ASSESSMENT OF GENETIC VARIABILITY BY COMBINED HYBRIDIZATION AND MUTATION IN BLACK GRAM [*Vigna mungo* (L.) Hepper]

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Thesis submitted to the
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DEPARTMENT OF GENETICS AND PLANT BREEDING
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CERTIFICATE

This is to certify that the thesis entitled **'ASSESSMENT OF GENETIC VARIABILITY BY COMBINED HYBRIDIZATION AND MUTATION IN BLACK GRAM [*Vigna mungo* (L.) Hepper]'** submitted in partial fulfillment of the requirements for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING** to the College of Agriculture, Shivamogga, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga is a bonafide record of research work carried out by **ANILKUMAR LALASING CHAVAN., ID. No. MA1TAI0341** (anilkumarchavan97@gmail.com) during the period of study in this university under my guidance and supervision and no part of this thesis has previously formed the basis for the award of any other degree, diploma, associateship, fellowship or any other similar titles.

Shivamogga
December, 2021

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(Anilkumar Lalasing Chavan)

Assessment of Genetic Variability by Combined Hybridization and Mutation in Black gram [*Vigna Mungo* (L.) Hepper.]

(ANILKUMAR LALASING CHAVAN)

ABSTRACT

A field experiment was carried out during *Rabi* 2020 at ZAHRS, Shivamogga, to determine the genetic parameters among 400 F_3M_2 progeny lines of cross (PU31 × Rashmi) in blackgram. Significant variations in progeny lines were documented for most of the traits through analysis of variance, indicating the vast genetic variability. High phenotypic coefficient of variation (PCV) was recorded for the trait seed yield per plant and moderate genotypic coefficient of variation (GCV) were observed for the traits viz., number of branches per plant, number of seeds per pod, number of pods per plant and seed yield per plant. The estimated GCV and PCV values depict the level of variability available in the population. High heritability combined with high genetic advance as *per cent* of mean were documented for number of pods per plant. This indicates that effective selection can be made for these traits. Correlation studies displayed that traits *viz*., days to 50 *per cent* flowering, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, 100 seed weight and number of seeds per pod were positively and significantly correlated with seed yield per plant. Path coefficient analysis revealed highest positive direct effect were observed for traits number of pods per plant and number of seeds per pod on seed yield per plant. Highest number of transgressive segregants were identified for plant height and number of clusters per plant. The results showed the existence of large count of transgressive segregants in early segregating generations for all the traits which showed a wide scope for the meticulous selection of these genotypes.

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ಉದ್ದಿನ ಬೇಳೆ [*ವಿಗ್ನಾ ಮುಂಗೊ*, (ಎಲ್) ಹೆಪ್ಪರ್] ಸಂಯೋಜಿತ ಸಂಕರೀಕರಣ ಮತ್ತು ರೂಪಾಂತರದಿಂದ ಅನುವಂಶೀಯ ಪರಿವರ್ತನಶೀಲತೆಯ ಮೌಲ್ಯಮಾಪನ

(ಅನಿಲಕುಮಾರ ಲಾಲಸಿಂಗ ಚವ್ಹಾಣ)

ಸಾರಂಶ

ಪ್ರಸ್ತುತ ಅಧ್ಯಯನವನ್ನು ವಲಯ ಕೃಷಿ ಹಾಗೂ ತೋಟಗಾರಿಕಾ ಸಂಶೋಧನಾ ಕೇಂದ್ರ, ಶಿವಮೊಗ್ಗ, ೨೦೨೦ ಹಿಂಗಾರುವಿನಲ್ಲಿ ೪೦೦ ಎಫ್‌೩ಎಮ್‌೨ ಸಂತಾನ ಸಾಲುಗಳ ಅನುವಂಶಿಕ ನಿಯತಾಂಕಗಳನ್ನು ನಿರ್ಧರಿಸುವ ಉದ್ದೇಶದಿಂದ ನಡೆಸಲಾಯಿತು ಅನೋವಾ ಪರೀಕ್ಷೆಯ ಮೂಲಕ ಪ್ರತಿಯೊಂದು ಸಂತಾನ ಸಾಲುಗಳ ಎಲ್ಲಾ ಗುಣಲಕ್ಷಣಗಳಲ್ಲು ಗಮನಾರ್ಹ ವ್ಯತ್ಯಸವಿದೆ, ಬೀಜದ ಇಳುವರಿಗೆ ಅಧಿಕ ಪಿಸಿವಿ ಹಾಗೂ ಸಸ್ಯದ ಶಾಖೆಗಳ ಸಂಖ್ಯೆ, ಕಾಯಿಯಲ್ಲಿರುವ ಬೀಜಗಳ ಸಂಖ್ಯೆ, ಗಿಡದಲ್ಲಿನ ಕಾಯಿಗಳ ಸಂಖ್ಯೆ ಹಾಗೂ ಕಾಯಿಯಲ್ಲಿರುವ ಬೀಜದ ಇಳುವರಿಗೆ ಮಧ್ಯಮ ಜಿ.ಸಿ.ವಿ.ಯು ಕಂಡು ಬಂದಿದೆ, ಸಸ್ಯದಲ್ಲಿರುವ ಕಾಯಿಗಳು ಹೆಚ್ಚಿನ ಅನುವಂಶಿಯತೆ ಮತ್ತು ಸರಾಸರಿ ಶೇಕಡಾವಾರು ಅನುವಂಶಿಕ ಮುಂಗಡವನ್ನು ಹೊಂದಿದೆ. ಸಸ್ಯದ ಬೀಜದ ಇಳುವರಿಯು ೫೦ ಪ್ರತಿಶತದಷ್ಟು ಹೂಬಿಡುವ ದಿನಗಳು, ಸಸ್ಯದ ಉದ್ದ, ಸಸ್ಯದಲ್ಲಿರುವ ಕಾಯಿಗಳ ಸಂಖ್ಯೆ, ಸಸ್ಯದ ಗೊಂಚಲುಗಳ ಸಂಖ್ಯೆ ಗೊಂಚಲಿನಲ್ಲಿರುವ ಕಾಯಿಗಳ ಸಂಖ್ಯೆ, ಕಾಯಿಯ ಉದ್ದ, ೧೦೦ ಬೀಜಗಳ ತೂಕ ಹಾಗೂ ಕಾಯಿಯಲ್ಲಿರುವ ಬೀಜಗಳ ಸಂಖ್ಯೆಯ ಗುಣಲಕ್ಷಣಗಳು ಗಮನಾರ್ಹ ಧನಾತ್ಮಕ ಸಂಬಂಧಗಳನ್ನು ತೊರಿಸಿದೆ ಎಂದು ಪರಸ್ಪರ ಸಂಬಂಧದ ಅಧ್ಯಯನ ಬಹಿರಂಗ ಪಡಿಸಿವೆ. ಗಿಡದ ಬೀಜದ ಇಳುವರಿಯ ಮೇಲೆ ಗಿಡದಲ್ಲಿ ಕಾಯಿಗಳು ಹಾಗೂ ಕಾಯಿಯಲ್ಲಿರುವ ಬೀಜದ ಸಂಖ್ಯೆ ಹೆಚ್ಚಿನ ಧನಾತ್ಮಕ ಮತ್ತು ನೇರ ಪರಿಣಾಮ ಬೀರುವುದನ್ನು ಮಾರ್ಗ ವಿಶ್ಲೇಷಣೆಯ ಅಧ್ಯಯನದಿಂದ ತಿಳಿದು ಬಂದಿದ್ದು ಗಿಡದ ಎತ್ತರ, ಗಿಡದಲ್ಲಿನ ಗೊಂಚಲುಗಳ ಸಂಖ್ಯೆಯ ಗುಣಲಕ್ಷಣಗಳಿಗೆ ಅತಿ ಹೆಚ್ಚಿನ ಸಂಖ್ಯೆಯ ಅತಿಕ್ರಮಣ ಪ್ರತ್ಯೇಕಗಳನ್ನು ಗುರುತಿಸಲಾಗಿದ್ದು ಫಲಿತಾಂಶಗಳು ಎಲ್ಲಾ ಗುಣಲಕ್ಷಣಗಳಿಗೆ ಆರಂಭಿಕ ಪೀಳಿಗೆಯಲ್ಲಿ ಅತಿಕ್ರಮಣ ಪ್ರತ್ಯಕಗಳ ದೊಡ್ಡ ಸಂಖ್ಯೆಯ ಅಸ್ತಿತ್ವವನ್ನು ತೊರಿಸಿರುತ್ತವೆ.

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ಡಿಸಂಬರ್-೨೦೨೧

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CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

INTRODUCTION

I INTRODUCTION

Black gram [*Vigna mungo* (L.) Hepper] (2n = 22) belongs to the family *Fabaceae* and the genus *Vigna.* Black gram (*Vigna mungo* (L.) Hepper) is a member of the Asian *Vigna* group of crop under subgenus Ceratotropics (Verdcourt, 1970).

Black gram is originated in India (Vavilov, 1926). The progenitor of black gram is believed to be *Vigna mungo* var. *silvestris*, (Lukoki *et al*., 1980). It is a staple crop in central and South-East Asia. However, it is extensively used only in India and now grown in the Southern United States, West Indies, Japan and other tropics (Delic *et al*., 2009).

Black gram is one of the highly priced pulse crop cultivated in India. It can be most appropriately referred as the "king of the pulses" due to its taste and numerous other nutritional qualities. Black gram is an ideal combination of all nutrients, which includes proteins, carbohydrates, fat, amino acids, vitamins and minerals (Karamany, 2006). It stands next to soybean in its protein content and it is rich in vitamin A, B1, B3 and has a small amount of thiamine, riboflavin, niacin and vitamin C (Das *et al*., 2002). Black gram also has high calorie content, *i.e.* 347 calories per 100 g of black gram. Therefore, black gram is one of the cheapest available protein sources for vegetarians (Tharanathan and Mahadevamma, 2003).

The biological value of black gram improves significantly when wheat or rice is combined with it because of the complementary relationship between the essential amino acids such as lysine and sulphur-containing amino acids, methionine and cysteine. In addition, being an important source of human food, it is also used as nutritional fodder, especially for milch animals. Black gram also has medicinal properties like curing diabetes, sexual dysfunction, nervous disorder, hair disorders, digestive system disorders and rheumatic afflictions. Furthermore, it is valued for its high digestibility and freedom from the flatulence effect (Fary, 2002).

Being a leguminous crop, it has the characteristics of restoring soil fertility by fixing atmospheric nitrogen through symbiotic association with *Rhizobium* bacteria present in the root nodules (Ahmad *et al.,* 2001). It is usually cultivated in a cereal-pulse cropping system to conserve soil nutrients and utilize the leftover soil moisture, particularly after rice cultivation. It is a short duration pulse crop (Delic *et al.,* 2009), usually flowering within 35-60 days of sowing and maturing within 65 to 90 days. It is generally cultivated as *a Kharif* crop and does well in the *Rabi* and summer season.

Black gram accounts for 13 *per cent* of the total pulse area and 10 *per cent* of total pulse production in India. It occupies an area of about 5.44 m ha, with a production of 3.56 mt and productivity of 604 kg ha^{-1}. Karnataka is one of the major black gram growing states of India with an area of 0.81 lakh hectares, with a production of 0.44 lakh tonnes and productivity of 821.5 kg ha^{-1} (Anonymous, 2020).

The critical position of pulse production, particularly black gram against the increased population, poses a challenge for breeders to develop high yielding, short duration, bold-grained and disease-resistant varieties. This can be achieved through a planned breeding programme along with the adoption of proper agronomic practices.

Grain yield is the most complex character and is influenced by several component characters such as days to 50 *per cent* flowering, plant height, number of pods per cluster, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length, 100 seed weight and grain yield per plant. In black gram yield can be enhanced by selecting highly heritable and correlated morphological attributes that contribute to yield in a given environment than combining them to identify genotypes with a desirable combination of traits.

A survey on genetic parameters such as variability, heritability and genetic advance involved in the inheritance of morphological attributes in the segregating populations will provide a systematic approach for quantitative traits under investigation.

The variability available in the breeding material helps in selecting the superior plant types. Heritability indicates the relative success of selection as it measures the relative amount of heritable portion of variability. High heritability combined with high genetic advance is more useful than heritability alone in predicting the resultant effect on selecting the best individual (Johnson *et al.,* 1955).

A clear understanding of the association of plant characters with yield is necessary for a successful crop improvement programme. Correlation coefficients show the magnitude and direction of the association of yield components and facilitate the plant breeders in identifying traits that are useful as selection criteria to improve crop yield under the target environment through correlated response.

