



Sodium azide induced genetic variability and character association in M_2 generation of mungbean

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Abstract : An experiment was conducted to study the mutagenic effects of different concentrations of sodium azide (0.01%, 0.02%, 0.03%, 0.04% and 0.05%) on ten different characters in mungbean cv. MALACCA LOCAL. High estimates of GCV and PCV were observed for primary branches, seeds per pod and pods per plant. Heritability was high for 100 seed weight, pod length and seed yield per plant. However, high genetic advance as per cent of mean was observed for seed yield per plant, primary branches per plant, pods per plant and 100 seed weight. Correlation coefficient analysis revealed that seed yield per plant exhibited significant and positive association with 100 seed weight, clusters per plant and pods per plant, suggesting that top priority should be given to these characters during selection for isolation of desirable mutant lines of mungbean.

Key Words : Mungbean, Heritability, Genetic advance, Correlation, M_2 generation, Sodium azide

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INTRODUCTION

Mungbean is one of the important and widely cultivated crop in different seasons in India and it ranks third after chickpea and pigeonpea in area and production. It is popular due to easily digestible component of the diet. It also improves soil fertility by adding atmospheric nitrogen. Genetic improvement in any organism rest on the platform architected by two components, genetic variability in the base population for selection of genotypes and stability of the genotypes identified through selection. When the natural genetic variability, becomes depleted through continuous selection endeavors, it becomes imperative to induce variability for selection of elite genotypes. Hybridization has played an important role through shuffling of genetic information of two or more parent genotypes to produce desirable recombination. Plant breeders require altogether new alleles and mutation is the ultimate origin of new genes and mutation has played an important role in the course of plant breeding endeavors.

Mutation breeding offers scope for achieving in many instances what cannot be accomplished through back cross and selection. The advantage of mutation breeding is that it can be applied for changing specific characters in otherwise good varieties by incorporating some useful variations in comparatively shorter period of time than the conventional breeding methods, since the induction of mutation has been accepted as a useful tool in breeding programme. Polygenic variation was earlier estimated in M_2 generation by Tadele *et al.* (2005) in chickpea, Singh and Kumar (2005) in mothbean and Barshile and Apparao (2008) in chickpea. Keeping in view, the impact of mutations in crop improvement, the present experiment was conducted with an objective to study the induced variation and character association in M_2 generation.

MATERIALS AND METHODS

Mungbean genotype namely Malaka Local was selected as parent genotype procured from Malaka village in Allahabad

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district. Hundred uniform healthy seeds each were treated with five different concentrations (0.01%, 0.02%, 0.03%, 0.04%, 0.05%) of sodium azide (NaN_3) after 6 hours of presoaking. The parent seeds treated in similar way but without mutagen served as control. After treatment the treated seeds were sown in the field to raise M_1 generation during *Kharif*, 2009. All M_1 plants were independently harvested to raise M_2 generation. Seeds from 10 normal looking M_1 plants of each treatment and control were sown in plant progeny rows in randomized block design with three replications to evaluate mutagenic population in M_2 generation during *Zaid*, 2010. In M_2 generation, observations were recorded for 10 plants of each concentration on days to 50 per cent flowering, plant height, no. of primary branches, no. of clusters/ plant, no. of pods/ plant, days to maturity, pod length (cm), no. of seeds/pod, 100-seed weight (g) and seed yield/ plant (g). The mean data over replications was used for calculating genotypic, phenotypic coefficient of variation (Burton and Devane, 1953), heritability (Lush, 1949) and genetic advance (Johnson *et al.*, 1955). The genotypic and phenotypic correlation coefficients (Al-Jibouri *et al.*, 1958) were also estimated.

RESULTS AND DISCUSSION

The analysis of variance for different characters showed significant differences for all characters under study at 1 per cent level and 5 per cent level of significance, indicating the presence of substantial amount of genetic variability among the mutant lines (Table 1). The estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) in broad sense and genetic advance were estimated for ten characters and furnished in Table 2. High genotypic and phenotypic coefficient of variation were observed for primary branches, seeds per pod and pods per plant. Barshile and Apparao (2008) reported that estimates of phenotypic and genotypic coefficient of variation

were high for plant height, number of pods per plant, number of seeds per pod, suggesting wide scope for selection for chickpea mutant lines.

