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# Characterization of Mungbean Mutants [*Vigna radiata* (L.) Wilczek] in $M_4$ and $M_5$ Generations

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## ABSTRACT

**Background:** An understanding the mungbean mutant lines with the check varieties can help in identifying mutants in better adoption. The present experiment was conducted to assess the genetic variation and morpho-metric characteristics of mungbean mutants in $M_4$ and $M_5$ generation.

**Methods:** A set of 7 $M_3$ progenies along with parent Pratap and 5 check was evaluated for $M_4$ and $M_5$ generation using randomized complete block design with three replications during *kharif* 2018 and summer 2019 in the experimental area of Instructional cum Research Farm, College of Agriculture, Assam Agricultural University, Jorhat, Assam.

**Result:** Significant differences were observed for most of the traits in both $M_4$ and $M_5$ generation. High heritability estimate coupled with high genetic advance as per cent of mean was documented for numbers of branches per plant, pods per plant, percentage of disease incidence, 100 seeds weight and seed yield per plant in both the generation indicate the pre-ponderance of additive gene action. Seed yield per plant was found to be significantly and positively correlated with numbers of pods per cluster, seeds per pod, pod length and 100 seeds weight at genotypic and phenotypic level in both $M_4$ and $M_5$ generation. The traits 100 seeds weight and branches per plant had showed positive direct effect on seed yield in both the generations; hence these two traits might be most effective for selection of higher yield mutants in mung bean.


**Key words:** Correlation, Genetic advance, Heritability, Mung bean, Path analysis.

## INTRODUCTION

Mungbean [*Vigna radiata* (L.) Wilczek] is one of the major pulse crops of India, which is cultivated from humid tropic to arid and semi arid regions. Mungbean is considered rather wild as it still gives low seed yield (<1 t/ha), with uneven maturity and year to year variation in yield is also remarkably high. This opens an ample room for mungbean breeders to improve the crop on the aspect of early and synchronous maturity. The conventional breeding approaches have their limitations in increasing production of crops with narrow range of variability. In such cases, mutation breeding may provide a suitable alternative. It has been established that radiations as well as chemical mutagens, when applied to plant provide many opportunities in exploitations of mutation, recombination and in increasing genetic variability of the quantitatively inherited characters. From the works already reported by several authors in self pollinated crops (Williams and Hanway, 1961; Chaturvedi and Singh, 1980). It is evident that the polygenic mutants result in release of considerable variability in mutagen treated populations. Keeping the above facts in view, the present investigation was undertaken to study the genetic variation and morpho-metric characterization of selected mutants of mung bean.

## MATERIALS AND METHODS

The seeds of cultivar Pratap were treated with Gamma rays (100, 200 and 300 *Gy)* and EMS (0.1%, 0.2% and 0.3%) in the year 2017. The gamma ray doses irradiation was done at Bidhan Chandra Krishi Vishwavidyalaya (BCKV), West Bengal (WB). About 240 plants selected in $M_2$ generation in 2017 were grown as single plant to progeny rows in $M_3$ generation during summer 2018. Uniform progenies with desirable traits like synchronous maturity, dense clustered, long podded and brown podded were identified and single plant harvested. A set of these 7 $M_3$ progenies along with parent *Pratap* and 5 checks *viz*., BARC-I, BARC-II, BARC-III, BARC-IV, BARC-V and SGC-20 (Table 1) was evaluated for $M_4$ and $M_5$ generations using randomized complete block design with three replications during *kharif* 2018 and summer 2019 in the experimental area of Instructional cum Research Farm, College of Agriculture, Assam Agricultural University, Jorhat, Assam. The progenies and checks were accommodated in a plot of 5 rows of 5 m length with a row to row and plant to plant spacing of 30 and 10 cm,

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respectively. Observations were recorded for characters namely days to 50% flowering (D50%F), days to pod initiation (DPI), days to maturity (DM), plant height (cm) (PH), number of branches per plant (BPL), cluster per plant (CPL), pods per cluster (PCL), seeds per pod (SPP), percentage of disease infection (%DI), pod length (cm) (PL), 100 seeds weight (g) (100SW) and seed yield (g) (SYD). The data generated were subjected to analysis of variance (ANOVA), genotypes as fixed effects in Windostat v.9.2 (indostat@hotmail.com).

