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EFFICIENCY OF EARLY GENERATION SELECTION FOR INDUCED POLYGENIC MUTATIONS IN LENTIL (*LENS CULINARIS* MEDIK.)

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ABSTRACT

The mutagenized populations exhibited increased variability over the control in M_2 and M_3 generations for flowering duration, primary branches/plant, peduncles/plant, pods/plant, seeds/pod, 1000-seed weight, and seed yield/plant. The interfamily analysis revealed a great deal of heterogeneity among M_2 families in each treated population with respect to character means. Using CV and mean as parameters, promising M_2 families were identified for multiple characters. The frequency of such promising families with different mutagens was in the following order: NEU>EMS>SA>gamma rays. Most of the M_3 families (75.0–85.7%) confirmed as promising for multiple characters were already identified in M_2, and some (4.6–7.2%) were isolated from the unselected group of M_2 generation. Although the contribution of the unselected M_2 progenies to the total promising M_3 families was greater (51.3–65.2%) than those obtained from the M_2 selected group (34.7–48.6%), the selection efficiency (proportion of desirable mutations selected), nevertheless, was higher in M_2 than in M_3 generation. About 75–85% selected M_2 plants from various treatments bred true in M_3 for the characters studied. The selection, started in early generation (M_2), can greatly increase the efficiency of mutation breeding for quantitatively inherited traits, such as, yield and maturity.

Key words: Lentil, induced polygenic variability, early generation selection.

The mutation breeding technique has been used as an important supplement to other conventional methods of plant breeding for improvement of crops by developing new plant type with superior biochemical composition and better adaptation. Unlike other crops, such as wheat, barley, rice and peas, where much work has been done to understand the mutation process per se and to use mutation breeding for yield improvement, very limited work has been carried out in lentil. The present study has been planned to know the quantum and direction of micromutational variability for some characters of economic importance in lentil. Another important aspect examined relates to the selection procedures for identifying useful variability. The success of mutation breeding depends not only on the quality of induced mutations, but also on the worker's ability to identify rare mutations among a large number of others that are of little value. Most mutation breeding programmes fail to give a definite advantage of this kind, especially in respect of the quantitative variation generated by micromutations. An attempt has been made in the present study to develop standard selection procedure for this purpose.

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MATERIALS AND METHODS

Four mutagens, viz., gamma rays, ethylmethane sulphonate (EMS), N-nitroso-N-ethyl urea (NEU), and sodium azide (SA), with three doses each, were used to treat the seeds of lentil strain L-3991. The treated and control seeds were sown to raise M_1 generation during 1981–1982 at the IARI farm, New Delhi. The seeds of individual M_1 plants were collected separately in each treatment. Individual M_1 plant progenies were sown in separate M_2 progeny rows during the 1982–1983 cropping season. Five competitive plants from each M_2 family were taken randomly to record observations as described in [1]. Inter- and intrafamily variances, CV and mean were estimated on family and population basis. The CV for each of the seven characters in each M_2 family was compared with the corresponding highest value observed in the control families. An M_2 family having CV value higher than the highest observed in the control families was considered as carrying induced mutations. Thereafter, the mutated families were divided into groups with higher, unchanged, and lower means as compared to the mean of the control. From such analysis it was possible to detect the promising (higher CV with lower mean for flowering period and higher CV with higher mean for the other six characters) M_2 families for different characters. Intrafamily selection was done by taking two best plants from each selected promising M_2 family. The selected M_2 plants were then identified as promising for single as well as multiple (2–7) characters. Finally, all the selected M_2 plants as well as those from the families not identified as promising were used to compare their performance in M_3. Each M_3 family was raised from the seeds of a single M_2 plant. The M_3 families of each population were raised in randomised complete block design with two replications during 1983–84. Some of the M_3 families (4 in gamma rays, 10 in EMS, 9 in NEU, and 16 in SA treatments), identified as promising for multiple characters in M_2, were damaged in the field. Observations were recorded on the same seven quantitative characters as in M_2. Five random plants of a family from each replication were studied. As the variance was expected to decrease in M_3, the comparison of mean values was considered to be most appropriate to determine the selection efficiency in M_2 generation. Thus, the character mean for each M_3 family was compared with the highest family mean recorded in the control. The M_3 families with higher mean than the highest value observed in the control families were identified as promising M_3 families for single and multiple characters.

