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# Assessment of genetic variances and effects for agronomic traits in mungbean (*Vigna radiata* (L.) Wilczek)

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**Abstract**
Mungbean holds significant importance as a pulse crop across Asia that run out with high high-quality protein (25%) and remarkable increase in quantity of thiamine, niacin, lysine and ascorbic acid during sprouting. Thus, breeding for developing mungbean genotypes with enhanced yield potential is paramount for maintaining mungbean productivity and safeguarding global food security.This study was performed for the mungbean crop at Agricultural Research Station, Badnapur during *Kharif* 2022-23 with an aim to estimate the genetic effects influencing yield and yield related traits in 54 mungbean crosses derived from mating six females and nine males in line × tester mating system. The results manifested that genotypes were highly significantly for all the yield and its contributing characters. Significant variations were also predicted among the lines, testers and line × tester for all the studied traits. The dominance variance ($\sigma^2D$) was in greater amount as compared to the additive variance ($\sigma^2A$) for most of the traits. Formerly, the value of $\sigma^2$ SCA variance was notably more than the value of $\sigma^2$GCA variance for all the traits which exerted non additive gene effects for substantial influence on the genetic manifestation of the studied traits. Therefore, it is advised that hybridization be pursued for characteristics influenced by non-additive genetic effect, followed by selection in later generations in mungbean.

**Keywords:** Mungbean, GCA, SCA, gene action

## Introduction
The country like India, pulses stand out as the most affordable and commonly consumed protein source 21 - 30% (Singh *et al*. 2021) [31] and provide double amount than that of cereal crops. (Danielle *et al*. 2017) [9]. The protein found in mungbean, like in other pulses, is abundant in lysine, an essential amino acid indeed for the human that lacks in cereal grains. Pulses popularly referred as "rich man's vegetable" (Singh *et al*. 2015) [30] as well "poor man's meat" (Patil *et al*. 2020) [7, 25] as it serves as the primary protein source for a significant portion of the global vegetarian community and has laid significant contribution to the nutritional security of the country. Among pulses, mungbean (*Vigna radiata* (L.) Wilczek, 2n=24) is a self-pollinated pulse crop and established itself as extravagant short duration grain legume crop grown in *kharif*, *Rabi* and *Summer*. (Casey and Wringley 1982) [6] and possess desirable features like wider adaptability with low inputs requirement (Kakde *et al*. 2019) [13]. India leads globally as the foremost producer as well as consumer of pulses, encompassing 33% of the world's cultivated area and contributing 22% to global production. (Patil *et al*. 2020) [7, 25]. Mungbean in India is cultivated on an about 4.5 million ha area with total 2.5 million tons production (Anonymous., 2021) [2]. While, current scenario according to 1st advance estimates of *kharif* 2022-23, displaying 33.37 lakh hectares cultivated area with 17.5 lakh tonnes production (agricoop.nic). Though, India has legimate pride being largest producer and consumer, but less than half of the country's productivity is being celebrated, thereby it indicates the scope for mungbean improvement in productivity potential. Currently, Inspite of high demand of growing papulation, the mungbean yield of worldwide is low (721 Kg ha) with yield gap 19.50% (Dixit *et al*. 2024) [11]. Therefore, to boost current crop yields, it is imperative to conduct the mungbean enhancement program by hybridization and comprehend the significance of genetic interplay in determining yield and

its components. Information about gene action provides the basis for selection of traits and usually measured by the components of genetic variances (Sharma *et al*. 2019., Khan *et al*. 2020) [29, 15]. This facilitates breeders in discerning the proportion both additive and non additive genetic variance in the inheritance of various characters and selecting suitable breeding method that can efficiently harness the existing genetic diversity. Among the different techniques readily upwarding the productivity in mungbean, the line × tester analysis has been suggested for early evaluation of parents, because of its clarity in experimental analysis (Dhillon, 1975) [10]. Previously, the line × tester design has been investigated for the yield and agronomic traits of mungbean (Chavan *et al*. 2019; Patil *et al*. 2020; Narasimhulu *et al*. 2016) [7, 25, 19]. With the considerations mentioned above, the prese study was determined to estimate the magnitude gene action for yield and its relevant traits using line × tester mating design. The findings obtained from this study will provide crucial insights for the advancement of mungbean varieties with high seed yield.

