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Differential behaviour of polygenic characters to mutagenic treatments and selection in *macrosperma* lentil (*Lens culinaris* Medik.)

I. S. Solanki* and B. Sharma

Division of Genetics, Indian Agricultural Research Institute, New Delhi 110 012

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Abstract

Healthy seeds of a *macrosperma* lentil (*Lens culinaris* Medik.) cv., Prevoz Selection, were treated with three doses each of gamma rays, ethylene imine (EI) and N-nitroso-N-ethyl urea (NEU). All three mutagenized populations (pooled over three doses of each mutagen) showed increased variability over control for all the eight polygenic characters studied in the M_2 and M_3. The economically most important characters like pods and seed yield/plant were not only highly mutable but also showed increased variability in positive direction which was exploited through effective selection. Despite similar pattern of variability in M_2 and M_3 for all the traits, they were not identical in the extent of change. The results demonstrate that some characters, like pods and seed yield/plant, have a tendency to stabilize sooner than others. Therefore, selection for such characters can be confined to M_2 only as not much increase in variability and genetic advance (GA) in M_3 over M_2 is observed.

Key words : Induced polygenic variability, *Lens culinaris*, *macrosperma*, mutagens, selection

Introduction

Lentil is an important pulse crop of India. Among *rabi* pulses, it is second to chickpea in area (1.2 million ha) and production (0.92 million tonne) [1]. In spite of its importance as a rich source of protein, little attention was paid to improve its yield potential. The existing lentil germplasm indicates limited variability for important economic traits. As the exploitation of variability through recombination breeding is tedious, mainly due to its tiny flower, mutation breeding is advisable. Various polygenic characters have been reported to respond differently to mutagenic treatments and selection [2-4]. The paucity of reports indicates that such differential behaviour of different characters has not been much exploited earlier. Therefore, the present study has been planned to assess the quantum and direction of micromutational variability for economic traits and quantify the differences in their response to mutagenic treatments and selection response in lentil.

Materials and methods

Dry healthy seeds of uniform size of a *macrosperma* lentil (*Lens culinaris* medik.) cv., Precoz Selection, were treated with three doses (0.005, 0.01 and 0.02%) each of ethylene imine (EI) and N-nitroso-N-ethyl urea (NEU), and gamma rays (5, 10 and 20 kR). The treated seeds along with control were sown immediately in the field to raise the M_1. The M_1 plants (Table 1) from each treatment and control were harvested individually and their seed used to grow M_2 progenies (4 m length) with the spacing between rows and plants 30 and 5 cm, respectively. Five normal looking plants from each M_2 progeny were taken randomly to record observations on eight quantitative characters of economic value, viz., days to maturity, plant height (cm), number of fruiting branches, effective clusters and pods/plant, seeds/pod, 100-seed weight and seed yield/plant (g). The M_2 progenies with higher intrafamily coefficient of variation (CV) for a particular trait than the highest CV in the control were taken to have mutated for that trait and the mean values of such progenies were compared with the population mean of control. The putative mutant progenies were then classified into three groups: those with lower, unchanged and higher mean than the control progenies for each character. The M_2 progenies with higher CV as well as mean for a character, and higher CV and lower mean for days to maturity (considering early maturity as the desirable character) were treated as promising from breeding point of view.

The M_3 generation was raised as single plant progenies (4 m length) of M_2 plants at 30 and 5 cm spacing between rows and plants, respectively, to

*Present address : Department of Plant Breeding, CCS Haryana Agricultural University, Hisar 125 004

confirm the change in character values due to micromutations. All M_2 progenies except those with very poor grain yield were advanced to M_3 generation. The progenies segregating for macromutations in M_2 generation were not considered for analysis of polygenic traits. Observations on the same eight quantitative characters as in M_2 were recorded in the M_3 progenies which were grown from five normal looking random plants from each M_2 progeny. As intrafamily variance was expected to decline in the M_3, the comparison to character means was considered to be the most important criterion to determine the effectiveness of M_2 selection. Here again, the mean value of each M_3 progeny was compared with the highest character mean (lowest for days to maturity) recorded in the control, and an M_3 progeny having higher mean than the highest in control was identified as 'promising' for that particular trait. The CV was computed on progeny and population basis, and genetic advance was estimated as percentage of mean in both M_2 and M_3 generations using the standard statistical procedure [5].