RESULTS AND DISCUSSION

Most selections based on family means and CV in M_2 generation were confirmed as promising families (80.6% with NEU, 75.3% with EMS, 72.2% with SA, and 64.0% with gamma rays) for multiple characters in M_3 [1]. The M_3 analysis showed that additional variability was released or detected in the mutagenic treatments. Our M_3 selection was mainly based on family means, which showed that a large proportion of M_3 families (69.0–78.2%) was promising for multiple characters (Table 1). Even more interesting was the observation that most of the plants selected from the M_2 families (75.0–85.7%) and a few (4.6–7.2%) unselected plant progenies carried desirable changes (Table 2). Although the relative contribution of the unselected

Table 1. Frequency of M_3 families promising for multiple characters

Mutagen	Total families studied	Promising families		Families with varying No. of favourable character combinations							Promising for multiple characters	
		total	%	1	2	3	4	5	6	7	total	%
Gamma rays	649	100	15.4	31	21	10	12	9	9	8	69	69.0
EMS	660	92	13.9	20	15	11	12	14	10	10	72	78.2
NEU	655	96	14.6	24	19	7	10	17	9	10	72	75.0
SA	445	46	10.3	14	5	6	3	8	6	4	32	69.5

group to the total selections was greater (51.3–65.2% promising selections as against 34.7–48.6% from the selected group; Table 3), the proportion of promising families with multiple mutations was much less among the total M_3 progenies examined (4.6–7.2%) than among the M_3 progenies of the plants already selected in M_2 (75.0–85.7% progenies promising). It is evident from these observations that selection in M_2, if practiced judiciously, can yield promising material a generation earlier, a large part of which is likely to be confirmed in later generations, whereas carrying forward the entire material from M_2 to M_3 means screening of a voluminous mass in M_3, more than 90% of which is not expected to yield any promising selections.

Table 2. **Efficiency of selection for progenies promising for multiple characters in M_2 and M_3 generations**

Mutagen	Selected group			Unselected group		
	plants selected in M_2	confirmed promising M_3 families with multiple mutations		unselected plants from M_2	promising families with multiple mutations in M_3	
		total	%		total	%
Gamma rays	28	24	85.7	621	45	7.2
EMS	40	33	82.5	620	39	6.2
NEU	41	35	85.3	614	37	6.0
SA	16	12	75.0	429	20	4.6

Different selection techniques have been used to detect and measure induced polygenic variability in many crops. An important difference between the earlier studies and the one presented here relates to the procedure of handling the material carrying induced variability from the standpoint of identifying the mutants which offer maximum promise at the earliest possible time. The common recommendation from the earlier studies has been to select normal looking plants in M_2 at random to raise M_3 families, where selection is to be applied for the first time. The main handicap in this procedure is that the random nature of selection makes the process highly uncertain and also involves continuation of voluminous material. In contrast, the emphasis in the present study has been on starting selection in the M_2 itself.

Most studies involving polygenic mutations have failed to yield positive results in terms of varieties, either because promising families of the kind discussed here do not exist, or they are lost in the process of random selection from the huge mass of unselected material. It can be concluded that the efficiency of mutation breeding for yield and other quantitative characters could be greatly increased by using more rigorous screening techniques of the kind discussed here. Selection in M_2 generation was also practiced by some earlier workers [2–4], however, they studied characters having high heritability, mostly under controlled conditions. Moreover, the selection techniques followed in these cases were not based on rigorous inter- and intrafamily selections, using family mean and CV as the criteria for selection, as has been done in the present study. Gupta and Swaminathan [5] suggested that different M_2 families should be analysed for their mean and variance and families showing superior mean and increased variance over the control should be selected. Later, Jana and Roy [6] selected M_2 families on the basis of significantly changed mean only. Bhadra [7] employed inter- and intrafamily selections in black gram on the basis of mean and CV in M_2 generation. The M_2 families thus selected for all characters bred true in M_3 generation. More recently, Kharkwal [8] also emphasized the effectiveness of such early selection for indentifying superior lines for polygenically inherited characters.

Table 3. **Contribution of M_2 and M_3 generations to the total promising M_3 selections for multiple characters**

Mutagen	Total No. of promising families	Proportion of promising families in M_3, %			
		from M_2 selections		from unselected M_2 Materials	
		total	%	total	%
Gamma rays	69	24	34.7	45	65.2
EMS	72	33	45.8	39	54.1
NEU	72	35	48.6	37	51.3
SA	32	12	37.5	20	62.5

The present study, in general, shows the possibility of improvement for polygenic traits in lentil through induced mutations coupled with efficient selection techniques. It has been possible to identify a number of M_3 families that are promising for multiple characters. Some of these promising families were initially identified from the M_2 material and most of them (75.0–85.7%) were confirmed to be promising in M_3. However, as observed by Mar'yushkin et al. [9] in wheat, a number of unselected M_2 plants were also found to be promising in M_3. Rigorous selection in M_2 can be of help in reducing the volume of material and also ensure economy of time and resources with greater probability of success. In such cases, one can increase the volume of M_2 material and reject a large part of the families showing poor performance. Although such procedure ignores the variability that escapes attention in M_2 and can be recovered only in M_3, the material selected in M_2 as promising has a very high chance of being confirmed as such in the succeeding assessments, as is evident from the fact that 104 out of 125 (83.2%) progenies selected in M_2 generation of these experiments were confirmed as promising in M_3 generation.

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