP (0.28–0.57%).

The intergroup D^2 (62.1) between white and blue flowered lines was higher than the intergroup distance between white and pink (36.3) and between blue and pink (59.8) flowered lines. However, the blue flowered lines by themselves recorded an intragroup distance (67.8) higher than the intergroup distances between the

Table 2. Intra- and intercluster D^2 values based on 11 clusters in *Lathyrus sativus* L.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	17.7	33.7	47.9	87.2	69.4	61.7	39.6	34.8	32.9	71.6	387.4
II		23.1	77.2	24.6	63.0	63.8	37.5	50.2	51.2	84.2	441.2
III			15.5	114.6	96.2	94.8	119.6	50.6	36.3	36.2	262.1
IV				9.8	63.4	80.3	44.2	73.6	87.5	109.4	500.1
V					0.0	129.1	94.8	116.8	101.6	95.9	415.8
VI						0	93.2	74.4	63.6	86.7	383.2
VII							0	65.7	93.1	154.2	569.8
VIII								0	38.1	88.2	381.0
IX									0	29.4	267.6
X										0	164.6
XI											0

three groups. This suggested that flower colour alone is not able to diversify lines in *Lathyrus sativus*. Quader [4] reported that white flower coloured varieties diversed much from blue flower varieties of grasspea. In the present investigation, EC 51, a white flowered line, was placed in a separate cluster. Likewise, P 50B also formed a separate cluster. The two lines appear to be exotic and might have got introduced in India somehow from Western hemisphere which is thought to be the origin of this crop. Such geographical difference in origin might have led to genetic diversity as suggested by Jackson and Yunus [5].

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