EFFICIENCY OF SELECTION FOR MICROMUTATIONS IN M_2 GENERATION IN PEAS

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Comparative studies of selection in M_2 and M_3 generations have revealed that in many cases the two populations may not differ in response to selection (4,5). On the other hand, some experiments have demonstrated that selection in M3 is more effective than in M_2 (1,2). This was, most probably, because the material already selected in M_2 was confirmed with higher probability in subsequent generations (3). Even if the material selected in M_3 or later generations has a higher probability of becoming fixed as promising strains, there is no evidence to suggest that the frequency of promising mutations per se is higher in M3 than in M_2. It can be argued that the variability manifested in M3 could not have arisen afresh without causing any impact on the M_2 population. Therefore in the present study selection was initiated in the M_2 generation on the basis of higher CV (variability) and desired shift in mean than the highest values in these parameters in the control (untreated population) for five polygenic traits (days to flowering, pods/plant, seeds/pod, 100-seed weight and yield/plant). The criterion for confirmation of the promising families in M_3 was the shift in mean values in the desired direction. The selection efficiency in M_2 generation, calculated on the basis of this criterion, is presented in Tables 1 and 2.

As can be seen from Table 2, 76.2-79.8% of M_2 selections were confirmed as promising in the M3 generation. This suggests that selection in M_2 was very effective and dependable. Some characters showed an increase in variance with the advance in generation to M_3, which is confirmed by the fact that a further 22.2-24.8% of promising progenies were identified in M_3. Nevertheless, early generation selection is of great help in reducing the volume of work, in saving time, and in isolation of confirmed mutations. As can be seen from Table 2, the contribution of the M_2 and M3 generations to total selections arising from the different treatments was 75.2-77.8% and 22.2-24.8%, respectively. Thus, although new mutated progenies (about one-fourth of total) were added in the M_3 generation (progenies which were either not identified in M_2 or were new additions as a result of release of additional variability), the volume of material has to be increased very substantially in order to recover this smaller additional variability of a promising nature.

The overall analysis of the results obtained reveals that there is tremendous possibility to improve polygenic characters through induced mutagenesis by employing an efficient selection technique. It is evident that rigorous selection can help identify promising variants from the mutagenized populations in the first segregating (M_2) generation. These variants can simultaneously be confirmed and their potential tested in the M_3 generation.

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Table 1. Selection efficiency for micromutations in M_2 and M3 generations (pooled over five traits).

Mutagen	M_2 generation		M_3 generation	
	Total progenies	Promising selections (%)	Total progenies	Promising selections (%)
Gamma rays	1200	16.6	786	30.3
EI	1200	21.2	786	35.9
NEU	1200	24.5	842	38.4

Table 2. Nature of M_2 selections and their contribution to total micromutations (pooled over five traits).

Mutagen	M_2 selections		Proportion of total selections (%)	
	Total	Confirmed in M_3 (%)	M_2 selections	M_3 selections
Gamma rays	189	76.2	76.2	23.8
EI	230	77.5	77.8	22.2
NEU	274	79.9	75.2	24.8

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