Burton (1952) suggested the genetic variation along with heritability estimates would give a better idea about the expected efficiency of selection thus a character possessing high GCV along the high heritability will be valuable in selection programme. In the present study, highest heritability in broad sense was recorded for 100 seed weight followed by pod length and seed yield per plant.

The highest genetic advance as per cent of mean was recorded for seed yield per plant followed by primary branches per plant, pods per plant and 100 seed weight. Johnson *et al.* (1955) suggested that heritability and genetic advance when calculated together would prove more useful in predicting the resultant effect of selection on phenotypic expression. High heritability coupled with high genetic advance as per cent mean was recorded for 100 seed weight and seed yield per plant. Tadele *et al.* (2005) reported that seed yield per plant, pods per plant and seeds per pod recorded high heritability coupled with high genetic advance as per cent mean in M_2 and M_3 generations of chickpea.

The correlation among various yield and yield contributing characters revealed that seed yield per plant was significantly and positively correlated with number of clusters per plant and number of pods per plant at both genotypic and phenotypic levels (Table 3). However, 100 seed weight and number of primary branches were significantly and positively associated with seed yield per plant at only genotypic level. It suggests that top priority should be given to these characters while making selection for yield improvement. Singh and Singh (2003) also reported that number of pods per plant, 100 seed weight, plant height and number of primary branches were positively and significantly correlated with seed yield.

For identification of important yield component characters the information about the inter-relationship among

Table 1 : Analysis of variance for yield and yield component characters in mungbean

| Sr. No. | Characters | Mean sum of square | | |
|---------|---------------------------|--------------------|-----------|-------|
| | | Replications | Genotypes | Error |
| | Degree of freedom | 2 | 50 | 100 |
| 1. | Days to 50% flowering | 6.71 | 3.25** | 0.19 |
| 2. | Plant height | 0.79 | 38.51** | 5.83 |
| 3. | No. of primary branches | 0.006 | 2.09** | 0.59 |
| 4. | No. of clusters per plant | 0.20 | 3.56** | 1.58 |
| 5. | No. of pods per plant | 7.14 | 43.93** | 3.93 |
| 6. | Days to maturity | 4.90 | 2.02** | 0.44 |
| 7. | Pod length | 0.0005 | 1.48* | 0.04 |
| 8. | No. of seeds per pod | 0.49 | 5.71** | 0.99 |
| 9. | 100 seed weight | 0.07 | 0.60 | 0.008 |
| 10. | Seed yield per plant | 0.032 | 2.36** | 0.08 |

* and ** indicate significance of values at $P=0.05$ and 0.01 , respectively

characters is necessary for developing efficient breeding strategy for yield improvement. Among the other characters, pod length had positive significant correlation at both genotypic and phenotypic levels with number of primary branches and number of seeds per pod, 100 seed weight had positive significant correlation with number of primary branches, number of pods per plant, pod length and number of seeds per pod and days to 50 per cent flowering had positive significant correlation with days to maturity at both genotypic and phenotypic levels. But number of seeds per pod positively and significantly correlated with plant height, number of primary branches, number of clusters per plant and number of

pods per plant and 100 seed weight also had positive and significant correlation with plant height and number of clusters per plant at only genotypic level, suggesting the inter-dependency of these characters and due consideration should be given during selection of mutant lines.