## RESULTS AND DISCUSSION

### Analysis of variance

Analysis of variance for seed yield and the yield attributing characters revealed highly significant differences among the genotypes for most of the characters except for days to pod initiation and pod length in $M_4$ generation and days to pod initiation and plant height in $M_5$ generation (Table 2 and Table 3).

### Mean performances

Among the genotypes grown in $M_4$ generation, SM-2 showed earliest flowering (35 days) with lowest pod maturation period (40 days) (Table 4a and 4b). Whereas LP (42 days) was observed to be the late flowering genotype and SM-1 (43 days) was documented to require more days for pod initiation than the rest of the genotypes. SGC-20 (62 days) was investigated to be the earliest maturing genotype and DC (75 days) was experimented to be showing late maturity. SM-3 showed highest number of branches per plant (9.22) along with highest number of clusters per plant (4.15). Percentage of disease infection was investigated lowest for SM-1 (13.31%) and 100-seed weight was found highest for BP (5.81 g). As for the $M_5$ generation, BARC-III was found to be the earliest flowering genotype (33 days) and also showed earliest maturity (58 days). LP (35 days) showed early pod maturation. SM-1 (42 days) was observed to be the late flowering genotype and DC (43 days) was detected to require more days for pod initiation than the rest of the genotypes. BARC-I was

**Table 1:** List of mutants/genotypes used in present investigation with their source of origin.

| Genotype code | Genotype name | Type | Source |
|---|---|---|---|
| SM-1 | Synchronous-maturity-I | Mutant | Department of Plant Breeding and Genetics, AAU, Jorhat-13 |
| SM-2 | Synchronous-maturity-II | Mutant | |
| SM-3 | Synchronous-maturity-III | Mutant | |
| DC | Dance-cluster | Mutant | |
| LP | Long-pod | Mutant | |
| BP | Brown-pod | Mutant | |
| BARC-I | TMB-122 | Check | Bhabha Atomic Research Centre, Mumbai |
| BARC-II | TMB-124 | Check | |
| BARC-III | TMB-127 | Check | |
| BARC-IV | TMB-148 | Check | |
| BARC-V | TMB-152 | Check | |
| SG-1 | Pratap | Parent | Department of Plant Breeding and Genetics, AAU, Jorhat-13 |
| SGC-20 | SGC-20 | Check | RARS, Shillongoni, AAU, Jorhat-13 |

**Table 2:** Analysis of variance for yield and yield component characters in *Vigna radiata* (L.) Wilczek for $M_4$ generation.

| Source of | | Mean squares | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| variations | df | D50%F | DPI | DM | PH (cm) | BPL | CPL | PCL | SPP | %DI | PL (cm) | 100 SW (g) | SYD (g) |
| Replicates | 2 | 2.33 | 1.00 | 1.25 | 10.04 | 0.005 | 0.004 | 0.008 | 0.284 | 5.41 | 0.25 | 0.003 | 0.001 |
| Genotype | 12 | 9.88* | 3.12 | 63.30* | 14.89* | 5.13* | 0.27* | 0.62* | 2.76* | 33.21** | 0.455 | 1.62** | 1.92** |
| Error | 24 | 2.30 | 2.72 | 12.15 | 3.077 | 0.006 | 0.067 | 0.002 | 0.43 | 1.39 | 0.205 | 0.002 | 0.024 |
| CV (%) | | 3.82 | 3.93 | 5.21 | 5.32 | 1.23 | 7.11 | 1.64 | 6.81 | 5.72 | 7.62 | 0.86 | 4.09 |

**Table 3:** Analysis of variance for yield and yield component characters in *Vigna radiata* L. Wilczek for $M_5$ generation.