## Experimental Materials and Methods

The present investigation was conducted at experimental farm of Agricultural Research Station, Badnapur. (Latitude 19.86° N, Longitude 75.70° E, 31°5 and Altitude 586.65 m) District Jalna. The experimental material consisting of 15 parents (six females *viz.*, BM 4, BM 2002-1, Phule chetak, Kopergaon, AKM 4 and PKV green gold and nine males (testers) *viz.*, BWMCD 5, BWMCD 10, BWMCD 7, BWMC 20, BWMC 20-1, BWMC 25, BWMC 30-2-1, IC 39564 and BM 21-21). The parents including lines and testers employed for present study and their characteristics are presented in (Table 1). In the mungbean growing season of *kharif* 2021-22, the six females and the nine males were mates as per a line × tester mating system to produce 54 $F_1$ hybrids as suggested by Kempthorne (1957) [14]. The parents and their $F_1$ crosses were sown during the *Kharif* 2022-23. The experimental materials were sown in a Randomized Block Design with two replications. Each replication was presented in two rows each of parents and $F_1$ crosses. The row was 4.00 m long and planted to plant with spacing of 20 × 10 cm. The observations was recorded on each character on selected five random plants. Analysis of variance was performed as per the standard method of Panse and Sukhatme (1985) [23]. The significance of the GCA and SCA effects was evaluated using the least significant difference test at both 5% and 1% levels of significance. The GCA:SCA ratio was computed to analyze the effects and gauge the relative significance of additive and non-additive gene effects, following the methodology outlined by Singh and Chaudhary (1977) [32].

## Results and Discussion

The information of the genetic basis relating agronomic characters of interest is extremely precise for any plant breeding programmes that seek to increase crop yield in areas where there is need of explicit selection of parents by means of generating superior crosses as well as segregants. In the present study, the analysis of variance for line × tester (Table 2) revealed significant mean square due to genotypes for all traits, revealed the existence of genetic variations in varying genotypes and justified the appropriate inclusion of genotypes for present investigation. A wide range of variation was also previously noted in different mungbean genotypes by Nath *et al*. (2018) [21], Rathod *et al*. (2020) [27], Vaidya *et al*. (2016) [34] and Bhagora *et al*. (2013) [4] in mungbean. Further, partitioning of mean square by genotype into parents and crosses exhibited highly significant variations for all studied characters, the comparison between the mean squares due to parents and crosses unveiled notable distinctions, indicating significant genetic variability between the parent plants and their crosses. This disparity suggests the potential for genetic enhancement through the exploitation of the mungbean diverse genetic pool. Moreover, it underscores the presence of a marked heterosis for the traits under investigation. Equivalent results for significant variation for one or more traits in mungbean was in consonance with Patil *et al*. (2020) [7, 25]. The primary distinction between additive and non additive gene action lies in how alleles manifest themselves. Additive gene action involves both alleles expressing themselves and contributing independently to a trait, making it simpler for breeders to manage. Conversely, non additive gene action entails one allele exerting a stronger influence than the other. Jinks and Jones (1958) [12] stated greater additive variance than dominance variance depict the trait with additive gene effect while greater former of dominance variance than additive one indicate non additive gene effect. In addition, when the variance reaches zero, it signals the presence of epistasis. Various types of interactions, such as A × A, A × D, and D × D, if significant, suggest non-allelic interaction. Panse (1942) [22] proposed that the presence of additive genetic variance enhances the probability of establishing superior genotypes in initial segregating generations. Nonetheless, when dominant and epistatic interactions are prevalent, the implementation of selection should be postponed to subsequent generations. This approach allows for the utilization of appropriate breeding strategies aimed at attaining desirable genotypes. In present study, analysis of variance (Table 3) showed that the mean square due to GCA and SCA were significant for all characters. Therefore, the significant differences in GCA and SCA variances suggested that both additive and non-additive genetic mechanisms contributed to the regulation of these traits across the mungbean genotypes (Table 3). The presence of both additive and non additive gene effects for yield and important yield component traits in mungbean has been documented by Anbumalarmathi *et al.* (2004) [1]; Barad *et al.* (2008) [3]. However, the proportion of variances due to $\sigma^2$ GCA/$\sigma^2$ SCA, the value stayed notably below one for all traits ranged from 0.571 to 0.997, indicated that non additive gene action was more influence in the inheritance of these characters in comparison to additive types. Cockerham (1961) [8] suggested that the presence of non-additive genetic effects serves as the main rationale for initiating a hybrid breeding program. The predominance of non additive genetic effects in the expression of various traits in mungbean was also accordance with Anbumalarmathi *et al*. (2004) [1] for days to 50% flowering, Kohakade *et al*. (2021) [16] for days to maturity, Bhagora *et al*. (2013) [4] for plant height, Marappa (2008) [17] for number of primary branches/plant, Mohan and Sheeba (2019) [18] for number of clusters/plant, Purohit *et al*. (2016) [26] for number of pods/plant, and number of seeds/pod, Chavan *et al*. (2019) [7] for pod length, Pathak *et al.* (2019) [24] for 100 seed weight and Singh *et al*. (2021) [31] for seed yield/plant. From the estimates of additive and dominance variance, revealed greater part of dominance variance was