Path coefficient analysis is a standardized partial regression coefficient. This splits the correlation into the measures of direct and indirect effects. Therefore it reveals whether the association of these characters with the yield is due to their direct effect on yield or it is a consequence of their indirect effect through some other character. If the correlation between yield and other characters is due to the direct effect of that particular character, it reflects the true relationship between them.

The success of selection in self-pollinated crops depends on the extent to which breeders can fix the transgressive segregation in early generations as high heterotic crosses would result in more productive transgressive segregants in later generations (Arunachalam 1981). Transgressive segregation creates an opportunity for new genotypes to arise that are more fit than their ancestors. Transgressive segregants are more adaptable under various environmental conditions. Transgressive segregants can be predicted and observed within progenies of an early segregating generation.

Therefore, by keeping all these in view, the present study in black gram was undertaken with F_3M_2 populations derived from hybridization of PU31 × Rashmi and mutation by using gamma radiation of 20 Kr dosage, which were selected based on high mean performance for seed yield. With this premise, the present investigation was undertaken with the following objectives.

1. To assess the genetic variability in F_3M_2 segregating lines of black gram
2. To study correlation and path analysis in F_3M_2 segregating lines of black gram
3. To identify the transgressive segregants for yield and its attributing traits in black gram

REVIEW OF LITERATURE

II REVIEW OF LITERATURE

Black gram is an important pulse crop of the tropic and sub-tropic areas and have been identified as a potential for low cost dietary protein in many countries (Girish *et al.,* 2012). The economic product of black gram is seed and the yield of black gram is very low because of the non-availability of high yielding cultivars. The lack of stable and high yielding cultivars is one of the major constraints in improving its production and productivity as the best cultivars may not necessarily repeat the performance in every year with change in weather variables. The available literature in connection with the objectives of the present investigation has been reviewed under the following sub-headings.

2.1 Variability, heritability and genetic advance

2.2 Character association and path coefficient analysis

2.3 To identify the transgressive segregants for yield and its attributing traits in black gram

2.1 Variability, heritability and genetic advance

In any plant breeding programme the ultimate aim is to improve the plant traits for agronomic and economic benefits. Variability is an essential pre-requisite in any crop improvement program and the presence of wide spectrum of variability will enhance the chance of selecting desired genotypes.

Meshram *et al*. (2012) studied genetic variability in 27 black gram genotypes revealed that the characters *viz*., plant height, number of pods per plant and grain yield per plant exhibited high genotypic variance and heritability coupled with genetic advance indicating the presence of high additive gene effects suggesting its utility for direct selection.

In the study of gamma irradiated (15kR, 25kR and 35kR) black gram varieties T-9, TPU-4 and AK U-18 recorded high variability for pods per plant and seed yield among the genotypes in M_3 generation (Meshram *et al*. 2013).

Narasimhan *et al.* (2013) recorded higher phenotypic and genotypic coefficients of variation among twelve black gram genotypes for total seed yield, number of pods per plant. High heritability estimates were recorded for plant height, number of branches, number of bunches, number of pods per plant, pod length, number of seeds per pod, test weight and total seed yield. High genetic advance expressed as percentage of mean was recorded for plant height, number of branches, number of clusters, number of pods per plant and total seed yield.

Sowmini and Jayamani (2013) studied genetic variability among 193 black gram lines along with their parents stated that GCV is high for the traits single plant yield, number of clusters per plant and number of pods per plant. High heritability *per cent* was observed for days to maturity, number of seeds per pod and hundred seed weight. High genetic advance as *per cent* of mean was observed for plant height, number of clusters per plant, number of pods per plant, single plant yield and hundred seed weight. High heritability coupled with high genetic advance as *per cent* of mean was observed for hundred seed weight.

Suresh *et al*. (2013) observed that the seed yield per plant had high significant positive correlation with pods per plant in mung bean. The trait, plant height had high positive significant correlation with pods per plant and seeds per pod. Days to 50 *per cent* flowering had high significant positive association with days to maturity. The genotypic correlation of days to 50 *per cent* flowering and number of pods per plant had positive significant association with seeds per pod. In F_1 generation, clusters per plant, pods per plant, days to maturity, days to 50 *per cent* flowering, pods per cluster and 100 seed weight showed high significant and positive association with seed yield per plant and suggested that these traits could be selected indirectly in order to improve the seed yield per plant in mung bean.

Deepshikha *et al.* (2014) observed high phenotypic coefficient of variation for number of pods per plant, plant height at maturity, grain yield per plant and high genotypic coefficient of variation for number of pods per plant and grain yield per plant. High heritability coupled with high genetic advance as *per cent* of mean was observed for number of pods per plant, number of clusters per plant, number of seeds per pod, seed index and grain yield per plant, suggesting their utility for effective selection for yield improvement of black gram.

Panigrahi *et al.* (2014) reported higher PCV than GCV for all the quantitative characters assessed in black gram during *rabi* season. It was concluded that the selection of the traits such as number of primary branches per plant, clusters per plant, pods per plant and seed yield with high GCV are important in improvement, while characters like 100 seed weight, pod length and plant height exhibited moderate GCV value whereas days to 50 *per cent* flowering, days to maturity and seeds per pod recorded low GCV values.

Patel *et al*. (2014a) evaluated 76 genotypes in randomized block design with three replications in summer season. The highest genotypic and phenotypic coefficient of variances were observed for grain yield per plant followed by number of pods per plant and number of cluster per plant. High genetic advance coupled with high heritability was observed for grain yield per plant, number of pods per plant and number of clusters per plant.

The presence of moderate magnitude of heritability in broad sense, genetic advance as *per cent* of mean, phenotypic and genotypic coefficients of variation in respect of number seeds per pod, plant height and yield has been reported by Mandal *et al.* (2014) while working with 135 black gram genotypes.

Ramya *et al.* (2014) studied M_2 generation of black gram, recorded high estimates of PCV and GCV for primary branches per plant, number of clusters per plant, number of pods per plant and single plant yield. High heritability coupled with high genetic advance as *per cent* of mean was observed for number of primary branches and seed yield per plant.

Kumar *et al.* (2015) studied genetic variability in 50 genotypes of black gram, high PCV and GCV were observed for number of pods per plant, number of clusters per plant, number of seeds per plant, seed yield per plant. High heritability was observed for days to 50 *per cent* flowering, seed yield per plant, days to maturity, number of pods per plant, number of clusters per plant, hundred seed weight, number of seeds per pod, number of pods per cluster, pod length. Low heritability was observed for plant height and genetic advance as *per cent* of mean was high for number of pods per cluster, number of clusters per plant, number of pods per plant, number of seeds per pod and seed yield per plant.

In an experiment carried out by Vijay *et al.* (2015) in black gram with fourteen lines, three testers and 42 F_1 plants, it was found that highest GCV is recorded for seed yield followed by clusters per plant, fodder biomass, seeds per pod, pod weight, total biomass and branches per plant. The highest heritability and genetic advance were recorded for days to 50 *per cent* flowering and clusters per plant respectively. High genetic advance as *per cent* of mean coupled with moderate to high heritability was observed for number of clusters per plant, pods per plant, seeds per pod, pod weight, seed yield per plant and fodder biomass.

Gowsalya *et al.* (2016) carried out an investigation among eighty genotypes of black gram to assess genetic variability and they recorded highest GCV for number of branches per plant, seed yield per plant, number of clusters per plant, pod length, number of pods per plant and plant height. High heritability coupled with high genetic advance was observed for pod length, number of branches, plant height, clusters per plant, seed yield per plant and number of pods per plant.

Priyanka *et al.* (2016a) conducted variability studies among 24 black gram lines and revealed that the genotypes were highly variable for number of clusters per plant, pods per plant, seeds per pod and seed yield per plant. Phenotypic coefficients of variation were greater than their corresponding genotypic coefficient of variability. Broad-sense heritability was higher for all the traits except for days to 50 *per cent* flowering and branches per plant. High heritability coupled with high genetic advance as *per cent* of mean was observed for the characters pods per cluster, pod length, test weight, seeds per pod and seed yield per plant indicating that these characters are mainly controlled by additive genes and selection of such traits might be effective for the improvement of grain yield.

Anu *et al*. (2017) evaluated 36 black gram genotypes for genetic variability and found that high phenotypic coefficient of variation has been recorded by clusters per plant while medium values were found for plant height and primary branches per plant. Medium genotypic coefficient of variation was reported for plant height and clusters per plant. High heritability was shown by traits like seed yield per plant, biological yield per plant, pods per plant and harvest index. Estimated genetic advance and genetic advance as percentage of mean were moderately high for plant height and moderate for other traits like cluster per plant, seed index, biological yield per plant and seed yield per plant.

Rolaniya *et al.* (2017) evaluated 36 black gram genotypes and found that moderate genotypic coefficient of variation and phenotypic coefficient of variation was recorded for number of clusters per plant, primary branches per plant and seed yield per plant. High broad sense heritability and high genetic advance as *per cent* of mean was recorded for seed yield per plant and plant height confirming the presence of additive gene action.

Variability studies conducted by Hemalatha *et al.* (2017) among 25 black gram genotypes revealed that maximum GCV and PCV were recorded for harvest index, pods per plant and seed yield per plant. High heritability was recorded for pods per plant, biological yield per plant, days to maturity, days to 50 *per cent* flowering, harvest index, seed yield per plant. High heritability coupled with high genetic advance as *per cent* of mean was recorded for pods per plant.

Genetic variability studies among 15 black gram accessions along with two checks and two local varieties by Jyothi *et al.* (2017) for grain yield revealed that heritability in broad sense was high for seed yield, test weight of seed and total biomass. High genetic advance as *per cent* of mean was observed for seed yield, test weight of seed and total biomass. High heritability coupled with high genetic advance as *per cent* of mean was observed for seed yield, total biomass and test weight of seed.

Kuralarasan *et al.* (2017) analyzed 26 mutant lines of urad bean for genetic variability. Presence of moderate magnitude of heritability in broad sense, genetic advance as percentage of mean, phenotypic and genetic coefficient of variability in respect of number of branches per plant, number of pods per plant, plant height and seed yield indicated predominance of additive gene action in governing the inheritance of these traits.

Ozukum and Sharma (2017) in their study on five urad bean breeding materials revealed that relatively higher estimate of phenotypic coefficient of variation were observed number of pods per plant and yield per plot which demonstrated the effect of environment upon the traits and there is sufficient genetic variability to justify selection for improvement in the urad bean lines. High broad sense heritability estimates were recorded for days to 80 *per cent* maturity, days to 50 *per cent* flowering and 100 seed weight. The highest genetic advance *per cent* of mean was recorded for yield per plot (28.92 %) followed by number of pods per plant.

Panda *et al.* (2017) evaluated 50 black gram genotypes and studied the magnitudes of heritability in broad sense and found to be low for number of seeds per pod, pod girth and pod length, moderate for days to maturity, days to 50 *per cent* flowering and number of branches per plant. High heritability for number of clusters per plant, hundred seed weight, plant height, number of pods per plant, number of seeds per plant and seed yield per plant was recorded. The high heritability in conjunction with high genetic advance was noted in number of seeds per plant and seed yield per plant.

Yusufzai et al. (2017) found considerable variation in F_2 population for days to 50 *per cent* flowering, days to 75 *per cent* maturity, plant height, branches per plant, pods per plant, pod length, seeds per pod, 100-seed weight and seed yield per plant in mung bean genotypes. Higher values of PCV than GCV were found for all the traits. Highest efficiency of genetic advance was observed in seed yield per plant followed by number of pods per plant, number of seeds per pod and plant height.

Aftab *et al.* (2018) examined 39 black gram genotypes including two checks (T9 and AZAD-1) to study genetic variability parameters for 13 traits. Number of clusters per plant followed by primary branches per plant and seed yield per plant exhibited moderate GCV and PCV, whereas higher estimates of GCV and PCV were obtained for biological yield, harvest index, seed yield per plant. High values of genetic advance for seed yield per plant revealed direct selection for improvement in black gram.

Blessy *et al.* (2018) studied genetic variability in 14 black gram genotypes along with one check (T-9) and noticed high estimates of phenotypic coefficients of variation than genotypic coefficients of variation. GCV and PCV were high for clusters per plant, primary branches and pods per plant. Clusters per plant, seed index, primary branches, pods per plant possessed high estimates of heritability coupled with high genetic advance.