The genetic architecture of seed yield is based on the balance or overall net effect produced by various yield components interacting with one another. Based on the studies on correlation, it may be concluded that number of clusters per plant and number of pods per plant being easily observable characters at field level, appeared to be primary yield contributing characters and could be relied upon these

Table 2 : Estimates of genetic variability parameters for various characters in mungbean

| Sr. No. | Characters | Coefficient of variation | | Heritability (%) bs | Genetic advance (GA) | GA as percent of mean |
|---------|-----------------------|--------------------------|-------|---------------------|----------------------|-----------------------|
| | | GCV | PCV | | | |
| 1. | Days to 50% flowering | 2.06 | 2.24 | 84.16 | 1.91 | 3.89 |
| 2. | Plant height | 7.78 | 9.64 | 65.11 | 5.49 | 12.93 |
| 3. | Primary branches | 16.72 | 24.80 | 45.46 | 0.98 | 23.22 |
| 4. | Clusters per plant | 8.42 | 15.56 | 29.28 | 0.90 | 9.39 |
| 5. | Pods per plant | 12.50 | 14.23 | 77.20 | 6.61 | 22.63 |
| 6. | Days to maturity | 1.06 | 1.44 | 54.45 | 1.10 | 1.62 |
| 7. | Pod length | 8.46 | 8.84 | 91.66 | 1.37 | 16.69 |
| 8. | Seeds per pod | 12.34 | 15.74 | 61.38 | 2.02 | 19.91 |
| 9. | 100 seed weight | 10.41 | 10.63 | 95.92 | 0.90 | 21.00 |
| 10. | Seed yield per plant | 4.02 | 12.87 | 90.26 | 1.71 | 23.92 |

Table 3 : Correlation coefficient (r) between 10 quantitative characters in mungbean at genotypic (r_g) and phenotypic (r_p) level

| Sr. No. | Characters | Level | Plant height | Primary branches | Clusters/ plant | Pods/ plant | Days to maturity | Pod length | Seeds/ pod | 100 seed weight | Yield/ plant |
|---------|-----------------------|----------------|--------------|------------------|-----------------|-------------|------------------|------------|------------|-----------------|--------------|
| 1. | Days to 50% flowering | r _g | 0.3214* | 0.0993 | -0.0678 | 0.2159 | 0.9858** | 0.0388 | 0.2223 | 0.2155 | 0.1154 |
| | | r _p | 0.2366 | 0.0627 | 0.0090 | 0.1531 | 0.8094** | 0.0374 | 0.1631 | 0.1700 | 0.1054 |
| 2. | Plant height | r _g | | 0.1133 | -0.0753 | -0.0328 | 0.2156 | 0.2408 | 0.3385* | 0.3312* | 0.0839 |
| | | r _p | | 0.0986 | -0.0373 | -0.0481 | 0.0771 | 0.1861 | 0.2188 | 0.2658 | 0.1097 |
| 3. | Primary branches | r _g | | | 0.0613 | 0.2368 | -0.0693 | 0.6369** | 0.4589** | 0.5735** | 0.4653** |
| | | r _p | | | 0.0631 | 0.1535 | -0.0319 | 0.4279** | 0.1907 | 0.3761** | 0.2452 |
| 4. | Clusters/ plant | r _g | | | | 0.1204 | -0.1496 | -0.0083 | 0.3572** | 0.4087** | 0.5488** |
| | | r _p | | | | 0.0268 | -0.0395 | -0.0063 | 0.1958 | 0.2064 | 0.2993* |
| 5. | Pods/ plant | r _g | | | | | 0.0168 | 0.1277 | 0.2775* | 0.4684** | 0.4403** |
| | | r _p | | | | | -0.0134 | 0.1172 | 0.2253 | 0.4124** | 0.3795** |
| 6. | Days to maturity | r _g | | | | | | -0.0687 | 0.0480 | -0.1163 | -0.1528 |
| | | r _p | | | | | | -0.0347 | 0.0037 | -0.1673 | -0.1385 |
| 7. | Pod length | r _g | | | | | | | 0.4059** | 0.3971** | 0.1991 |
| | | r _p | | | | | | | 0.3072* | 0.3713** | 0.1882 |
| 8. | Seeds/ pod | r _g | | | | | | | | 0.5221** | 0.2655 |
| | | r _p | | | | | | | | 0.4130** | 0.2156 |
| 9. | 100 seed weight | r _g | | | | | | | | | 0.7125** |
| | | r _p | | | | | | | | | 0.6750** |

* and ** indicate significance of values at P=0.05 and 0.01, respectively

characters for selection of desirable mutant lines to improve the genetic yield potential of mungbean.

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