| Source of | | Mean squares | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| variations | df | D50%F | DPI | DM | PH (cm) | BPL | CPL | PCL | SPP | %DI | PL (cm) | 100 SW (g) | SYD (g) |
| Replicates | 2 | 15.87 | 3 | 2.87 | 4.29 | 0.01 | 0.08 | 0.01 | 0.02 | 1.17 | 0.61 | 0.01 | 0.22 |
| Genotype | 12 | 22.36* | 12.58 | 46.81** | 10.46 | 0.57** | 0.56** | 0.56** | 2.90** | 47.89** | 0.77* | 1.62** | 0.54* |
| Error | 24 | 3.96 | 4.17 | 4.54 | 3.03 | 0.01 | 0.03 | 0.01 | 0.10 | 0.55 | 0.15 | 0.00 | 0.08 |
| CV (%) | | 5.28 | 5.34 | 3.37 | 5.15 | 1.97 | 5.16 | 1.42 | 3.98 | 2.63 | 6.50 | 0.89 | 8.07 |

*, **Significant at 5% and 1% level, respectively.

observed to have lowest percentage of disease infection (22.20%). Genotype BP showed highest pod length (6.65 cm) and highest 100 seeds weight (5.56 g). However, seed yield per plant was observed to be highest in SGC-20 (4.09 g).

**Genetic parameters**

High phenotypic and genotypic coefficient of variation was registered for seed yield per plant and number of branches per plant in $M_4$ generation (Table 5). In the case of $M_5$ generation, none of the traits showed a high phenotypic and genotypic coefficient of variation but the number of clusters per plant, pods per cluster, seeds per cluster, seeds per pod, percentage of disease infection, 100-seed weight and yield showed a moderate phenotypic and genotypic coefficient of variation. High estimates of genotypic coefficient of variation indicated the presence of wide variation for the character under study to allow further improvement by the selection of individual traits. These results align with that of Pathak and Patil (1993), Longnathan *et al.* (2001), Samad and Lavanya (2005) and Makeen *et al.* (2007). High heritability estimate coupled with high genetic advance as per cent of mean was registered for the number of branches per plant, pods per plant, percentage of disease infection, 100-seed weight and seed yield per plant in $M_4$ and for number of clusters per plant, pods per cluster, seeds per pod, percentage of

**Table 4a:** Mean performance of yield and yield attributing traits of mung bean mutants.

| Genotype | D 50% F | | DPI | | DM | | PH | | BPL | | CPL | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | $M_4$ | $M_5$ | $M_4$ | $M_5$ | $M_4$ | $M_5$ | $M_4$ | $M_5$ | $M_4$ | $M_5$ | $M_4$ | $M_5$ |
| SM-1 | 41.67 | 42 | 43.33 | 37.67 | 62.67 | 65 | 32.67 | 31.97 | 6.27 | 4.7 | 4.1 | 3.59 |
| SM-2 | 34.67 | 40.33 | 39.67 | 35.33 | 68.67 | 64.33 | 34.4 | 33.82 | 7.27 | 4.3 | 3.47 | 3.77 |
| SM-3 | 40.33 | 39 | 43 | 38 | 74 | 64.67 | 30.56 | 36.03 | 9.22 | 5.22 | 4.15 | 3.5 |
| DC | 39.33 | 39 | 41.67 | 43 | 75 | 64.67 | 35.53 | 34.26 | 6.18 | 4.64 | 3.9 | 3.49 |
| LP | 41.67 | 34.33 | 42.67 | 34.67 | 68 | 72.67 | 33.87 | 34.58 | 7.51 | 5.62 | 3.43 | 3.27 |
| BP | 40.67 | 35.67 | 42.33 | 38.67 | 72.67 | 65.33 | 33.73 | 34.98 | 7.48 | 5.23 | 3.22 | 3.4 |
| BARC-I | 41.33 | 34.33 | 42.33 | 38.33 | 66.33 | 63 | 33.53 | 30.33 | 5.43 | 4.17 | 3.67 | 3.53 |
| BARC-II | 40 | 38.67 | 41 | 37.67 | 66.33 | 59.67 | 33.13 | 35.4 | 7.18 | 4.35 | 3.4 | 4.33 |
| BARC-III | 39.67 | 33.33 | 42.33 | 39 | 60.67 | 58 | 32.07 | 33.19 | 6.17 | 5.35 | 3.57 | 3.55 |
| BARC-IV | 38.67 | 37.67 | 40.67 | 38.67 | 64.67 | 62.33 | 37 | 37.19 | 6.19 | 4.65 | 3.57 | 2.62 |
| BARC-V | 39.67 | 38.67 | 42.67 | 37.67 | 64.33 | 64 | 32.2 | 33.06 | 6.08 | 4.94 | 3.4 | 3.28 |
| SG-1 | 39.33 | 40.67 | 41.67 | 38 | 64.33 | 61 | 28 | 32.36 | 4.61 | 4.76 | 3.5 | 3.59 |
| SGC-20 | 38.67 | 35.67 | 41.67 | 40.33 | 62 | 57 | 32 | 32.31 | 4.29 | 4.6 | 4 | 4.28 |
| Mean | 39.67 | 37.64 | 41.92 | 38.23 | 66.9 | 63.21 | 32.98 | 33.81 | 6.45 | 4.81 | 3.64 | 3.55 |
| Range | 35-42 | 33-42 | 40-43 | 35-43 | 62-75 | 57-73 | 28-37 | 30.33-37.19 | 4.29-9.22 | 4.3-5.62 | 3.22-4.15 | 2.62-4.33 |
| C.D. 5% | 2.57 | 3.37 | 2.69 | 3.46 | 5.91 | 3.61 | 2.97 | 2.95 | 0.13 | 0.16 | 0.44 | 0.31 |