Chauhan *et al.* (2018) studied 21 black gram genotypes to estimate genetic variability, heritability and genetic advance in black gram. The experimental study was mainly relied on selection of transgressive segregants. They reported that families and progenies within families were significantly different for majority of the traits and found to be highly variable for biological yield, harvest index and seed yield. High heritability coupled with high genetic advance were recorded for plant height, branches per plant, biological yield and seed yield, thus reflecting the significance of selection to develop superior genotypes in black gram breeding program.

Gandi *et al*. (2018) evaluated nine crosses of black gram in F_2 and F_3 generations to estimate genetic variability, heritability and genetic advance and they construed that the estimates of PCV were higher than GCV. The genotypic variance was observed highest for clusters per plant, pods per cluster and single plant yield in both the generations. High heritability coupled with high genetic advance as *per cent* of mean was recorded for the characters like clusters per plant, pods per cluster, pods per plant, seeds per pod and single plant yield indicating that MASH 114 x TNY LOCAL and IPU 0233 x TNY LOCAL crosses were amenable for selection.

Patidar *et al*. (2018) estimated genetic variability for 12 qualitative as well as quantitative characters in 29 black gram genotypes. They recorded high GCV values for seed yield per plant, biological yield per plant, number of pods per plant and number of branches per plant. High heritability was obtained in number of branches per plant, 100 seed weight, plant height, number of pods per plant. High heritability in association with genetic advance were noted for number of branches per plant and number of pods per plant.

Shobha *et al.* (2018) studied genetic variability in 120 black gram genotypes revealed high PCV and GCV for the traits *viz.*, single plant yield, number of clusters per plant, number of pods per plant and number of primary branches per plant. High heritability coupled with high GAM was recorded for the traits *viz.,* plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant and single plant yield.

Sushmitharaj *et al*. (2018) studies 32 black gram genotypes and revealed high GCV and PCV for the traits *viz.*, number of clusters per plant, number of pods per plant, hundred seed weight and single plant yield. High heritability coupled with high GAM were observed for the traits *viz.,* plant height, number of clusters per plant, number of pods per plant and single plant yield.

Tank *et al*. (2018) analyzed 45 black gram genotypes to study genetic variability for 14 traits *viz.,* days to 50 *per cent* flowering and days to 75 *per cent* maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, pod length, number of seeds per pod, seed yield per plant, biological yield per plant, harvest index, 100 seed weight and seed protein content. Experimental findings revealed that number of branches per plant followed by 100 seed weight, number of clusters per plant, number of pods per plant and plant height showed moderate to high GCV, heritability and genetic gain.

Chaithanya *et al*. (2019) investigated 28 black gram genotypes to estimate genetic variability for 12 traits and reported high PCV and GCV for harvest index and seed yield per plant. High heritability coupled with moderate genetic advance were obtained in number of pods per plant, pod length, number of primary branches per plant, harvest index, biological yield and seed yield per plant.

Panwar *et al*. (2019) observed significant differences between PCV and GCV for yield and its contributing traits among 46 black gram genotypes. High values of PCV were noted for seed yield per plant, number of seeds per plant, biological yield per plant, number of pods per plant and harvest index. Whereas highest GCV was observed in seed yield per plant followed by number of pods per plant, biological yield and number of seeds per plant.

Sathees *et al*. (2019a) evaluated 162 F_2 plants derived from the cross IC 436656 x KKB 14045 in black gram. High PCV and GCV were observed for number of primary branches, number of clusters per plant, number of pods per plant and single plant yield. High heritability coupled with high genetic advance was registered for the traits *viz.,* days to 50 *per cent* flowering, number of clusters per plant, hundred seed weight, pod length and single plant yield suggesting the additive gene action.

Senthamizhselvi *et al*. (2019) studied variability and inter relationship among seven yield and its attributing traits in 112 black gram genotypes. They reported significant differences for all the characters under study. Heritability and genetic advance estimates were high for plant height, primary branches per plant, pods per plant, 100 seed weight and yield per plant, whereas high heritability with low genetic advance was noted for days to 50 *per cent* flowering.

Chowdhury *et al*. (2020) studied the genetic variability, character association among nine yield and related traits in 51 varieties and advance breeding lines of urad bean. They recorded significant variation for all the quantitative characters studied. The GCV and PCV estimates were high for branches per plant, pods per plant and yield per plant, whereas moderate GCV and PCV were recorded of plant height, seeds per pod and pod length. High heritability coupled with high GA as *per cent* of mean was observed for number of branches per plant, number of pods per plant and seed yield per plant. Days to 50 *per cent* flowering, number of seeds per pod, days to maturity and 100 seed weight showed high heritability estimates with moderate to low genetic advance such that their response to selection would be poor.

Gomathi *et al*. (2020) evaluated 140 F_3 progenies derived from the cross IC 436656 × KKB14045 in black gram. High heritability was recorded for plant height, days to 50 *per cent* flowering, number of primary branches per plant, number of clusters per plant, number of pods per plant, 100 seed weight and total seed yield.

Khan *et al*. (2020a) studied genetic variability in 60 black gram genotypes revealed high GCV for seed yield per plant, number of pods per plant, number of clusters per plant and high heritability was found for 100 seed weight followed by number of pods per plant and pod length. High genetic gain was observed for number of pods per plant followed by seed yield per plant. The characters *viz.,* number of clusters per plant, number of pods per plant, seed yield per plant and harvest index showed high GCV, heritability and genetic gain.

Sarvani *et al*. (2020) conducted variability studies among the F_3 population of three black gram crosses *viz*., LBG-787 × LBG-752, TU-94-02 × KU-1006 and TU-94-02 × LBG-752 along with their parents. High PCV and GCV were recorded for plant height, number of clusters per plant, number of pods per plant and seed yield per plant in two crosses, LBG787 × LBG-752 and TU-94-02 × KU-1006 indicating the existence of wide variability for these traits. High heritability coupled with high genetic advance as *per cent* of mean were recorded for plant height, number of clusters per plant, number of pods per cluster, number of pods per plant and seed yield per plant in the cross LBG-787 × LBG-752. This indicates the scope of selection for these traits in a particular population since there is a wide range of variation and additive gene action for the traits.

Singh *et al*. (2020) evaluated 100 urad bean genotypes for assessment of genetic variability, broad sense heritability and genetic advance as *per cent* of mean (GAM) under two locations. They recorded significant variation for all the characters with significant G × E interaction across both locations. High estimates of PCV and GCV were recorded for plant height, pod maturity, pods per plant, yield per plant and harvest index. Moderate to high heritability coupled with higher GAM was noted for plant height, pod maturity, nodes per plant, clusters per plant, biological yield per plant, seed yield per plant and harvest index.

Surekha *et al*. (2020a) evaluated 25 black gram genotypes which revealed that PCV was higher than GCV for all the traits and high heritability was observed for seed yield per plant, number of pods per cluster and number of clusters per plant suggesting that these traits are primarily under genetic control.

Rahikaben and Bala (2021) studied genetic variability in 50 black gram genotypes and revealed high heritability coupled with high genetic advance as *per cent* of mean was recorded for plant height, number of branches per plant, number of clusters per plant, pods per plant, seed yield per plant and straw yield. The higher magnitude of genotypic coefficient of variation was observed for plant height, clusters per plant, 100 seed weight, seed yield per plant and straw yield indicating the inherent connection between genotypic and phenotypic expression of these traits.

Rehman *et al*. (2021) conducted variability studies among 31 F_4 genotypes of black gram. Analysis of variance revealed significant differences among the genotypes for all the traits except days to 50 *per cent* pod setting and high heritability coupled with high genetic advance as *per cent* of mean were recorded for the traits *viz.,* seed yield per plant, seed index, days to maturity, plant height, harvest index, biological yield, pod length and number of primary branches per plant.

2.2 Character association and path coefficient analysis

2.2.1 Correlation for yield and its yield attributing traits

The correlation coefficient is a statistical measure used to determine the degree and direction of the relationship between two variables and is independent of the unit of measurement. In plant breeding, correlation coefficient analysis provides a measure of the mutual relationship between various plant characters and determines the component characters on which selection can be made for genetic improvement in yield through indirect selection. Phenotypic correlation is the observable correlation between two variables, and it includes both genotypic and environmental effects. It measures the environmental deviation together with non-additive gene action. Genotypic correlation is the inherent association between two variables, and it may be either due to the pleiotropic action of genes, linkage or more likely both. The knowledge of the association between different characters is highly essential for planning a sound breeding programme.

Chand and Rao (2002) evaluated 625 biparental progenies in F_3 generation of black gram of cross PDU-3 × L-400 to study the character association. They observed positive and significant correlations of grain yield with plant height, branch number, cluster number, pod number, seeds per pod, pod length and 100 seed weight.

Vaithiyalingan (2002) carried out correlation studies for 12 traits in 11 parents and 30 hybrids of black gram and noticed significant positive association of seed yield with branches per plant, pods per plant, seeds per pod and harvest index.

Srividhya *et al.* (2005) observed significant positive association of seed yield with number of pods per plant, number of clusters per plant, number of seeds per pod, 100 seed weight and total biomass meaning that the selection of these traits would be beneficial for yield improvement in F_2 generation of urad bean.

Umadevi and Meenakshi (2005) reported highly significant positive phenotypic and genotypic correlation of clusters per plant, pods per plant, pod length, seeds per pod and 100-seed weight with grain yield from their assessment of 60 diverse black gram germplasm during kharif season. It was also noticed that seeds per pod had highly significant positive correlation with days to maturity, clusters per plant, pods per plant and pod length and a highly significant negative correlation with plant height. Hundred seed weight recorded highly significant positive correlation with plant height and significant positive correlation with clusters per plant.

Bhagowati and Hazarika (2006) found significant and positive association of plant height, number of pods, pod length, number seeds per pod, 100 seed weight, harvest index with seed yield in black gram. They also recorded variations with respect to degree and magnitude of correlation coefficients for various crosses of segregating generations.

Rao *et al.* (2006) evaluated 12 black gram genotypes under four different environments for seven traits and found that the seed yield was found to be positively associated with days to maturity and number of pods per plant.

Sarkar *et al.* (2006) analysed seven genotypes of diverse origin for estimating the eight components for correlation coefficient and path coefficient analysis. The study revealed that seed yield was in positive and strong association with clusters per plant, pods per plant and seeds per pod in urad bean.

Singh *et al.* (2007) recorded significant positive correlation of seed yield with number of pods per plant following plant height, pod length, number of seeds per pod, days to flower initiation and days to maturity, while negative correlation with primary branches per plant in black gram.

Ali *et al.* (2008) studied the character association pattern and measured the direct and indirect influence of different yield contributing characters towards the final economic seed yield per plant of 31 urad bean genotypes. It was observed that, the characters *viz*., pods per plant, pod length, seeds per pod and 100 seed weight were significantly and positively correlated with seed yield per plant. Similarly the characters namely, number of pods per plant, 100 seed weight and number of seeds per pod exhibited positive association coupled with positive direct effect at both phenotypic and genotypic level on seed yield per plant.

Gul *et al.* (2008) noticed plant height at maturity was significantly and positively correlated with days to maturity, seeds per pod and dry weight per plot while it was negatively correlated with 100 seed weight and harvest index in an experiment carried out with 26 mung bean genotypes during summer. While days to flowering was positively associated with days to maturity, pods per plant, plant height and dry weight per plot and had negative association with seeds per pod, seed yield, 100-seed weight and harvest index. 100-seed weight had significant positive correlation with pods per plant and harvest index, while it had significant negative correlation with days to maturity, seeds per pods and plant height. Seed yield per plot was found to be non-significantly correlated with 100 seed weight. Seed yield per plant was significantly positively correlated with pods per plant and harvest index. On the other hand, its correlation with plant height was significantly negative.

Kadam *et al.* (2008) stated that yield in black gram had a highly significant and positive correlation with plant height, leaf area, total dry weight, number of pods per plant, number of grains per pod and 100 seed weight and negatively correlated with flowers shredded.

Malik *et al.* (2008) evaluated 18 genotypes of black gram and found that pods per plant, branches per plant and biological yield per plant showed highly significant and positive correlation with grain yield and concluded that selection of genotypes on the basis of these traits can be useful.

Konda *et al*. (2009) obtained positive correlation of branches per plant, clusters per plant, pods per plant, seeds per pod, pod length and 100 seed weight with seed yield in 40 black gram genotypes.