predominant for all the characters except plant height, number of clusters/plant and number of seeds/pod. Further the degree of dominance less than one was observed for plant height (0.934), number of clusters/plant (0.715) and number of seeds/pod (0.936) indicated inheritance in these traits due to partial dominance while, degree of dominance displayed higher than one indicated over dominance in inheritance for days to 50% flowering (1.259), days to maturity (1.349), number of primary branches/plant (1.073), number of secondary branches/plant (1.320, number of pods/plant (1.785), pod length (1.210), 100 seed weight (1.248) and seed yield/plant (1.038). These results were accordance with the similar findings of Sujatha and Kajjidoni (2013) [33], and Bhavani *et al.* (2016) [5]. A thorough examination of the results from these investigations figure out that, both additive and non additive genes governed yield and its associated traits but leveraging the potential of both types of gene actions, non additive gene effects paved a precise role in the genetic inheritance of all these investigated traits.

**Table 1:** Source of seed and salient characteristics of the parents.

| Sr. No | Parents | Source | Characteristics of parents |
|---|---|---|---|
| | **Females** | | |
| 1. | BM 4 | ARS, Badnapur | Short poded and medium size seed. |
| 2. | BM 2002-1 | ARS, Badnapur | Dull colour and bold seeded |
| 3. | Phule Chetak | MPKV, Rahuri | Shiny seeded |
| 4. | Kopergoan | Dr. PDKV, Akola | Long poded and bold seeded. |
| 5. | AKM 4 | Dr. PDKV, Akola | Short poded. |
| 6. | PKV Green gold | Dr. PDKV, Akola | Tolerant to powdery mildew. |
| | **Males** | | |
| 1. | BWMCD 5 | ARS, Badnapur | Tolerant to *Insitu* germination |
| 2. | BWMCD 10 | ARS, Badnapur | Tolerant to *Insitu* germination |
| 3. | BWMCD 7 | ARS, Badnapur | Tolerant to *Insitu* germination |
| 4. | BWMC 20 | ARS, Badnapur | Long poded |
| 5. | BWMC 20-1 | ARS, Badnapur | Long poded |
| 6. | BWMC 25 | ARS, Badnapur | Long poded |
| 7. | BWMC 30-2-1 | ARS, Badnapur | Black seeded and long poded. |
| 8. | BM 21-21 | ARS, Badnapur | Yellow seeded and long poded. |
| 9. | IC 39564 | ICAR-NBPGR, New Delhi | Bold seeded. |