**Table 4b:** Mean performance of yield and yield attributing traits of mung bean mutants.

| Genotype | PCL | | SPP | | %DI | | PL (cm) | | 100 SW (g) | | SYD (g) | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | $M_4$ | $M_5$ | $M_4$ | $M_5$ | $M_4$ | $M_5$ | $M_4$ | $M_5$ | $M_4$ | $M_5$ | $M_4$ | $M_5$ |
| SM-1 | 2.58 | 2.42 | 8.37 | 8.51 | 13.31 | 25.18 | 5.58 | 5.95 | 4.79 | 4.68 | 3.28 | 3.05 |
| SM-2 | 2.18 | 2.62 | 9.13 | 8.36 | 19.53 | 26.53 | 5.63 | 6.04 | 4.12 | 4.01 | 2.53 | 3.64 |
| SM-3 | 2.48 | 2.29 | 8.73 | 8.41 | 21.67 | 27.96 | 5.41 | 6.14 | 3.14 | 3.03 | 2.62 | 2.71 |
| DC | 2.15 | 2.61 | 9.31 | 7.57 | 23.22 | 26.53 | 6.06 | 5.3 | 5.67 | 5.58 | 4.45 | 3.91 |
| LP | 1.77 | 2.82 | 9.13 | 9.52 | 23.65 | 29.32 | 5.36 | 6.4 | 4.79 | 4.68 | 2.75 | 4.04 |
| BP | 2.77 | 2.64 | 9.76 | 8.37 | 22.5 | 32.08 | 5.78 | 6.65 | 5.81 | 5.69 | 4.44 | 3.81 |
| BARC-I | 2.75 | 2.02 | 10.13 | 8.07 | 17.58 | 22.2 | 5.85 | 6.1 | 4.7 | 4.59 | 4.55 | 3.58 |
| BARC-II | 3.19 | 2.15 | 9.75 | 7.3 | 17.4 | 37.85 | 6.24 | 6.13 | 5.21 | 5.1 | 4.63 | 3.58 |
| BARC-III | 2.78 | 3.14 | 8.8 | 7.41 | 21.47 | 30.64 | 5.85 | 4.86 | 4.71 | 4.62 | 4.4 | 3.53 |
| BARC-IV | 1.7 | 3.17 | 9.63 | 7.42 | 22.25 | 31.26 | 6.28 | 6.32 | 5.67 | 5.56 | 3.65 | 3.02 |
| BARC-V | 2.45 | 3.45 | 9.53 | 5.29 | 18.58 | 25.57 | 6.16 | 6.15 | 5.13 | 5.02 | 3.69 | 3.45 |
| SG-1 | 3.05 | 2.82 | 11.33 | 8.14 | 20.36 | 25.29 | 6.63 | 5.43 | 4.21 | 4.14 | 4.1 | 3.98 |
| SGC-20 | 2.75 | 3.18 | 11.67 | 7.5 | 26.14 | 27.28 | 6.37 | 5.44 | 5.15 | 5.03 | 4.66 | 4.09 |
| Mean | 2.51 | 2.72 | 9.64 | 7.84 | 20.59 | 28.28 | 5.94 | 5.92 | 4.85 | 4.75 | 3.83 | 3.57 |
| Range | 1.70-2.78 | 2.02-3.45 | 8.37-11.67 | 5.29-9.52 | 13.31-26.14 | 22.2-37.85 | 5.36-6.63 | 4.86-6.65 | 3.14-5.81 | 4.01-5.69 | 2.53-4.66 | 2.71-4.09 |
| C.D. 5% | 0.07 | 0.07 | 1.11 | 0.53 | 2 | 1.26 | 0.77 | 0.65 | 0.07 | 0.07 | 0.27 | 0.49 |