Bhareti *et al.* (2011) estimated correlation among yield and related traits in advanced lines of black gram. They showed that genotypic correlation coefficients were superior in magnitude to the phenotypic correlation coefficients. The trait like days to maturity was highly correlated with days to 50 per cent flowering, while days to 50 *per cent* flowering had negative association with grain yield per plant.

Isha *et al.* (2011) reported that the number of pods per plant, harvest index and number of clusters per plant were significantly and positively correlated with seed yield in black gram. Hence, these traits could be utilized in direct selection so as to improve the seed yield per plant. Plant height showed significant positive association with pod length, seeds per pod, 100 seed weight and days to maturity. They suggested that selection of the tall plants could result in attaining longer pods with more number of seeds, increased seed weight and also increase in days to maturity. Plant height showed highly significant negative association with harvest index and explained that selection of tall plants reduces the harvest index. Clusters per plant exhibited highly significant positive association with pods per plant and harvest index. On the contrary, highly significant negative association of clusters per plant with number of seeds per pod.

Saima *et al*. (2011) observed a significant positive correlation between numbers of pods per plant, pod length, seed yield per plant and number of seeds per plant, 100 seed weight and biological yield by investigating 34 black gram genotypes.

Shivade *et al*. (2011) carried out a study among 36 genotypes of black gram and concluded that the yield contributing characters *viz.,* plant height, number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, length of pod, number of seeds per pod and dry matter per plant had positive correlation with seed yield per plant at both the phenotypic and genotypic level.

Ahmad *et al*. (2013) observed that clusters per plant had positive and significant correlation with primary branches per plant, pods per plant, seeds per pod and seed yield per plant but had significant and negative correlation with 100 seed weight in mung bean during *Kharif.* It was also observed that pods per plant exhibited positive and significant correlation with number of seeds per pod and seed yield per plant, while it was significant and negatively correlated with 100 seed weight at both genotypic and phenotypic levels. 100 seed weight is significant and positively correlated with pod length at both the levels but negatively correlated with clusters per plant. Positive and significant correlations of seed yield with clusters per plant, branches per plant, pods per plant, pod length and seeds per pod were observed in mung bean.

Reni *et al.* (2013) reported that the pods per plant and plant height had highly significant genotypic and phenotypic correlation with grain yield. Plant height showed significant positive association with pods per plant days to 50 *per cent* flowering and days to maturity. They suggested that these traits could be used to improve grain yield resulting in the evolution of high yielding varieties of black gram.

Bharti *et al.* (2014) observed a very strong positive association of grain yield per plant with number of clusters per plant, number of pods per cluster, number of seeds per pod, biological yield per plant, harvest index and negative correlation with days to maturity. Selection is effective for those traits having positive correlation with yield in black gram.

Meghana *et al.* (2014) made an attempt to estimate genotypic, phenotypic and environmental correlations in all possible character combinations for 28 genotypes of urad bean. They observed a negative association of yield with 50 *per cent* flowering, days to maturity and pod length whereas positive association was observed towards plant height, biological yield and seed yield.

Patel *et al*. (2014b) studied 11 characters in black gram during the summer season. Grain yield per plant was positively and significantly correlated with days to 50 *per cent* flowering, days to maturity, number of branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length and 100 seed weight. The studies suggest that selection for days to maturity, number of pods per plant, 100 seed weight and number seeds per pod to evolve high yielding varieties of black gram.

Correlation studies by Singh *et al.* (2014) among 128 urad bean genotypes indicated that pods per plant, branches per plant, pod length, seeds per pod and 100 seed weight exhibited high significant and positive correlation with seed yield.

A significant positive association of seed yield per plant with plant height, number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, 100 seed weight and total dry matter production has been recorded by Kanimoli *et al.* (2015)

Correlation coefficient analysis involving 35 genotypes of urad bean by Sharma (2015) revealed that seed yield per plant has a positive and significant association with number of branches per plant, number of pods per plant, biological yield per plant, 100 seed weight and harvest index and a negative association with days to maturity and plant height. The characters like number of branches per plant, number of pods per plant, 100 seed weight and harvest index were also positively associated among themselves indicating the simultaneous improvement of these characters by selection.

Monika *et al*. (2016) estimated genotypic and phenotypic correlations in all possible combinations for 75 accessions of black gram. The results indicated that the characters plant height, number of primary branches per plant, number of pods per plant, number of seeds per plant, number of seeds per pod and 1000 seed weight showed positive correlation with seed yield both at phenotypic and genotypic level.

Priyanka *et al*. (2016b) carried out an experiment on 24 genotypes of black gram for the estimation of correlation coefficient and path coefficient analysis. Number of branches per plant showed significantly positive correlation with yield both at phenotypic as well as genotypic level. Plant height showed significant negative correlation with yield both at phenotypic as well as genotypic level. Maximum direct effect of number of branches per plant on seed yield was observed.

Baroowa and Gogoi (2016) assessed response pattern of black gram (T9, KU 301) and green gram (Pratap, SG 21-5) genotypes under drought stress imposed at vegetative, early reproductive and pod filling stages. The results revealed the existence of positive correlation of seed yield with plant height, leaf number and shoot: root biomass.

Mehra *et al.* (2016) concluded that number of seeds per plant, number of pods per plant, plant height and 100 seed weight were significantly and positively associated with seed yield per plant both at phenotypic and genotypic levels. He also found that the degree of association was highest between seed yield per plant and number of seeds per plant followed by number of pods per plant, biological yield per plant, plant height and 100 seed weight.

Miah *et al*. (2016a) evaluated ten black gram cultivars for estimating correlation and path coefficient through 11 traits. They observed positive correlation of yield with number of pods per plant, pod length, weight per pod, harvest index and 100 seed weight but had negative association with plant height.

Sateesh *et al.* (2016) estimated genotypic and phenotypic correlations in all possible combinations for 75 accessions of black gram. The results indicated that the characters plant height, number of primary branches per plant, number of pods per plant, number of seeds per plant, number of seeds per pod and 100 seed weight showed positive correlation with seed yield both at phenotypic and genotypic level.

Singh *et al*. (2016) found that the characters plant height, number of primary branches per plant, number of pods per plant, number of seeds per plant, number of seeds per pod and 100 seed weight showed positive correlation with seed yield both at phenotypic and genotypic level among diverse genotypes of black gram. The magnitude of genotypic correlation was higher than phenotypic correlation.

Sohel *et al.* (2016) revealed that yield per plant in black gram was positively and significantly associated with pods per plant, pod length, pod weight, harvest index and 100 seed weight but negatively associated with plant height, fresh weight and dry weight.

Arya *et al*. (2017) estimated correlation studies for yield and related components in 30 black gram genotypes and they found that seed yield per plant had significant and positive correlation with number of pods per plant followed by biological yield per plant and harvest index.

Correlation coefficient analysis carried out by Hemalatha *et al*. (2017a) among 35 black gram genotypes revealed that seed yield per plant had a significant and positive correlation with harvest index and number of pods per plant both at genotypic and phenotypic levels.

Patidar *et al*. (2017) by analyzing 29 black gram genotypes concluded that seed yield per plant was positively and significantly correlated with number of branches per plant, number of pods per plant, biological yield per plant and harvest index.

Rajasekhar *et al*. (2017a) evaluated 40 black gram genotypes for the analysis of correlation and path coefficient. The study specified the significant positive association of primary branches, number of pods per plant, seed index and harvest index with the seed yield per plant at both genotypic and phenotypic levels while path coefficient indicated the direct effects of primary branches, pods per plant, harvest index with seed yield. Hence, selection of these traits would be helpful in enhancing yield in black gram.

The association studies carried out by Suguna *et al.* (2017) among 12 hybrids and four parents of black gram indicated that single plant yield was highly correlated with plant height, number of branches per plant, number of pods per plant, pod length and number of seeds per pod.

Bandi *et al.* (2018) carried out character association studies among 36 black gram genotypes and the results indicated that number of clusters per plant, number of pods per plant, number of seeds per pod and 100 seed weight showed positive significant association with seed yield per plant both at phenotypic and genotypic levels, whereas days to 50 *per cent* flowering, days to maturity exhibited negative and significant association with seed yield per plant.

Gopinath *et al*. (2018) revealed 64 germplasm lines in black gram association studies that seed yield per plant was positively and significantly correlated with plant height, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length and protein content at both phenotypic and genotypic level indicating that these six traits could be important for improving the seed yield in black gram.

Sathya *et al*. (2018) studied association among yield and related attributes in the F_2 population of five black gram crosses. The research revealed that plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, total number of pods per plant, pod length, number of seeds per pod and 100 seed weight had positive correlation with seed yield. The traits *viz.,* number of clusters per plant, number of pods per plant, number of seeds per pod and 100 seed weight had positive direct effect on yield.

Hadimani *et al*. (2019) studied correlation among 13 characters in black gram and found that seed yield was significantly and positively correlated with pods per plant, 100 seed weight, grain yield per hectare and pod length. They also noticed greater positive direct effects of 100 seed weight and pod length on grain yield.

Sathees *et al*. (2019b) evaluated 162 F_2 plants of black gram for correlation and path analysis for yield and yield contributing traits and reported significant positive correlation of seed yield with plant height, primary branches, cluster per plant, pods per plant, seeds per pod, pod length and 100 seed weight.

Singh *et al*. (2019) recorded that biological yield per plant, number of pods per plant, number of seeds per plant, number of primary branches per plant, test weight, plant height, number of seeds per pod, days to 50 % flowering and number of pods per plant had strong and positive correlation with seed yield whereas days to 50 *per cent* flowering and test seed weight possessed maximum direct effects on yield in black gram.

Vadivel *et al*. (2019) analysed F_2 populations of black gram for evaluating correlation coefficients and found strong and positive association among seed yield per plant and plant height, number of branches per plant, number of cluster per plant, number of pods per cluster, number of pods per plant, pod length and 100 seed weight, highlighting their selection for yield improvement.

Chowdhury *et al*. (2020b) studied character association among nine yield and related traits and found that the genotypic correlation coefficient was higher than the phenotypic correlation coefficient for all the concerned traits. They noticed that yield per plant exhibited significant positive correlation with plant height, no. of branches per plant, no. of pods per plant, no. of seeds per pod and 100 seed weight at genotypic level. At phenotypic level all these characters revealed significant positive association with yield except plant height in urad bean.

Surekha *et al*. (2020b) estimated genotypic and phenotypic correlations in all possible combinations for 26 genotypes of black gram. The results indicated that the characters number of pods per cluster and number of clusters per plant showed significant positive correlation with seed yield per plant.

Teja *et al*. (2021a) studied 27 black gram genotypes. Correlation coefficient analysis revealed that seed yield per plant exhibited positive and significant correlation associated with plant height, number of pods per plant, biological yield and harvest index at both genotypic and phenotypic levels.

2.2.2 Path analysis for yield and its yield attributing traits

Chand and Rao (2002b) evaluated 625 biparental progenies in F_3 of black gram cross PDU-3 × L-400. Pods per plant followed by number of clusters per plant and seeds per pod exhibited highest positive direct effect on yield. They also suggested that inconsistent performance of different characters might have been caused by genetic shift or breakage of gene linkages.

Ninety three urad bean genotypes were evaluated by Raika *et al*. (2002) using path coefficient analysis for grain yield and yield components. They reported that biological yield has a high direct effect on grain yield, as well as indirect effect through harvest index, pod length and number of primary branches per plant.

Hassan *et al.* (2003) carried out path coefficient analysis among 25 black gram genotypes and concluded that harvest index has high direct effect on seed yield followed by biological yield per plant. They also found that traits like plant height, number of pods per plant and 100 seed weight show a small direct effect on yield but had high indirect effects via biological yield.

Path analysis by Venkatesan *et al.* (2004) using 49 genotypes of black gram revealed that pods per plant, pod length and plant height had positive direct effects on yield. Days to first flowering, plant height, branches per plant, clusters per plant, pods per plant, seeds per pod and hundred seed weight showed positive indirect effects on yield via most of the characters.

Seed yield in black gram had significant and positive correlation with plant height, branches per plant and pods per plant at genotypic as well as phenotypic level except for number of branches per plant which showed positive but non-significant association with yield per plant due to environment interaction (Parameswarappa and Lamani 2005). The characters like plant height, number of branches per plant and pods per plant may be attributed as important components of seed yield. Seed yield correlated with pods per plant, branches per plant and total biomass. Harvest index and total biomass were also positively and significantly correlated with each other.