Results and discussion

All the eight polygenic characters studied in this study did not respond in identical manner to the mutagenic treatments (Table 1). Seed yield showed maximum induced variation (CV 83.8-86.1% in M_2 and 84.5-87.7% in M_3), followed by number of pods (CV 73.6-76.1% in M_2 and 74.1-77.0% in M_3), clusters (CV 72.1-74.7% in M_2 and 72.6-75.3% in M_3) and branches per plant (CV 55.7-63.3% in M_2 and 64.2-65.4% in M_3). The remaining four characters showed less mutability. It is interesting that the economically most important characters gave maximum response to mutagenic treatments. Being highly mutable they also showed greater variability (CV) in positive direction which could be exploited through selection (Fig. 1). The highest

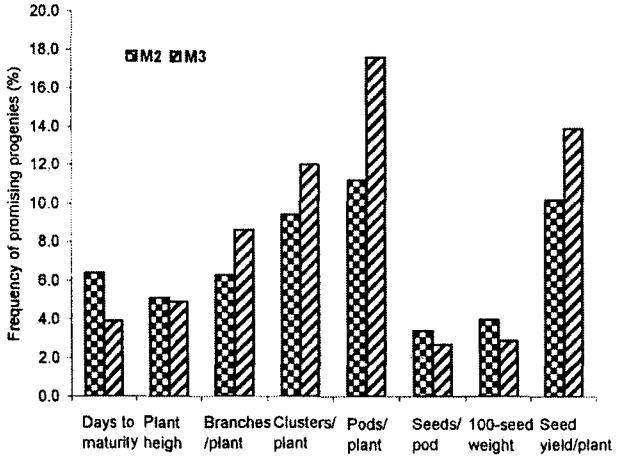

Fig. 1. Frequency of promising progenies for different characters in M_2 and M_3 generation lentil

frequency of promising progenies was obtained for pods/plant (11.2% in M_2 and 17.6% in M_3), followed by seed yield (10.2% and 13.9%), clusters (9.4% and 12.0%) and branches/plant (6.3% and 8.6%), whereas the lowest frequency of promising progenies was obtained for seeds/pod (3.4% in M_2 and 2.7% in M_3). Similar results were reported earlier in pea [2, 4], pigeonpea and chickpea [6], black gram [7] and lentil [8, 9]. The trend appears to be universally confirmed.

Another important feature of this investigation was that, despite similar pattern of variability in M_2 and M_3 for all the eight traits, they were not identifical in the extent of change due to selection (Table 2). The increase in variability (CV) due to generation advance was very small for fruiting clusters (0.7%), pods (0.8%) and seed yield/plant (1.9%), and seeds/pod (3.0%). It was significantly higher for the remaining four characters, viz., days to maturity (133.3%), plant height (17.1%), 100-seed weight (11.3%) and branches/plant (8.2%). In contrast, Singh [4] reported negligible increase in variability due to generation advance for days to flowering and 100-seed weight in peas. It remains to be determined whether character-to-character differences can be attributed to the intra-populational structure or previous selection history of different varieties [3]. Such a possibility, however, cannot explain the present situation as the untreated material of the same variety did not show a regular increase in variance with advancing generation.

Even though it cannot be readily explained why some characters reveal greater variability in later generations than others, these results clearly demonstrate that some characters have a tendency to stabilize sooner than others. This may be partly related with the number and distribution (coupling or repulsion phase) of polygenes controlling them. From the present discussion, it can be argued that selection for some characters (pods, seed yield and branches per plant) could be confined to M_2 only, as much advantage is not expected by further selection in later generations. Genetic advance (GA) for pods (5.0% of mean), seed yield (8.3% of mean) and branches/plant (14.9% of mean) did not increase much in the M_3 over M_2 (Table 2). Although these characters are believed to be controlled by a large number of genes, their stabilization in early generations seems difficult, yet the process may be facilitated by accumulation and fixation of more favourable genes (positive mutations) in the population. Shakoor and Haq [10] also selected mutants in M_2 generation for grains/pod, pod number and seed yield/plant which bred true in the M_3, suggesting that some polygenic characters are stabilized in early generations. At least for these characters both time and labour can be saved and only the M_2 selections