disease infection and 100-seed weight in $M_5$ generation indicate the preponderance of additive gene action. The similar findings were observed by Singh *et al.* (2009) and Narasimhulu *et al.* (2013) were supportive of the present study. Hence, the results of the most of the traits showed high heritability in $M_5$ generation compare with the $M_4$ generation indicates selection of the traits would be effective in present investigation.

**Correlation**

In the present study, seed yield per plant was found to be significantly and positively correlated with the number of pods per cluster, seeds per pod, pod length and 100- seed weight at the genotypic and phenotypic level in $M_4$ generation and with the number of clusters per pod, pod length and 100 -seed weight in $M_5$ generation (Table 6 and Table 7). The significant negative correlation of seed yield per plant at the genotypic level was recorded in the number of branches per pod for $M_4$ generation and plant height for $M_5$ generation. Similar findings were also reported by Nazir *et al.* (2005), Singh *et al.* (2009) and Ahmed *et al.* (2013). Percentage of disease infection showed a significant negative correlation with days to pod initiation and number of pods per cluster in $M_4$ generation, while in $M_5$ generation, number of clusters per pod showed a significant positive correlation with days to maturity, plant height, number of branches per plant and pods per cluster. The present correlation result is due to multiple effects of the same gene, the selection for one character will improve another character simultaneously. Hence, correlations among traits influence the effectiveness of selection. These results are in agreement with the findings of Ahmad *et al.*, (2013) and Narasimhulu *et al.*, (2013).

**Path analysis**

The genotypic correlation coefficients were used for carrying out path coefficient analysis in 13 genotypes and the analyzed had revealed low residual value 0.398 and 0.278 in $M_4$ and $M_5$ generation, respectively (Table 8 and Table 9). Considering the direct effect of the component traits on seed yield in the genotypes it was observed that 100 seeds weights had the highest direct effect (2.974)

**Table 5:** Estimates the genetic parameters of different characters in green gram [*Vigna radiata* (L.) Wilczek] for $M_4$ and $M_5$ generation.

| Character | PCV (%) | | GCV (%) | | $h^2_{b.s.}$ (%) | | GA (% of mean) | |
|---|---|---|---|---|---|---|---|---|
| | $M_4$ | $M_5$ | $M_4$ | $M_5$ | $M_4$ | $M_5$ | $M_4$ | $M_5$ |
| D50% F | 5.54 | 8.44 | 4.01 | 6.58 | 52.30 | 60.80 | 5.97 | 10.57 |
| DPI | 4.03 | 6.91 | 0.87 | 4.38 | 4.64 | 40.22 | 0.39 | 5.72 |
| DM | 8.08 | 6.83 | 6.17 | 5.94 | 58.40 | 75.64 | 9.72 | 10.64 |
| PH | 8.03 | 6.94 | 6.02 | 4.66 | 56.13 | 45.00 | 9.29 | 6.43 |
| BPL | 20.30 | 9.20 | 20.26 | 8.99 | 99.64 | 95.44 | 41.66 | 18.09 |
| CPL | 10.01 | 12.87 | 7.05 | 11.79 | 49.60 | 83.91 | 10.23 | 22.24 |
| PCL | 18.11 | 15.99 | 18.04 | 15.93 | 99.18 | 99.21 | 37.00 | 32.69 |
| SPP | 11.39 | 12.97 | 9.13 | 12.34 | 64.30 | 90.57 | 15.09 | 24.20 |
| %DI | 16.82 | 14.29 | 15.82 | 14.04 | 88.41 | 96.62 | 30.64 | 28.44 |
| PL (cm) | 9.04 | 10.09 | 4.86 | 7.72 | 28.96 | 58.52 | 5.39 | 12.16 |
| 100 SW (g) | 15.15 | 15.47 | 15.12 | 15.45 | 99.68 | 99.67 | 31.1 | 31.77 |
| SYD (g) | 21.16 | 13.60 | 20.76 | 10.94 | 96.27 | 64.77 | 41.96 | 18.14 |