Path coefficient analysis by Sharma *et al*. (2005) using ten black gram genotypes revealed that number of pods per plant and 100 seed weight had positive direct effects on grain yield per plant. Days to maturity, plant height, number of pods per plant and 100 seed weight showed positive indirect effects on grain yield per plant.

Veeramani *et al.* (2005) analysed F_2 generation of black gram for estimating path coefficient and recorded maximum positive direct effect of number of clusters per plant, number of pods per plant and pod length on seed yield whereas plant height exhibited indirect effects on number of pods per plant and clusters per plant.

Bhagowati and Hazarika (2006b) found significant and positive association of plant height, number of pods, pod length, seeds per pod, 100 seed weight, harvest index with seed yield in black gram. They also recorded variations with respect to degree and magnitude of correlation coefficients for various crosses of segregating generations.

Makeen *et al.* (2009) based on their studies on 22 micromutants of T_9 black gram variety revealed that pod length, pod bearing clusters per plant and 100-seed weight had positive and direct effect on seed yield per plant.

Shivade *et al.* (2011b) conducted a study to know direct and indirect effects of various yield component characters on yield among 36 genotypes of black gram and revealed that the characters days to 50 *per cent* flowering, number of clusters per plant, number of pods per cluster, length of pod, 100 seed weight, dry matter per plant, harvest index, number of seeds per pod and number of branches per plant had positive direct effect on seed yield per plant.

Yashoda *et al.* (2013) assessed 46 genotypes of black gram and the results of path analysis revealed that days to 50 *per cent* flowering, days to maturity, plant height, number of secondary branches per plant, number of pods per plant, number of seeds per pod and hundred seed weight had positive direct effects on grain yield. While the characters *viz*., number of primary branches per plant, number of clusters per plant and pod length had negative direct effects on grain yield.

Punia *et al.* (2014) conducted path analysis among 133 urad bean accessions and reported that number of pods per plant and number of branches per plant had major direct and indirect effect on yield contributing traits in urad bean.

Days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per pod and 100 seed weight had a positive direct effect, while the traits like days to 50 *per cent* flowering and pod length showed direct negative effect on seed yield as reported by Singh *et al.* (2014) among 28 promising urad bean genotypes.

Babu *et al.* (2016) carried out an experiment on 25 genotypes of black gram for the estimation of path coefficient analysis. Number of branches per plant showed significantly positive correlation with yield both at phenotypic as well as genotypic level. Plant height showed significant negative correlation with yield both at phenotypic as well as genotypic level. Maximum direct effect of number of branches per plant on seed yield was observed.

Jyothsna *et al.* (2016) examined 12 black gram genotypes for estimation of direct and indirect effects of various quantitative characters on yield by path analysis and revealed that number of pods per plant showed true relationship by establishing positive and direct effect on seed yield both at genotypic and phenotypic levels and plant height and length of pod at phenotypic level and number of seeds per pod at genotypic level.

Miah *et al.* (2016b) found that pod weight, harvest index, number of branches per plant and 100 seed weight had shown the highest level of coefficient of variation in black gram. The relationship between physiological and yield contributing characters was studied through analysis of correlation between them. It was observed that biomass per plant had maximum positive direct effects on yield per plant followed by number of pods per plant, seeds per pod by path coefficient analysis. Plant height had negative direct effect on seed yield followed by dry weight, 100 seed weight and number of branches per plant.

Rasel *et al.* (2016) by assessing ten black gram germplasm lines by path coefficient analysis, observed that biomass per plant had maximum positive direct effects on yield per plant followed by pods per plant, seeds per pod. Plant height had negative direct effect on seed yield followed by dry weight, 100 seed weight and branches per plant.

Arya *et al.* (2017b) assessed 30 black gram genotypes for knowing the cause and effect of different yield components. Path analysis revealed that harvest index, biological yield per plant, pods per plant and seeds per pod had high positive direct effect on grain yield at both genotypic and phenotypic level. Conversely, the other characters *viz.,* plant height, clusters per plant, primary branches, pod length, and days to 50 *per cent* flowering revealed negative direct effect of given magnitudes towards seed yield per plant.

Dhoot *et al.* (2017) reported significant and positive association of pods per plant and harvest index with seed yield in F_2 population of mung bean. They also found maximum positive direct effects of pods per plant, plant height, clusters per plant, seeds per pod, 100 seed weight and harvest index on seed yield per plant.

Gill *et al.* (2017) studied 45 advanced mutant lines of black gram and observed that direct effect of number of pods per plant is high on grain yield followed by 100 seed weight and number of branches per plant. Seeds per pod showed negative direct effect on seed yield but it exhibited indirect positive effect through days to maturity, pods per plant and pod length.

Rajasekhar *et al.* (2017b) assessed 40 black gram genotypes and found that primary branches, pods per plant and harvest index has shown the true relationship with seed yield by establishing the direct positive effects at both genotypic and phenotypic levels, while clusters per plant at genotypic levels and seed index at phenotypic levels.

Path analysis by Rekha and Reddy (2017) among 31 mung bean accessions revealed that harvest index has maximum direct effect on seed yield per plant followed by plant height, number of clusters per plant and number of pods per plant under water stress conditions. Hence these characters showed high possibility of gain from indirect selection.

Hemalatha *et al.* (2017b) evaluated 35 black gram genotypes under saline conditions and reported that characters, pods per plant and pod length had high positive direct effect of on seed yield per plant.

Blessy and Naik (2018) evaluated 14 black gram genotypes, path coefficient analysis revealed that characters biological yield , number of pods per plant, plant height, harvesting index, days to 50 *per cent* flowering, number of primary branches, have positive direct effect on seed yield per plant. While the characters number of clusters per plant, number of seeds per pod, pod length (cm), seed index, days to 50 *per cent* pod setting, days to 50 *per cent* maturity have negative direct effect on the seed yield per plant at genotypic level.

Ragul *et al.* (2018) subjected 52 progenies in F_5 generation derived from an interspecific cross between green gram (*Vigna radiata* cv. VBN-2) and black gram (*Vigna mungo* cv. Mash 114), path analysis studies revealed that number of pods per plant recorded significant and positive association with seed yield per plant. This trait alone recorded high direct effect on seed yield per plant.

Sathya *et al.* (2018b) studied association among yield and related attributes in F_2 population of five black gram crosses. The research revealed that plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, total number of pods, pod length, number of seeds per pod and 100-seed weight had positive correlation with seed yield. The traits *viz*., number of clusters per plant, number of pods per plant, number of seeds per pod and 100 seed weight had positive direct effect on yield.

Shanti *et al*. (2019) studied 25 black gram genotypes, path analysis revealed that number of clusters per plant is the principle component responsible for increasing seed yield in black gram and it showed high positive significant direct effects on seed yield. The indirect effect of number of pods per cluster and total number of pods per plant were positive on yield. Improving these characters also indirectly helps to improve the yield.

Partap *et al*. (2019) carried out path analysis studies among 40 black gram genotypes and indicated that the seed yield per plant received the highest direct effect from biological yield per plant, harvest index and days to 50 *per cent* flowering for both phenotypic and genotypic level. These characters suggest direct selection and would help in selecting the high yielding genotypes in black gram.

Khan *et al*. (2020b) studied 60 genotypes of black gram. Highest positive direct effect on seed yield per plant was exhibited by cluster per plant followed by harvest index. While high indirect effect on seed yields per plant exhibited positive and negative effects through other characters.

Shridhar *et al*. (2020) evaluated 35 black gram genotypes. Path analysis showed that days to maturity, plant height and number of clusters per plant showed positive direct effect coupled with positive indirect effects through number of pods per plant and 100 seed weight on seed yield per plant resulting in positive significant correlation with seed yield (kg/ha).

Teja *et al*. (2021b) studied 27 black gram genotypes. Path coefficient analysis revealed that characters plant height, number of primary branches, days to maturity, biological yield and harvest index have positive direct effect on seed yield per plant at genotypic and phenotypic levels.

2.3 To identify the transgressive segregants for yield and its attributing traits in black gram

Jayalakshmi (2000) studied the frequency of transgressive segregates in 21 crosses in F_2 and F_3 generations for yield attributes. Cross ICG 2716 × ICGV 86031 exhibited higher frequency of transgressive segregants for majority of the characteristics in addition to kernel yield. Among others, ICG 2716 × TAG 24, ICG 2716 ×TG 26, ICG 86031 × TG 26, TG 26 × TMV2-NLM expressed transgressive segregates for kernel yield and other attributes like harvest index and number of pods per plant in groundnut.

Rajavindran *et al.* (2000) studied the six cross combinations of Sesame. The crosses Si 833 × CO 1 and EC 132836 × TMV4 gave a high frequency of transgressive segregants for seed yield per plant, primary branches per plant and capsule number per plant.

Girase and Deshmukh (2002) observed the transgressive segregation for all the seven characters in three crosses of Chickpea. They observed the highest transgressive segregation for plant height (27 %) followed by pods per plant, fruiting branches per plant and yield per plant in both F_2 and F_3 generations of all the three crosses, except F_3 generation of JG-62 × Vijay. They also reported the simultaneous transgressive segregation for yield in combination with other characters. They reported that the proportion of transgressive segregants were more in backcross population with increasing parent than straight F_2 population.

Rahman *et al.* (2002) studied transgressive segregation in the backcross populations, involving three crosses in long bean. Trends were different for different crosses. In cross 1, high mean variance and significant transgressive segregation pattern was exhibited by BC_2F_1 generation for shelf life, pod yield per plant and pod weight. In cross 2, high means were shown by BC_1F_1 generations for shelf life and pod yield per plant but high transgressive segregants were observed in BC_2F_1 generation for shelf life, BC_1F_1 for pod yield per plant and BC_1F_2 for pod weight. In cross 3, BC_1F_2 generation revealed high variances for shelf life, pod yield per plant and number of pods per plant but the highest STS values were revealed in BC_1F_3 (selected) for shelf life and pod yield per plant, BC_2F_1 for number of pods per plant, and BC_1F_2 for pod weight. In general, shelf life exhibited high mean and STS in the BC_2F_1 generation. Pod length in general did not show good transgressive segregation in these crosses.

Kotzamanidis (2006) studied the thirteen successful crosses in peanut (*Arachis hypogaea* L.) in 1985 belonging to the crossing schemes: Virginia × Spanish, Virginia × Valencia, Valencia × Virginia, Virginia × Virginia, Valencia × Valencia, Valencia × Spanish and seven successful crosses in 1986 belonging to two crossing scheme: Virginia × Valencia, Virginia × Virginia. Transgressive segregation for yield characters of 100 pod weight and 100 seed weight was studied. Pedigree selection was applied from F_3 and F_5 generations and segregated materials together with the parental varieties were evaluated. Most of the selections that showed transgressive segregation belong to the cross type Virginia × Spanish. Yield and quality of peanut could be improved by exploiting the phenomenon of transgressive variation occurring in cross between Virginia × Spanish.

Dhole and Reddy (2011) reported that total of eight transgressive segregants (2.56 %) in mung bean was recorded in the cross- I, which ranged from 8.52 to 9.29 g for 100 seed weight. No transgressive segregants were obtained in cross-II and cross-III for 100 seed weight. Among the F_2 populations, the mean seed yield per plant was the highest in the cross-I (3.89 g) followed by the cross-III (2.74 g) and cross-II (1.88 g). For seed yield per plant, fifteen (4.79 %) and one (0.003 %) transgressive segregants were recorded in the cross-I (ranged from 7.95 to 11.93 g) and cross-III (15.01 g), respectively.

Karkute and Girase (2013) studied transgressive segregants for all the characters in F_2 generation of three crosses. The highest proportion of transgressive segregants were recorded for pods per plant (46) followed by grain yield per plant (43), pod length (41), number of clusters per plant (40), number of seeds per pod (36) and 100 seed weight (28) irrespective of crosses. They also observed the simultaneous transgressive segregants for grain yield in combination with other character.

Shivakumar *et al.* (2013) found more number of transgressive segregants for number of seeds per plant followed by number of pods per plant and yield per plant in F_2 population and F_2 derived F_3 population from the cross between ICC 13124 and WR 315 of chickpea.

Ajay *et al.* (2014) evaluated F_2 and F_3 population derived from cross between BRG-1×ICP-8863, TTB-7 × ICP-8863 and TTB-7 × ICPL87119 in pigeonpea. Transgressive segregants identified for pods per plant and seed yield per plant in F_2 and F_3 generations. In F_2 generation twenty four transgressive segregants were observed with seed yield per plant and pods per plant. In F_3 generation of a cross BRG-1 × ICP-8863 twenty six transgressive segregants were observed with seed yield and pods per plant. In cross TTB-7 × ICP-8863 twenty transgressive segregants were observed with seed yield per plant and pods per plant. Whereas, in cross TTB-7 × ICP-87119 forty five transgressive segregants were observed with seed yield and pods per plant. Cross TTB-7 × ICPL87119 recorded more number of transgressive segregants compared to other two crosses.