Table 1. Effect of mutagens (pooled over three doses) on induced variability (CV %) for different polygenic characters in M_2 and M_3 generations in *macrosperma* lentil

Population size/Character	M_2 generation				M_3 generation			
	Control	Gamma rays	EI	NEU	Control	Gamma rays	EI	NEU
No. of M_1 plants	174	931	1009	973				
No. of M_2 and M_3 plants	500	3710	3440	3735	1185	5415	5330	5025
Days to maturity	1.3	2.0	2.6	2.7	2.5	5.4	5.7	5.8
Plant height (cm)	11.2	14.8	16.2	18.2	10.0	17.9	19.1	20.5
Branches/plant	42.2	63.3	60.3	55.7	26.3	64.2	64.5	65.4
Clusters/plant	45.2	72.1	73.4	74.7	24.4	72.6	73.7	75.3
Pods/plant	54.0	73.6	74.8	76.1	30.3	74.1	75.4	77.0
Seeds/pod	17.2	19.3	20.1	20.2	12.5	20.1	20.5	21.0
100-seed weight (g)	17.7	24.4	26.0	23.6	27.0	26.1	27.8	28.6
Seed yield/plant (g)	66.8	83.8	86.1	83.9	48.4	84.5	86.4	87.7

Table 2. Induced variability (CV %) and genetic advance (% of mean) for different polygenic characters in M_2 and M_3 generations in *macrosperma* lentil

Population size/character	CV in M_2		CV in M_3		Increase in CV in M_3 over M_2 (%)	GA in M_2		GA in M3		Increase in GA in M3 over M_2 (%)
	Control	Mutagenized population	Control	Mutagenized population		Control	Mutagenized population	Control	Mutagenized population	
Population size	500	10885	1185	15770						
Days to maturity	1.3	2.4	2.5	5.6	133.3	0.5	2.7	0.7	6.0	122.2
Plant height (cm)	11.2	16.4	10.0	19.2	17.1	3.8	9.7	4.6	15.3	57.7
Branches/plant	42.2	59.8	26.3	64.7	8.2	11.1	26.9	8.2	30.9	14.9
Clusters/plant	45.2	73.4	24.4	73.9	0.7	9.2	36.6	11.7	51.3	40.2
Pods/plant	54.0	74.8	30.3	75.4	0.8	13.5	39.8	9.7	41.8	5.0
Seeds/pod	17.2	19.9	12.5	20.5	3.0	2.1	5.8	4.4	7.8	34.5
100-seed wt. (g)	17.7	24.7	27.0	27.5	11.3	2.4	10.4	8.0	13.5	29.8
Seed yield/plant (g)	66.8	84.6	48.4	86.2	1.9	2.8	36.0	22.1	39.0	8.3

can be advanced to M_3 for confirmation, further selection, preliminary testing and multiplication.

The same rule can also be applied for other characters as well, even though their variability increased in the M_3 over M_2 appreciably. The M_2 progenies can be classified as promising on the basis of their higher CV and shift in mean in desired direction than the highest value of control and only these progenies should be advanced for the second cycle of selection in a larger M_3 population.

Therefore, irrespective of whether a character shows increase in variability with the advancing generations or not, preliminary screening in early generations should be of great help in reducing the volume of work and saving time. The reduced volume of material with a definite indication of induction of change as a result of mutagenic treatment can be subjected to thorough evaluation in the subsequent generations.

Only one genotype (Precoz Selection) was used for mutagenic treatments in this study. The possibility of genotypic differences cannot be ruled out as different experiments carried out in the past showed divergent results. The dependence of the direction and magnitude of induced polygenic variability on the genotypic background of the material has been emphasized earlier [2, 11].

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