**Table 6:** Genotypic (upper diagonal) and phenotypic (lower diagonal) correlation coefficients between different characters in [*Vigna radiata* (L.) Wilczek] for $M_4$ generation.

| | D50% F | DPI | DM | PH (cm) | BPL | CPL | PCL | SPP | %DI | PL (cm) | 100SW (g) | SYD (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| D50% F | | 2.400** | 0.001 | -0.096 | 0.091 | 0.253 | 0.199 | -0.082 | -0.246 | -0.381* | 0.142 | 0.241 |
| DPI | 0.516** | | -0.068 | -0.746** | 0.393* | 0.936** | 0.447** | -0.934** | -0.700** | -0.655** | -0.387* | -0.173 |
| DM | -0.011 | 0.004 | | 0.232 | 0.706** | 0.073 | -0.273 | -0.342* | 0.287 | -0.570** | -0.077 | -0.227 |
| PH (cm) | -0.242 | -0.336* | 0.233 | | 0.182 | -0.195 | -0.748** | -0.467** | 0.146 | -0.215 | 0.678** | 0.001 |
| BPL | 0.060 | 0.061 | 0.532** | 0.149 | | -0.031 | -0.267 | -0.768** | -0.054 | -0.992** | -0.345* | -0.603** |
| CPL | 0.033 | 0.224 | 0.017 | -0.097 | -0.032 | | -0.035 | -0.144 | -0.034 | -0.343* | -0.426** | -0.159 |
| PCL | 0.127 | 0.072 | -0.211 | -0.541** | -0.263 | -0.047 | | 0.418** | -0.317* | 0.497** | -0.126 | 0.583** |
| SPP | -0.228 | -0.100 | -0.154 | -0.181 | -0.623** | -0.099 | 0.338* | | 0.426** | 1.053** | 0.187 | 0.587** |
| %DI | -0.145 | -0.024 | 0.191 | 0.067 | -0.056 | -0.028 | -0.291 | 0.350* | | 0.277 | 0.171 | 0.114 |
| PL (cm) | -0.111 | -0.345* | -0.227 | -0.173 | -0.534** | -0.063 | 0.270 | 0.540** | 0.021 | | 0.513** | 0.899** |
| 100 SW (g) | 0.095 | -0.099 | -0.056 | 0.517** | -0.344* | -0.293 | -0.126 | 0.150 | 0.161 | 0.275 | | 0.603** |
| SYD (g) | 0.161 | 0.033 | -0.211 | -0.048 | -0.588** | -0.130 | 0.572** | 0.480** | 0.135 | 0.444** | 0.588** | |

*, **Significant at 5% and 1% level, respectively.

followed by number of branches per plant (0.877), cluster per plant (0.782) and days to pod initiation (0.070) in $M_4$ generation. Although in $M_5$ generation the trait hundred seed weights showed highest direct effect (1.261) followed by number of branches per plant (1.047), seeds per pod (0.552), pod length (0.407), percentage of disease

**Table 7:** Genotypic (upper diagonal) and phenotypic (lower diagonal) correlation coefficients between different characters in [*Vigna radiata* (L.) Wilczek] for $M_5$ generation.