Baliram (2014) observed transgressive segregants for all the characters in B_1F_2 and B_2F_2 generations of three crosses. In general, the highest proportion of transgressive segregants were recorded for pod length (63) followed by grain yield per plant (48), number of pods per plant (37), number of seeds per pod (37), number of clusters per plant (36) and 100 seed weight (36) in B_1F_2 generation. In B_2F_2 generation highest proportion of transgressive segregants were recorded for number of clusters per plant (51), followed by number of pods per plant (46), grain yield per plant (45), pod length (35), number of seeds per pod (30) and 100 seed weight (28).

Jambormias *et al.* (2015) evaluated three F_3 population derived from a cross Gelatik × Mamasa Lere Butsiw in greengram. Transgressive segregants were observed for seed weight and harvest index which ranged between 11 to 18 g and 0.56 to 0.65.

Shashikumar *et al.* (2016) evaluated three F_2 population derived from three crosses KCG-6 × ICGV-91114, KCG-6 × TG-69 and TMV-2 × ICGV-00350. Good number of transgressive segregants were observed over better parent for pod yield, oil content and matured pods per plant in the cross KCG-6 × ICGV-9114 of groundnut.

Showkath *et al*. (2016) evaluated F_3 population of cross FPB 21 × RIL 180 and 25 transgressive segregants were identified in FPB 21 × RIL 180 for number of pods per plant in dolichos bean.

Kerem *et al*. (2017) evaluated F_2 and F_3 population derived from cross between *Cicer arietinum* and *Cicer reticulatum* of chickpea. They reported highest transgressive segregants for seeds per plant, number of pods per plant, biological yield and seed yield.

Chouhan *et al*. (2018b) generated transgressive segregants in respect of seed yield and its components in F_3 generation of black gram. High frequency of transgressive segregation was shown by the different progenies of crosses namely DU-1 × Palampur93, HPBU-124 × HPBU-111, TU-17-4 × Palampur-93, IPU-02-33 × Palampur-93, KU-223 × HPBU-111, KU-553 × Palampur-93, HPBU-126 × HPBU-111, KU-553 × HPBU-111 and HPBU-126 × Palampur-93 for all of the studied traits. The results suggested the existence of large count of transgressive segregants in early segregating generations for almost all the traits which provides a wide scope for the meticulous selection of these genotypes.

Guindon *et al*. (2019) made a cross between two pea varieties, namely DDR14 and Explorer to find out transgressive segregants in F_2 progeny and F_3 families. The cross showed high frequency of transgressive segregation for characters number of pods per plant (15.5 %) and number of seeds per plant (13.6 %) in F_3 generation.

Kuralarasan and Jayamani (2021b) developed an inter sub specific mapping population (RIL) by crossing VBN (Bg) × *Vigna mungo* var. *silvestris* by using single seed decent method. Transgressive segregants were observed for all the traits. Five RILs *viz*., RIL 11, RIL12, RIL67, RIL73 and RIL168 showed superiority over cultivated variety VBN (Bg) for all traits except branches per plant. 36 RILs were identified for single plant yield which was above VBN (Bg). A total of 54 RILs were identified as bold seeded with hundred seed weight exceeding the VBN (Bg). Early flowering lines with short stature are the preferable traits for the intercropping situation. A total of 174 lines were found to be early flowering.

MATERIAL AND METHODS

III MATERIAL AND METHODS

The present investigation was undertaken to study genetic variability in F_3M_2 population of black gram [*Vigna mungo* (L.) Hepper] including four checks. The experiment was conducted during *Rabi* 2020 at Zonal Agricultural and Horticultural Research Station (ZAHRS), Navile, Shivamogga, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga, Karnataka, India, which is situated in 13.28° North latitude and 75.34° East longitude and at an altitude of 617.0 meters above mean sea level.

3.1 Experimental material

The experimental material consisted of 400 F_3M_2 progeny lines of cross (PU31 × Rashmi) in black gram [*Vigna mungo* (L.) Hepper] including four checks (PU31, Rashmi, DBGV5 and DU1). Pod characteristics and seed characteristics of parents depicted in plate 1.

3.2 Experimental details and the layout of the experimental field

The experiment was laid out at research plots in the D-8 block of ZAHRS, Navile, Shivamogga in an augmented experimental design (Federer, 1961) with ten blocks, each block with 40 lines and a total of 400 progeny lines. The genotypes were unreplicated, while checks were replicated twice in all the blocks to obtain the estimate of an error and blocking effects. Individual genotypes were directly sown by dibbling two seeds per hill on 13th November 2020 for *Rabi* 2020 in a row of 4 meters length with 30 cm of spacing between the plants and 45 cm between the rows. The field management was done by following the recommended package of practices to raise a healthy crop. The soil was fertilized with farmyard manure at the rate of 5 t ha^{-1} and NPK in the ratio of 25: 50: 25 kg ha^{-1}. Nitrogen was provided in the form of urea (46 % N) in split doses *i.e.,* 50 *per cent* at basal and 50 *per cent* at 30 days after sowing. Phosphorous was provided as single super phosphate (16 % P_2O_5) and potassium as muriate of potash (60 % K_2O). Irrigation was done once in a week, and necessary measures were taken to manage pest and disease infestation. The overview of the research plots of *Rabi*-2020 are depicted in plate 2.

3.3 Cropping history in the research plot

The previously grown crops in the experimental field used in the present investigation are brinjal, field bean, bhendi, green gram, and cowpea.

3.4 Observations recorded

Fifteen plants from each progeny rows were selected based on individual plant basis and tagged for further observation and the mean values were considered for analysis. The traits studied are described below.

Table 1 Summary of experimental material for seed yield and its component traits for F_3M_2 black gram [*Vigna mungo* (L.) Hepper]

1	Number of genotypes	400
2	Experimental design	Augmented
3	Number of blocks	10
4	Number of checks	04
5	Number of genotypes in a block	40
6	Row length	4 m
7	Spacing between the rows	0.3 m
8	Spacing between the plants within row	0.1 m

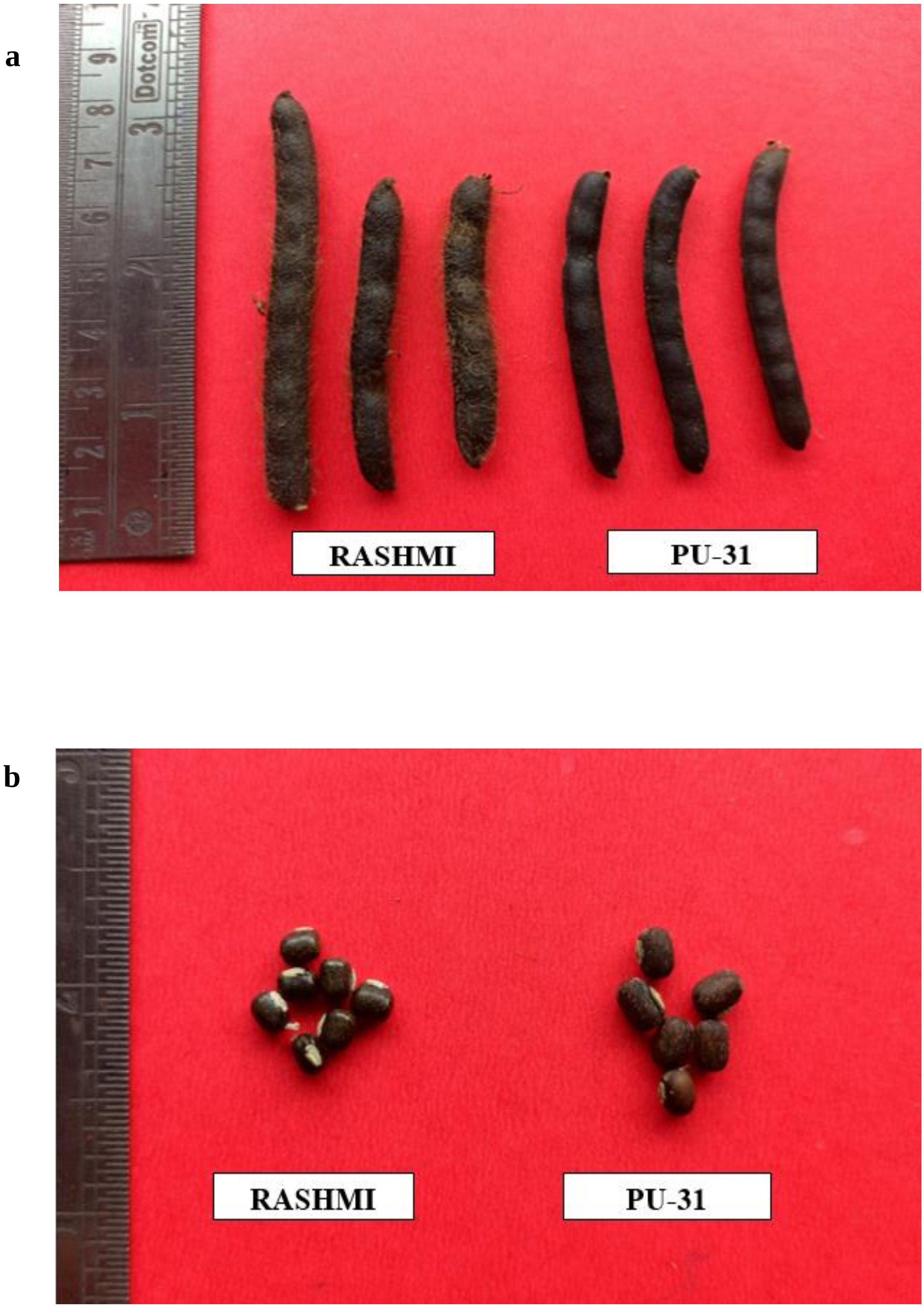


Plate 1: (a) Pod characteristics of parents, (b) Seed characteristics of parents

Plate 2 Overall view of experimental field layout

Table 2 Characteristics of parents.

SL. No.	Parents	Characteristics
1.	Rashmi	Long duration variety (70-75days) susceptible to YMV, pods are hairy with shiny seeds, which produces potential yield of 600 – 900 kg/ha.
2.	PU31	Medium duration variety tolerant to YMV, pods are non-hairy with dull seeds, which produces potential yield of 600-700 kg/ha.

3.4.1 Number of days to 50 per cent flowering

The number of days taken from the date of sowing to the day on which 50 *per cent* of plants in a progeny row show anthesis was recorded.

3.4.2 Plant height (cm)

Height of the selected plants from the base of the plants to the tip of main raceme was measured and averaged.

3.4.3 Number of branches per plant

Total number of branches originating from the main axis were counted at harvest and recorded.

3.4.4 Number of clusters per plant

Number of clusters per plant recorded by counting the total number of pod bearing clusters from selected plants and averaged

3.4.5 Number of pods per cluster

Number of well filled pods from all the effective clusters of each plant was counted and averaged per cluster.

3.4.6 Number of pods per plant

Number of pods were counted at harvest stage from selected plants and averaged.

3.4.7 Pod length (cm)

The average length of five pods selected at random in each plant is measured and recorded in centimeters.

3.4.8 Number of seeds per pod

The number of seeds present in fully matured pod was counted and the mean was computed from observations.

3.4.9 Hundred Seed weight (g)

Completely dried hundred seeds were weighed, and weight was recorded in grams.

3.4.10 Seed yield per plant (g)

The mature pods were harvested from tagged plants in each entry and threshed and the average weight in grams was taken as seed yield per plant.

3.5 Statistical analysis

The experimental data were compiled and subjected to the following statistical analysis. Statistical analysis was performed on the data of traits means recorded on

15 selected plants for yield and its attributing traits using WINDOWSTAT version 9.2 software and R software. The following statistical methods were employed for data analysis and interpretation of yield attributing traits.

3.5.1 Analysis of Variance (ANOVA)

Analysis of variance was performed to split the total variability into different sources (Federer *et al.,* 1975) (Table 3).

