Chapter 6

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The present investigation was carried out using ethylmethane sulphonate (EMS) – an alkylating agent, hydrazine hydrate (HZ) – a base analogue and sodium azide (SA) – a respiratory inhibitor on mungbean (Vigna radiata (L.) Wilczek). The main objective of this study was to enhance the genetic variability for quantitative traits in two varieties viz; PDM-11 and NM-1 of mungbean and to increase the yield potential of crop by isolating promising lines. Various other aspects of this study were:

1. biological damage in M₁ generation
2. frequency and spectrum of chlorophyll and morphological mutations
3. effectiveness and efficiency of the mutagens
4. estimation of variance (genetic and non-genetic), heritability and genetic advance, and
5. evaluation of seed protein content in the high yielding mutants isolated in M₃ generation.

Biological damage, induced in M₁ generation, was estimated in the form of immediate effects of the mutagens on seed germination, seedling height, plant survival at maturity and pollen fertility. A dose dependent reduction in these parameters, except plant survival at maturity, was observed in both the varieties of mungbean. However, the mutagens differed in the extent of damage caused. Variety NM-1 was found to be more sensitive than the var. PDM-11.
Various types of anomalies in the cotyledonary and vegetative leaves (shape and number) were recorded in the treated population, their frequency being maximum with EMS treatments and minimum with SA treatments.

A wide spectrum of chlorophyll mutants was obtained in $M_2$ generation. All these chlorophyll deficient mutants were lethal except maculata, viridis and virescent. Chlorina followed by xantha types were predominant in both the varieties. EMS treatments induced the highest frequency of chlorophyll mutations followed by HZ and SA treatments. The frequency of chlorophyll mutations was dose dependent and increased with the mutagen concentration. Based on effectiveness in both the varieties, the order of the mutagens was HZ>SA>EMS. Two criteria viz., pollen sterility ($Mp/S$) and seedling injury ($Mp/I$) were taken into consideration to determine the efficiency of the mutagens. EMS was found to be the most efficient mutagen followed by HZ and SA. Moderate concentrations of the mutagens were most effective and efficient in inducing mutations.

A wide range of morphological mutants were identified in $M_2$ population of mungbean. The frequency of morphological mutants differed in different mutagenic treatments and also between the varieties. The highest frequency was noticed in the EMS treated population and the lowest in the SA treated one, HZ treatments being the intermediate. Variety NM-1 gave the broader spectrum and frequency of morphological mutations than the var. PDM-11. Of all the mutant types, yield and plant height were of maximum occurrence in the two varieties studied.

Attempts were made to ascertain the effects of the mutagenic treatments on mean and the coefficient of variation (CV) in $M_1$ itself. Induced variability was studied for nine quantitative traits, namely, days to
flowering, plant height (cm), days to maturity, number of fertile branches, number of pods, pod length (cm), seeds per pod, 100-seed weight (g) and total plant yield (g). Means for all the nine quantitative traits remained unchanged in the treated population. However, the coefficient of variation (CV) differed from trait to trait and the highest CV over control was recorded for fertile branches per plant. The mean values for traits like days to flowering, plant height and days to maturity shifted to negative direction in both M2 and M3 generations. Days to maturity were reduced by approximately four days in both the varieties after the mutagenic treatments in M3 generation. The mean values for yield and yield components increased in all the treatments, with some exceptions, in both the varieties of mungbean. The exceptions were noticed in M2, whereas M3 generation showed a complete positive trend of shift. However, the mean pod length did not differ significantly in most of the mutagenic treatments. The genotypic coefficient of variation, heritability and genetic advance increased manifold in the treated population and varied from trait to trait in M2 and M3 generations. The studies of heritability and genetic advance suggest that the induced polygenic variability can be utilized in plant improvement programme.

A considerable increase in mean values for fertile branches per plant, pods per plant and seed yield per plant was noticed among the isolated mutant lines in M3 generation. Estimates of genotypic coefficient of variation, heritability and genetic advance for yield and yield components were also recorded to be higher. Increase in fertile branches and pods per plant played a significant role in boosting the seed yield in mutants isolated in M3 generation. Increase in mean values coupled with an increase in
genetic variability especially for yield contributing traits of these mutants suggest further possibilities of selecting more promising lines with high yield potential.

Phenotypic correlation between various character pairs of the mutants isolated in M₃ generation showed a positive and significant relationship among number of fertile branches, number of pods and seed yield per plant. The present findings support the view that the mutagenic treatments could alter the mode of association between traits apart from generating genetic variability.

Seed protein content of the mutants isolated in M₃ generation showed a slight but insignificant improvement over the controls. The coefficient of variation for seed protein content of the mutants did not differ much from the control plants, indicating no further improvement in seed protein content is possible. Seed protein content was found to have a negative correlation with the total plant yield in the mutants and the controls of both the varieties.

Results showed that the moderate concentrations of various mutagens proved to be effective and efficient in generating genetic variability in both the varieties of mungbean. Therefore, polygenic variability induced by chemical mutagens can be effectively exploited in mungbean improvement programme.