| | D 50% F | DPI | DM | PH (cm) | BPL | CPL | PCL | SPP | %DI | PL (cm) | 100 SW (g) | SYD (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| D 50% F | | -0.257 | 0.009 | -0.002 | -0.424** | 0.107 | -0.187 | -0.092 | -0.186 | 0.101 | -0.272 | -0.389* |
| DPI | 0.171 | | -0.629** | -0.293 | -0.231 | 0.137 | 0.096 | -0.445** | -0.093 | -0.713** | 0.532** | 0.166 |
| DM | 0.082 | -0.312* | | 0.155 | 0.459** | -0.500** | -0.183 | 0.532** | -0.164 | 0.759** | -0.074 | -0.028 |
| PH (cm) | 0.153 | 0.160 | 0.255 | | 0.391* | -0.398* | 0.115 | 0.062 | 0.813** | 0.522** | 0.131 | -0.390* |
| BPL | -0.293 | -0.145 | 0.359* | 0.219 | | -0.371* | 0.364* | 0.234 | 0.197 | 0.061 | -0.100 | 0.001 |
| CPL | 0.034 | 0.013 | -0.419** | -0.302 | -0.326* | | -0.332* | -0.030 | 0.161 | -0.369* | -0.169 | 0.398** |
| PCL | -0.138 | 0.084 | -0.160 | 0.075 | 0.351* | -0.309* | | -0.513** | -0.019 | -0.286 | 0.301 | 0.199 |
| SPP | -0.046 | -0.262 | 0.434** | 0.026 | 0.221 | 0.046 | -0.476** | | -0.030 | 0.203 | -0.321* | 0.107 |
| %DI | -0.143 | -0.032 | -0.142 | 0.569** | 0.193 | 0.174 | -0.021 | -0.027 | | 0.221 | 0.326* | -0.018 |
| PL (cm) | -0.014 | -0.344* | 0.381* | 0.242 | 0.030 | -0.251 | -0.206 | 0.197 | 0.172 | | 0.100 | -0.311* |
| 100SW (g) | -0.205 | 0.337* | -0.063 | 0.102 | -0.098 | -0.153 | 0.299 | -0.306 | 0.322* | 0.075 | | 0.397* |
| SYD (g) | -0.252 | 0.049 | 0.011 | -0.296 | 0.004 | 0.311* | 0.178 | 0.105 | -0.036 | -0.187 | 0.313* | |

*, **Significant at 5% and 1% level, respectively.

**Table 8:** Genotypic path analysis direct (diagonal values in bold face) and indirect effects of component characters on seed yield per plant in [*Vigna radiata* (L.) Wilczek] for $M_4$ generation.

| | D50 % F | DPI | DM | PH (cm) | BPL | CPL | PCL | SPP | %DI | PL (cm) | 100S W (g) | R |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| D50%F | -0.808 | 0.169 | 0.000 | 0.231 | 0.080 | 0.198 | -0.107 | 0.005 | 0.047 | 0.004 | 0.421 | 0.241 |
| DPI | -1.938 | 0.070 | 0.016 | 1.792 | 0.345 | 0.733 | -0.241 | 0.060 | 0.135 | 0.007 | -1.151 | -0.173 |
| DM | -0.001 | -0.005 | -0.232 | -0.557 | 0.619 | 0.057 | 0.147 | 0.022 | -0.055 | 0.006 | -0.228 | -0.227 |
| PH (cm) | 0.078 | -0.052 | -0.054 | -2.401 | 0.159 | -0.152 | 0.403 | 0.030 | -0.028 | 0.002 | 2.017 | 0.001 |
| BPL | -0.074 | 0.028 | -0.164 | -0.436 | 0.877 | -0.024 | 0.144 | 0.049 | 0.010 | 0.011 | -1.025 | -0.603** |
| CPL | -0.205 | 0.066 | -0.017 | 0.468 | -0.027 | 0.782 | 0.019 | 0.009 | 0.007 | 0.004 | -1.266 | -0.159 |
| PCL | -0.161 | 0.031 | 0.063 | 1.795 | -0.234 | -0.027 | -0.539 | -0.027 | 0.061 | -0.005 | -0.375 | 0.583** |
| SPP | 0.066 | -0.066 | 0.079 | 1.121 | -0.674 | -0.112 | -0.225 | -0.064 | -0.082 | -0.011 | 0.555 | 0.587** |
| %DI | 0.199 | -0.049 | -0.067 | -0.350 | -0.047 | -0.027 | 0.171 | -0.027 | -0.193 | -0.003 | 0.508 | 0.114 |
| PL (cm) | 0.308 | -0.046 | 0.132 | 0.517 | -0.871 | -0.268 | -0.267 | -0.067 | -0.053 | -0.011 | 1.526 | 0.899** |
| 100S W (g) | -0.114 | -0.027 | 0.018 | -1.629 | -0.302 | -0.333 | 0.068 | -0.012 | -0.033 | -0.005 | 2.974 | 0.603** |