3.5.1.1 Estimation of Mean, Range and Standard Error

3.5.1.1.1 Mean

The mean value of every character was determined by summing up all the observations and dividing them by corresponding number of observations.

$$\overline{X} = \sum_{i=1}^{n} X_i/n$$

Where,

$\overline{X}$ = Mean

$\sum_{i=1}^{n} X_i$= Sum of all observations

n = Number of observations

3.5.1.1.2 Range

It is the difference between the highest mean value and the lowest mean value of each character.

$$\text{Range} = X_{max} - X_{min}$$

Where,

X_{max} = the highest mean value of the character

X_{min} = the lowest mean value of the character

3.5.1.1.3 Standard error

It is the measure of uncontrolled variation present in a sample, which is estimated by dividing the standard deviation (SD) by the square root of the number of observations (n) in the sample and denoted by SE.

$$SE = \frac{SD}{\sqrt{n}}$$

3.5.1.2 Variance and covariance

3.6.1.2.1 Variance

Variance is defined as the average of the squared deviation from the mean and is expressed as the sum of squares of the deviations of all the observations of a sample from its mean and divided by (n-1), where n is the number of observations. It is estimated by the following formula.

$$\text{Variance} = \frac{\sum(\text{Xi} - \overline{\text{X}})^2}{\text{n} - 1}$$

Where,

Xi = i^{th} observation of a population

n = Number of observations

3.5.1.2.1.1 Genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated using the formula given by Cochran and Cox (1957).

$$\text{Genotypic variance } (\sigma_g^2) = \frac{\text{MSS (genotype)} - \text{MSS (error)}}{\text{Number of blocks}}$$

$$\text{Phenotypic variance } \left(\sigma_p^2\right) = \sigma_g^2 + \sigma_e^2$$

$$\text{Environmental variance } (\sigma_e^2) = \text{MSS (error)}$$

3.5.1.2.2 Covariance

The analysis of covariance was carried out by taking two characters at a time. The genotypic and phenotypic covariance were calculated as per the formula given below described by Singh and Chaudhary (1977).

$$\text{Environmental covariance} = \text{EMSP}$$

$$\text{Genotypic covariance} = \frac{\text{TrMSP} - \text{EMSP}}{\text{r}}$$

$$\text{Phenotypic covariance} = \text{genotypic covariance} + \text{environmental covariance}$$

Where,

EMSP = Error mean sum of products

TrMSP = Treatment mean sum of products

r = number of replications

3.5.1.3 Phenotypic and Genotypic coefficient of variability

Phenotypic and Genotypic coefficient of variation was calculated by the formula suggested by Burton and De vane (1953).

$$\mathrm{PCV} = \frac{\text{Phenotypic standard deviation}}{\text{General mean}} \times 100$$

$$\mathrm{PCV} \ = \frac{\sigma_{\mathrm{p}}}{\overline{\mathrm{X}}} \times 100$$

$$\mathrm{GCV} = \frac{\text{Genotypic standard deviation}}{\text{General mean}} \times 100$$

$$\mathrm{GCV} \ = \frac{\sigma_{\mathrm{g}}}{\overline{\mathrm{X}}} \times 100$$

Categorization of the range of variability as proposed by Sivasubramanian and Madhavamenon (1973) is as follows.

Scales	Value of GCV and PCV (%)
Low	Less than 10
Moderate	10 – 20
High	More than 20

3.5.2 Heritability and Genetic advance

3.5.2.1 Heritability

Hanson *et al.* (1956) defined heritability in broad sense as the ratio of genotypic variance to the total variance in the non-segregating populations. Heritability was calculated by the formula given by Allard (1960).

$$\mathrm{H} \ = \frac{\sigma_{\mathrm{g}}^2}{\sigma_{\mathrm{p}}^2} \times 100$$

Where,

H = Heritability in broad sense ($\mathrm{h}_{\mathrm{bs}}^2$)

σ_{g}^2 = Genotypic variance

σ_{p}^2 = Phenotypic variance

As suggested by Johnson *et al.* (1955b), ($\mathrm{h}_{\mathrm{bs}}^2$) estimates were categorized as follows:

Scales	Values of heritability in broad sense (%)
Low	Less than 30
Moderate	30 – 60
High	More than 60

3.5.2.2 Genetic Advance (Expected)

Genetic advance denotes the improvement in the genotypic value of the new population over the base population, and it is estimated by the following formula suggested by Allard (1960b).

$$\text{Genetic Advance (Expected)} = \mathrm{H} \times \sqrt{\sigma_p^2} \times \mathrm{K}$$

Where,

H = Heritability coefficient

$\sqrt{\sigma_p^2}$ = Phenotypic standard deviation

K = Selection differential in the standard units which is 2.06 at 5 *per cent* selection intensity

3.5.2.3 Genetic advance as percent of mean (GAM)

Genetic advance as *per cent* of mean was calculated by following formula.

$$\mathrm{GAM} = \frac{\mathrm{GA}}{\overline{\mathrm{X}}} \times 100$$

Where,

GA = Expected genetic advance

$\overline{X}$ = General mean of the character in the population

The range of GAM was classified as suggested by Johnson *et al.* (1955b).

Scales	Value of Genetic Advance (%)
Low	Less than 10
Moderate	10 – 20
High	More than 20

3.5.2.4 Skewness

As implied by the term, the skewness is a measure of the extent to which the distribution of the respective variable skewed to the left (negative value) or right (positive value), relative to the standard normal distribution (for which the skewness is 0). The measure of skewness is related to the third moment of the distribution. The skewness defined as:

$$\text{Skewness} = \frac{n\sum_{i=1}^{n}(X_I - \overline{X})^3}{(n-1)(n-2)\sigma^3}$$

Where,

'X' is independent variable

'n' is the valid number of cases

'σ^3' is the standard deviation (sigma) raise to the third power.

The lack of symmetry, *i.e.,* skewness, was recognized based on the coefficient of skewness. Its values range from -3 to + 3. The type of distribution based on the skewness values are as follows.

If skewness value zero = symmetrical distribution

If skewness value negative = negatively skewed distribution, If skewness value positive = positively skewed distribution

3.5.2.5 Kurtosis

The Kurtosis is a measure of how "wide" or skinny ("Flat" or "Peaked") the distribution is for the respective variable, relative to the standard normal distribution (for which the kurtosis is equal to 0). It is also sometimes referred to as the fourth moment of the distribution. The kurtosis defined as:

$$\text{Skewness} = \frac{n\,(n+1)\sum_{i=1}^{n}(X_I - \overline{X})^4}{(n-1)(n-2)(n-3)\sigma^4} - \frac{3\,(n-1)^2}{(n-2)(n-3)}$$

Where,

'X' is independent variable

'n' is the valid number of cases

'σ^4' is the standard deviation (sigma) raise to the fourth power

Three types of kurtosis were recognized based on the kurtosis value, which depends on the distribution curve.

If kurtosis value = 3 = Normal curve = Mesokurtic

If kurtosis value > 3 = Leaping curve = Leptokurtic

If kurtosis value < 3 = Flat curve = Platykurtic

3.5.3 Correlation coefficient analysis

The concept of correlation was first given by Galton (1889), which was further elaborated by Fisher (1919) to initiate an effective selection program aimed at genetic enhancement of the economic yield of the crop plants.

The correlation coefficients were calculated to determine the degree of association of characters with yield and yield components. The phenotypic correlation coefficient helps to determine the selection index, whereas, the genotypic correlation coefficient provides a close measure of association between characters, which may be useful for the overall yield improvement.

Genotypic correlation is the inherent association between the two variables, and it may be either due to the pleiotropic action of genes or linkage. If the correlation between yield and a character is due to the direct effect of the character, it reflects a true relationship between them, and selection can be practiced for such characters. However, if the correlation is mainly due to the indirect effect of the character through another component trait, the breeder has to select for the trait through which the indirect effect is expected. An excellent yield response is obtained when indirect selection is practiced for the character having high heritability and positive correlation with yield. Both genotypic and phenotypic coefficients of correlation between two characters were determined by using the variance and covariance components, as suggested by Al-Jibouri *et al.* (1958).

$$r_g(xy) = \frac{Cov_g(xy)}{\sqrt{\sigma_g^2(x) \times \sigma_g^2(y)}}$$

$$r_p(xy) = \frac{Cov_p(xy)}{\sqrt{\sigma_p^2(x) \times \sigma_p^2(y)}}$$

Where,

$r_g(xy)$, $r_p(xy)$ are the genotypic and phenotypic correlation coefficients respectively.

Cov_g and Cov_p are the genotypic and phenotypic covariance respectively.

σ_g^2 and σ_p^2 are the genotypic and phenotypic variance respectively.

x and y are the two traits for which correlation coefficient is estimated.

3.5.3.1 Test of significance

For testing the significance of correlation coefficients, the estimated values were compared with the table value (Fisher and Yates, 1938) at n-2 degrees of freedom (where n denotes the number of genotypes tested) at 5 % and 1 % levels of significance.

The range of correlation coefficients were classified as suggested by Searle (1965).

Scales	**Value of Correlation Coefficients**
Very strong	More than 0.65
Moderately strong	0.50 to 0.64
Moderately weak	0.30 to 0.49
Very weak	Less than 0.30

3.5.4 Path coefficient analysis

Path coefficient analysis is a standardized partial regression coefficient that splits the correlation coefficients into the measures of direct and indirect effects. Wright (1934), suggested Path coefficient analysis, and it was further elaborated by Dewey and Lu (1959). The whole system of variables represented in the form of a diagram is called a path diagram.

Path coefficient is the ratio of the standard deviation of the effect due to a given cause to the total standard deviation of the effect *i.e.* if seed yield per plant (Y) is the function of the causal factor X_1, then path coefficient for the path from causal factor X_1 to the effect Y is given by the formula, σ_{X_1}/σ_Y

In this experiment seed yield per plant (Y) was taken as an effect of the other traits (X) like the number of days to 50 *per cent* flowering, number of days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, hundred seed weight, seed yield per plant, biomass yield per plant, biological yield per plant and harvest index as the causal factors.

3.5.4.1 The path-coefficients were obtained by solving a set of simultaneous equations given below

$$r_{X_1Y} = P_{X_1Y} + r_{X_1X_2}P_{X_2Y} + r_{X_1X_3}P_{X_3Y} + \dots\dots\dots\dots\dots\dots\dots\dots\dots + r_{X_1X_{14}}P_{X_{14}Y}$$

$$r_{X_2Y} = r_{X_2X_1}P_{X_1Y} + P_{X_2Y} + r_{X_2X_3}P_{X_3Y} + \dots\dots\dots\dots\dots\dots\dots\dots\dots + r_{X_2X_{14}}P_{X_{14}Y}$$

$$\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots$$

$$\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots$$

$$r_{X_{14}Y} = r_{X_{14}X_1}P_{X_1Y} + r_{X_{14}X_2}P_{X_2Y} + r_{X_{14}X_3}P_{X_3Y} + \dots\dots\dots\dots\dots\dots\dots\dots + P_{X_{14}Y}$$

Where,

r_{X_1Y} to $r_{X_{14}Y}$ denotes coefficient of correlation between independent characters X_1 to X_{14} and dependent character Y

$r_{X_1X_2}$ to $r_{X_{13}X_{14}}$ denotes coefficient of correlation between all possible combination of independent characters.

P_{X_1Y} to $P_{X_{14}Y}$ denotes direct effects of character X_1 to X_{14} on Y

3.5.4.2 The indirect effects of the causal factors were calculated by the formula given below

$$\text{Indirect effects} = r_{ij} \times P_{ij}$$

Where,

$i = 1 \dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots n$

$j = 1 \dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots n$

$P_{ij} = P_{1Y}, P_{2Y}, P_{3Y} \dots\dots\dots\dots\dots P_{nY}$

3.5.4.3 The residual factor(P_{RY})

The variation in yield unaccounted by the causal effects under consideration is called residual effect and is calculated using the following formula.

$$(P_{RY}) = \sqrt{1 - R^2}$$

Where,

$$(R^2) = \sum_{i=1}^{15} P_{X_iY} r_{X_iY}$$

Therefore,

$$(P_{RY}) = \sqrt{1 - P_{1Y}\, r_{1Y} + P_{2Y}\, r_{2Y} + \dots\dots\dots\dots\dots\dots\dots\dots\dots\dots + P_{14Y}\, r_{14Y}}$$

Where,

P_{RY} = Residual effect

R^2 = Coefficient of determination

P_{iY} = Direct effect of X_i on Y

r_{iY} = Correlation coefficient of X_i and Y

The range of path coefficients were classified as suggested by Lenka and Mishra (1973).