**Table 2:** ANOVA for combining ability in a Line × Tester analysis for yield and its component in Mungbean.

| Source | D.f | Days to 50% flowering | Days to maturity | Plant height (cm) | No. of primary branches/ plant | No. of secondary branches/ plant | No. of clusters/ plant | No. of pods/ plant | No. of seeds/ pod | Pod length (cm) | 100 seed weight (g) | Seed yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Replications | 1 | 1.22 | 0.11 | 14.47 | 0. 18 | 0.01 | 1.32 | 9.67 | 0.50 | 2.11 | 0.10 | 6.88 |
| Genotypes | 68 | 10.37** | 14.83** | 71.95** | 5.70** | 4.14** | 8.78** | 106.74** | 2.42** | 6.96** | 1.00** | 24.6** |
| Parents | 14 | 8.69** | 16.56** | 28.88** | 0.76** | 4.48** | 0.79** | 4.88** | 2.12** | 5.65** | 0.86** | 8.63** |
| Parent v/s crosses | 1 | 0.65** | 293.42** | 104.62** | 66.56** | 89.37** | 227.15** | 4289.36** | 1.38** | 31.18** | 1.08** | 706.10** |
| Crosses | 53 | 11.00** | 9.12** | 82.71** | 5.85** | 3.23 ** | 6.77** | 54.73** | 2.54** | 6.85** | 1.03** | 15.05** |
| Lines | 5 | 7.15** | 19.13** | 28.39** | 0.48** | 1.58** | 1.01** | 9.96** | 3.28** | 4.42** | 0.82** | 10.83** |
| Testers | 8 | 10.72** | 11.88** | 22.71** | 0.74** | 0.99** | 0.75** | 2.31** | 1.64** | 6.78** | 0.95** | 8.33** |
| Lines × testers | 40 | 8.51** | 8.57** | 50.86** | 4.18** | 2.66** | 3.53** | 53.66** | 1.66** | 5.45** | 0.81** | 12.06** |
| Error | 68 | 1.91 | 4.42 | 4.75 | 0.34 | 0.30 | 1.18 | 4.96 | 0.30 | 0.51 | 0.06 | 4.76 |

**Table 3:** Estimation of GCA and SCA, Additive and Dominance variances for yield and its contributing traits in Mungbean.

| Sr. No. | Source | $\sigma^2$ GCA | $\sigma^2$ SCA | $\sigma^2$ GCA/$\sigma^2$ SCA | $\sigma^2$ A | $\sigma^2$ D | $(\sigma^2 A/\sigma^2 D)^{1/2}$ | Degree of dominance |
|---|---|---|---|---|---|---|---|---|
| 1 | Days to 50% flowering | 1.041** | 3.300** | 0.315 | 2.082 | 3.300 | 0.631 | 1.259 |
| 2 | Days to maturity | 0.570* | 2.074* | 0.275 | 1.139 | 2.074 | 0.549 | 1.349 |
| 3 | Plant height | 13.207** | 23.056** | 0.573 | 26.414 | 23.056 | 1.146 | 0.934 |
| 4 | No. of primary branches/plant | 0.833** | 1.918** | 0.434 | 1.665 | 1.918 | 0.868 | 1.073 |
| 5 | No. of secondary branches/plant | 0.338** | 1.179** | 0.287 | 0.677 | 1.179 | 0.574 | 1.320 |
| 6 | No. of clusters/plant | 1.150** | 1.175** | 0.979 | 2.301 | 1.175 | 1.958 | 0.715 |
| 7 | No. of pods/plant | 3.822* | 24.348* | 0.157 | 7.644 | 24.348 | 0.314 | 1.785 |
| 8 | No. of seeds/pod | 0.388** | 0.679** | 0.571 | 0.775 | 0.679 | 1.142 | 0.936 |
| 9 | Pod length | 0.843** | 2.470** | 0.341 | 1.687 | 2.470 | 0.683 | 1.210 |
| 10 | 100 seed weight | 0.122** | 0.378** | 0.323 | 0.243 | 0.378 | 0.642 | 1.248 |
| 11 | Seed yield/plant | 2.102** | 4.533** | 0.464 | 4.205 | 4.533 | 0.928 | 1.038 |

Where,

1. Ratio $\sigma^2$ GCA/$\sigma^2$ SCA is < 1 indicated non additive gene action., Ratio of $\sigma^2$ GCA/$\sigma^2$ SCA > 1 indicated additive gene action.
2. Degree of dominance is > 0 < 1 indicated partial dominance., Degree of dominance is > 1 indicated over dominance.

**Conclusion**:

The investigation findings indicated that most traits are influenced by additive and non-additive gene effect. However, non-additive gene action was formerly more dominated in genetic interaction of yield and its attributes. Therefore, it is suggested that, hybridization followed by

selection in later generations will be pave swift progress in mungbean improvement.

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