

## Genetic diversity among induced mutants of grasspea (*Lathyrus sativus* L.)

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### Introduction

Knowledge about genetic diversity is a prerequisite of any breeding programme. Inclusion of diverse parents in hybridisation programmes serves the purpose of combining desirable genes in new recombinations. Mahalanobi's  $D^2$  statistic <sup>(7)</sup> is a powerful tool in quantifying the degree of divergence at genotypic level. Several workers have used this method to quantify the degree of divergence based on phenotypic observations in different crops <sup>(1,2,4,5,6,8,11,12)</sup>. These studies have shown that accessions from the same geographical region may differ genetically as well as phenotypically and also in adaptability. In the present study, this analysis was used to determine the divergence among 81 induced mutants and 6 parental lines of grasspea (*Lathyrus sativus* L.).

### Material and Methods

In a study on induced mutants in cvs. Nirmal, LSD-3, DL-250, PLK-750, Roma-2 and P-24 of *Lathyrus sativus* using gamma rays, ethyl methyl sulphonate (EMS), diethyl sulphate (DES) and N-nitroso-N-methyl urea (NMU), a number of macromutants were isolated. Of these, 81 elite mutants were selected for the present study.  $M_3$  populations of these mutants were grown along with their parental lines (controls) in a randomised block design with five replications. Each replication comprised of three rows 45 cm apart, with plant to plant spacing of 45 cm. Observations were recorded on five randomly selected plants for eight characters viz. days to first flowering, plant height, number of primary branches, pods/plant, seeds/pod, seeds/plant, 100 seed weight and seed yield/plant.

Estimates of divergence among the 87 genotypes were based on multivariate analysis using Mahalanobi's  $D^2$  statistic <sup>(7)</sup>. The formation of clusters was done by Toucher's method <sup>(9)</sup>.

### Results and Discussion

Analysis of variance showed significant differences among the genotypes. Based on the degree of divergence, 87 genotypes (including parental lines) were grouped into 12 clusters. Cluster V was the largest one having 17 genotypes (Table 1) and cluster

VIII the smallest with only one genotype. The pattern of cluster formation shows that there is a wide genetic diversity with regard to yield and its components in the genotypes isolated on the basis of macromutations from the same parent variety. On the other hand it is also interesting to note that several mutants isolated from genetically diverse varieties fall under the same cluster i.e. they are genetically closer to each other. This is in agreement with findings for pigeonpea <sup>(3)</sup>, where genetic diversity was claimed not be parallel with geographical diversity and has been supported in other pigeonpea studies <sup>(10)</sup>.

Inter and intra-cluster distances have been given in Table 1. Maximum intra-cluster distance (3.87) was observed for cluster XII, whereas the minimum distance (2.45) was recorded for cluster XI (excluding cluster VIII with only one genotype). Maximum inter-cluster distance was found between cluster VII and VIII (9.57) followed by clusters I and VIII (9.43), VIII and IX (8.29), III and VIII (8.12), VIII and XI (8.00) and VIII and X (7.62) suggesting wide diversity between these clusters. Minimum inter-cluster distance between IX and X (1.41) indicated close relationship among genotypes falling in these clusters.

Mean performance of different clusters for various characters is given in Table 2. The table reveals considerable differences between the clusters. Early maturity was found in clusters IV, VIII and XI, while cluster I showed delayed maturity over the general mean. Significant increased plant height was recorded in clusters II, VIII, and IX, while dwarf plant height was recorded in clusters I, III, VII and XI. Maximum number of primary branches was recorded in cluster II. Maximum numbers of pods, number of seeds and yield per plant were recorded in cluster VI and VIII. Maximum 100 seed weight was recorded in cluster X. Minimum number of seeds/plant, yield/plant and minimum number of pods/plant, 100 seed weight and yield/plant were recorded in clusters I and VII, respectively. Thus, in overall performance, cluster VI and VIII were the best since the mean values for most traits were higher. Cluster I showed minimum values for almost all the traits, indicating poorest performance.

**Table 1: Number of genotypes in clusters and average intra and inter-cluster distances between cluster centroids in induced mutants of grasspea.**

Cluster	No. genotypes	Cluster											
		I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	8	<i>3.05</i>	4.83	2.07	5.47	2.72	6.73	1.78	9.43	3.85	3.87	3.13	4.86
II	5		<i>3.81</i>	3.95	3.06	2.91	3.63	4.86	6.22	3.02	3.05	4.31	2.49
III	6			<i>2.94</i>	3.98	1.95	5.52	2.36	8.12	2.96	2.50	1.98	3.50
IV	3				<i>3.21</i>	3.71	3.27	5.52	4.62	4.67	3.72	3.65	2.97
V	17					<i>2.73</i>	4.34	2.30	7.47	3.19	3.21	2.41	2.19
VI	3						<i>2.77</i>	6.55	3.69	5.67	5.42	5.58	2.88
VII	10							<i>2.46</i>	9.57	4.30	4.40	2.52	4.25
VIII	1								<i>0.00</i>	8.29	7.62	8.00	6.13
IX	9									<i>2.48</i>	1.41	4.38	3.85
X	5										<i>3.07</i>	3.73	3.72
XI	10											<i>2.45</i>	3.42
XII	10												<i>3.87</i>

Note: figures in italics denote intra-cluster values.

**Table 2: Mean performance of different clusters for various characters in M<sub>3</sub> generation of grasspea mutants.**

	Days to first flower	Plant height (cm)	No. primary branches	Pods/ plant	Seeds/ pod	Seeds/ plant	100 seed weight	Yield/ plant (g)
I	105*	45*	4.8	25.4	1.78	43.4	4.42	2.06*
II	96	80*	8.6*	71.4	2.33	164.9	6.46	10.47
III	94	49*	4.6	41.7	2.06	89.2	7.17	5.97
IV	74*	70	6.5	103.9	2.08	215.2	6.06	12.66
V	101	57	5.6	55.4	2.55	138.3	5.24	7.44
VI	97	71	6.8	125.6*	2.58	325.3	5.92	19.69*
VII	102	40*	4.7	21.7*	2.61	54.0	3.93*	2.19*
VIII	76*	84*	7.2	203.8*	1.91	390.5	6.04	23.67*
IX	102	85*	6.6	33.7	2.01	66.4	9.97*	6.69
X	90	73	6.4	45.4	1.81	81.2	10.23*	7.66
XI	80*	44*	4.7	44.2	2.52	110.0	4.84	5.40
XII	94	67	6.4	70.4	3.00*	208.3	6.56	13.23
Mean	93	64	6.1	70.2	2.27	157.2	6.40	9.76
CD 5%	12.0	13.6	1.70	41.85	0.57	95.28	2.15	9.19

\* differs significantly (P<0.05) from the mean.

Of the two best performing clusters, cluster VI contained three genotypes (AKM-5, AKM-24 and AKM-79), while cluster VIII contained only genotype (AKM-26). These four genotypes hold promise for further use in future grasspea improvement programs.

The relative importance of plant height, number of primary branches, number of pods and number of seeds besides seed yield in contributing towards divergence was established when inter cluster groups means were compared. This study has clearly brought out in quantitative terms, the wide divergence induced

in the mutants isolated from the different parental genotype and falling under the same cluster through mutagenic treatments. Thus it could be concluded that while selecting genotypes from a particular cluster, the inter cluster distance, cluster mean and per se performance should be taken into consideration.

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