Residual effect 0.39973.

**Table 9:** Genotypic path analysis direct (diagonal values in bold face) and indirect effects of component characters on seed yield per plant in [*Vigna radiata* (L.) Wilczek] for $M_5$ generation.

| | D50 % F | DPI | DM | PH (cm) | BPL | CPL | PCL | SPP | % DI | PL (cm) | 100 SW (g) | r |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| D50%F | 0.181 | 0.253 | -0.014 | 0.003 | -0.443 | -0.013 | 0.032 | -0.051 | -0.035 | 0.041 | -0.343 | -0.389* |
| DPI | -0.047 | -0.982 | 0.926 | 0.426 | -0.241 | -0.017 | -0.017 | -0.245 | -0.018 | -0.290 | 0.670 | 0.166 |
| DM | 0.002 | 0.617 | -1.472 | -0.225 | 0.480 | 0.061 | 0.031 | 0.294 | -0.031 | 0.309 | -0.093 | -0.028 |
| PH (cm) | 0.000 | 0.288 | -0.229 | -1.453 | 0.409 | 0.048 | -0.020 | 0.034 | 0.155 | 0.212 | 0.165 | -0.390* |
| BPL | -0.077 | 0.226 | -0.675 | -0.568 | 1.047 | 0.045 | -0.062 | 0.129 | 0.038 | 0.025 | -0.126 | 0.001 |
| CPL | 0.019 | -0.135 | 0.737 | 0.578 | -0.388 | -0.122 | 0.057 | -0.017 | 0.031 | -0.150 | -0.213 | 0.398** |
| PCL | -0.034 | -0.094 | 0.269 | -0.167 | 0.381 | 0.040 | -0.172 | -0.283 | -0.004 | -0.117 | 0.379 | 0.199 |
| SPP | -0.017 | 0.436 | -0.784 | -0.090 | 0.245 | 0.004 | 0.088 | 0.552 | -0.006 | 0.083 | -0.405 | 0.107 |
| % DI | -0.034 | 0.091 | 0.241 | -1.181 | 0.207 | -0.020 | 0.003 | -0.017 | 0.190 | 0.090 | 0.411 | -0.018 |
| PL (cm) | 0.018 | 0.700 | -1.117 | -0.758 | 0.064 | 0.045 | 0.049 | 0.112 | 0.042 | 0.407 | 0.126 | -0.311* |
| 100SW (g) | -0.049 | -0.522 | 0.109 | -0.190 | -0.105 | 0.021 | -0.052 | -0.177 | 0.062 | 0.041 | 1.261 | 0.397* |

Residual effect 0.27817.

*, **Significant at 5% and 1% level, respectively.

incidence (0.190) and days to 50% flowering (0.181). The traits hundred seeds weight and number of branches per plant had showed positive direct effect on seed yield in both the generation; hence these two traits might be most effective for selection of higher yield mutants in green gram. This is in broad conformity with path analysis studies in greengram as reported by Mishra and Singh (2012), Prasanna *et al*. (2013); Makeen *et al*. (2007); Rahim *et al*. (2010) and Muthuswamy *et al*. (2019).

## CONCLUSION

The study of variability parameters among 7 mungbean mutants for 12 traits has provided valuable information regarding the genetic variability, heritability and genetic advance for the characters and efficacy of different mutagenic treatment. Genetic parameters of traits, correlation among traits and path analysis revealed that selection for 100 seeds weight and number of branches per plant would be effective in observation of high yielding mutants.

### Conflict of interest

All authors declared that there is no conflict of interest.

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