Scales	**Value of direct and indirect effects**
Negligible	0.00 to 0.09
Low	0.10 to 0.19
Moderate	0.20 to 0.29
High	0.30 to 0.99
Very high	More than 1.00

3.5.6 Transgressive Segregation:

Transgressive segregation is considered as an important tool by the plant breeder to bring about crop improvement. Due to segregation and recombination in certain cases transgressive segregants are produced in F_2 or latter generations by accumulation of favorable genes from both the parents involved in hybridization.

In the present study, transgressive segregants were identified by finding the number of plants exceeding the mean value of superior parent or lagging behind the mean value of inferior parent. The data recorded on all the plants from F_3M_2 population was used for calculating the number of transgressive segregants.

Table 3 Structure of ANOVA for Augmented design

Sources of variations	**Degrees of freedom**	**Mean sum of squares (MSS)**	**'F' ratio**
Blocks (b)	b – 1	MSS(b)	MSS(b)/ EMSS
Entries (e) (Genotypes + checks)	e – 1	MSS(e)	MSS(e)/EMSS
Genotypes (g)	g – 1	MSS(g)	MSS(g)/EMSS
Checks	c – 1	MSS(c)	MSS(c)/EMSS
Genotypes *vs* Check (gc)	1	MSS(gc)	MSS(gc)/EMSS
Error	(b-1) (c-1)	EMSS	

Where,

b = Number of blocks

g = Number of genotypes

c = Number of checks

e = Number of entries (genotypes + checks)

EXPERIMENTAL RESULTS

IV EXPERIMENTAL RESULTS

The experimental results obtained in the present investigation are presented in this chapter under the following headings.

4.1 Analysis of Variance

4.2 Genetic variability parameters

4.3 Correlation coefficient analysis

4.4 Path coefficient analysis

4.5 Transgressive segregants for yield and its attributing traits in black gram

4.1 Analysis of variance

4.1 Analysis of variance for growth, yield, yield attributes

Analysis of variance was carried out for yield and its attributes in 400 F_3M_2 progeny lines along with four checks. Analysis of variance revealed significant differences among the genotypes for all the traits studied, indicating the presence of sufficient genetic variability and the choice of the material for the investigation was appropriate (Table 4).

This was further supported by the fact that range has been also relatively wider for all the characters also pointing out extreme genotypes for selection. The mean values of all the characters are presented in Appendix 1.

4.2 Genetic variability parameters

The genetic variability parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2) and expected genetic advance as *per cent* of mean (GAM) for all the traits under study are depicted in the Table 5.

4.2.1 Days to 50 per cent flowering

Substantial variation was found for number of days to 50 *per cent* flowering in the study material with a mean value of 42.16 days and it was ranging from 37 to 47. Progeny line 161 took minimum number of days to 50 *per cent* flowering (37 days), whereas progeny line 46, progeny line 62 and progeny line 252 have taken maximum number of days to 50 *per cent* flowering (47 days). Estimates of GCV and PCV were low with the values of 3.56 and 4.29 *per cent* respectively. Further, high heritability (68.92%) coupled with low genetic advance as *per cent* of mean (6.09%) was observed for this trait. The frequency distribution for this trait was negatively skewed (-0.119) with platykurtic (0.335).

Table 4 ANOVA for grain yield and its component traits in F_3M_2 blackgram [*Vigna mungo* (L.) Hepper]

Source of Variation	Degrees of freedom	Mean Sum of Square									
		DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
Block (eliminating Treatments)	9	0.79	2.08	0.03	0.64	0.0039	8.41	0.14	0.12	0.02	3.55
Genotypes + Checks (Ignoring blocks)	403	3.39 **	7.44 *	0.16 **	3.28 **	0.15 **	41.56 **	0.21 **	0.47 **	0.17 **	5.08 **
Genotypes	399	3.26 **	7.15 *	0.15 **	2.81 **	0.14 **	37.27 **	0.2 **	0.45 **	0.16 **	4.49 **
Checks	3	9.29 **	29.11 **	0.63 **	12.04 **	0.82 **	467.36 **	0.48 **	1.76 **	0.51 **	42.47 **
Checks vs. Genotypes	1	38.39 **	55.66 **	1.35 **	163.27 **	1.05 **	475.72 **	4.67 **	3.16 **	0.78 **	127.63 **
Error	27	1.01	3.72	0.03	0.73	0.03	9.86	0.08	0.12	0.03	1.88

* - Significant @ 5%, ** - Significant @ 1%

DFF = Days to 50% flowering
PH = Plant height (cm)
NB = Number of branches^{-1}
NCP = Number of clusters plant^{-1}
NPC = Number of pods cluster^{-1}
NPP = Number of pods plant^{-1}
PL = Pod length (cm)
NSP = Number of seeds pod^{-1}
TW = Test weight (g)
TSY = Total seed yield (g)

Table 5 Estimates of parameters specifying variability for seed yield and its component traits in F_3M_2 blackgram [*Vigna mungo* (L.) Hepper]

Sl No	Traits	Mean	Range		GCV (%)	PCV (%)	h^2_{bs} (%)	GAM (%)	Skewness	Kurtosis	Kurtosis type
			Minimum	Maximum							
1	Days to 50 % flowering	42.16	37.00	47.00	3.56	4.29	68.92	6.09	-0.119	0.335	P
2	Plant height (cm)	30.82	24.00	37.00	6.02	8.68	48.04	8.6	-0.100	0.014	P
3	Number of branches plant^{-1}	3.33	2.40	4.12	10.39	11.75	78.2	18.96	-0.037	-0.354	P
4	Number of clustersplant^{-1}	15.72	11.00	19.00	9.18	10.68	73.9	16.28	-0.460	-0.115	P
5	Number of pods cluster^{-1}	3.70	2.80	4.70	9.00	10.28	76.79	16.28	0.077	-0.703	P
6	Number of pods plant^{-1}	45.16	31.00	58.00	11.61	13.53	73.55	20.54	-0.137	-0.518	P
7	Pod length (cm)	4.86	3.80	6.00	7.07	9.23	58.74	11.18	0.241	-0.346	P
8	Number of seeds pod^{-1}	5.39	4.10	7.00	10.74	12.46	74.3	19.1	-0.617	-0.346	P
9	100 seed weight (g)	4.61	2.98	5.30	7.88	8.76	80.9	14.62	-0.683	1.168	P
10	Seed yield plant^{-1} (g)	10.48	5.20	16.40	15.45	20.26	58.13	24.3	0.045	-0.099	P

GCV = Genotypic coefficient of variation
PCV = Phenotypic coefficient of variation
h^2(bs) = Broad sense heritability
GAM = Genetic advance as *per cent* mean
P = Platykurtic

4.2.2 Plant height (cm)

The plant height was in the range of 24 to 37 cm with a mean value of 30.82 cm. Progeny line 107 and progeny line 264 showed minimum plant height of 24 cm, whereas progeny line 48 and progeny line 64 exhibited maximum plant height of 37 cm. The estimates of GCV and PCV were found to be low with the values of 6.02 and 8.68 *per cent,* respectively. Plant height exhibited moderate heritability (48.04 %) combined with low genetic advance as *per cent* of mean (8.6 %). The frequency distribution for this trait was negatively skewed (-0.100) with platykurtic (-0.014)

4.2.3 Number of branches per plant

Number of branches per plant ranged from 2.40 to 4.12 with a mean value of 3.33. Progeny line 180 had minimum number of branches whereas, progeny line 98, progeny line 114 and progeny line 283 had maximum number of branches. The estimates of GCV and PCV were found to be moderate with the values of 10.39 and 11.75 *per cent* respectively. High heritability (78.2 %) coupled with moderate genetic advance as *per cent* of mean (18.96%) was observed for this character. The frequency distribution for this trait was negatively skewed (-0.037) with platykurtic (-0.354).

4.2.4 Number of clusters per plant

Number of clusters per plant ranged from 11 to 19 with a mean value of 15.72. Progeny line 39 had minimum clusters whereas, progeny line 43, progeny line 79, progeny line 250 and progeny line 276 had maximum clusters. This trait recorded low GCV (9.18 %) and moderate PCV (10.68 %). High heritability (73.9 %) coupled with moderate genetic advance as *per cent* of mean (16.28 %) was observed for this character (Table 4.2). The frequency distribution for this trait was negatively skewed (-0.460) with platykurtic (-0.115)

4.2.5 Number of pods per cluster

Number of pods per cluster ranged from 2.80 to 4.70 with a mean value of 3.70. progeny line 69 and progeny line 260 had minimum pods per cluster whereas, progeny line 10, progeny line 28 and progeny line 218 had maximum pods per cluster. This trait recorded low GCV (9 %) and moderate PCV (10.28 %). High heritability (76.79 %) coupled with moderate genetic advance as *per cent* of mean (16.28 %) was observed for this character. The frequency distribution for this trait was positively skewed (0.077) with platykurtic (-0.703).

4.2.6 Number of pods per plant

Number of pods per plant ranged from 31 to 58 with a mean value of 45.16. Progeny line 185 and progeny line 261 had minimum pods per plant whereas, progeny line 43 and progeny line 47 had maximum number of pods per plant. This trait recorded moderate GCV (11.61 %) and moderate PCV (13.53 %). High heritability (73.55 %) coupled with high genetic advance as *per cent* of mean (20.54 %) was observed for this character. The frequency distribution for this trait was negatively skewed (-0.137) with platykurtic (-0.518).

4.2.7 Pod length (cm)

Pod length ranged from 3.8 cm to 6 cm with a mean value of 4.86. Progeny line 6 and progeny line 22 had minimum pod length whereas, progeny line 147 had maximum pod length. This trait recorded low GCV (7.07 %) and low PCV (9.23 %). Moderate heritability (58.74 %) coupled with moderate genetic advance as *per cent* of mean (11.18 %) was observed for this character. The frequency distribution for this trait was positively skewed (0.241) with platykurtic (-0.346).

4.2.8 Number of seeds per pod

Number of seeds per pod ranged from 4.10 to 7 with a mean value of 5.39. Progeny line 285 and progeny line 293 had minimum number of seeds per pod whereas, progeny line 123 and progeny line 159 had maximum number of seeds per pod. This trait recorded moderate GCV (10.74 %) and moderate PCV (12.46 %). High heritability (74.30 %) coupled with moderate genetic advance as *per cent* of mean (19.10 %) was observed for this character. The frequency distribution for this trait was negatively skewed (-0.617) with platykurtic (-0.346).

4.2.9 100 seed weight (g)

Test weight or 100 seed weight exhibited considerable variation and was ranging from 2.98 g to 5.30 g with a mean of 4.61 g. Progeny line 67, progeny line 257 had minimum test weight whereas progeny line 153 had maximum test weight. The estimates of GCV and PCV were found to be low with the values of 7.88 and 8.76 *per cent*, respectively. Further this trait exhibited high heritability (80.90%) combined with moderate genetic advance as *per cent* of mean (14.62%). The frequency distribution for this trait was negatively skewed (-0.683) with platykurtic (1.168).

4.2.10 Total seed yield per plant (g)

Total seed yield per plant exhibited considerable variation and ranging from 5.2 g to 16.4 g with a mean of 10.48 g. Progeny line 130 and progeny line 146 had minimum total seed yield per plant whereas progeny line 47, progeny line 63 had maximum total seed yield per plant. This trait recorded moderate GCV (15.45 %) and high PCV (20.26 %). Further, this trait exhibited moderate heritability (58.13 %) combined with high genetic advance as *per cent* of mean (24.3 %). The frequency distribution for this trait was positively skewed (0.045) with platykurtic (-0.099).

4.3 Correlation coefficient analysis

The economic yield of a crop plants is a complex trait as it is governed by the action and interaction of various agro-morphological attributes. Association of economic yield with other agro-morphological component characters should be studied because sometimes due to low heritability selecting directly for high seed yield per plant may be ineffective. Correlation studies will provide reliable information, in particular the breeder wants to combine superior yield potential with desirable agronomic attributes. The relations between yield and yield attributing component traits studied presented in (Table 6).

4.3.1 Days to 50 per cent flowering

Days to 50 *per cent* flowering exhibited significant positive association with number of branche*s* per plant (0.110), number of clusters per plant (0.241), number of pods per cluster (0.244), number of pods per plant (0.255), number of seeds per pod (0.176), test weight (0.198), total seed yield per plant (0.263) and positive association non-significantly with the pod length (0.023). In contrast, a significant negative correlation was exhibited with the plant height (-0.104).

4.3.2 Plant height (cm)

Plant height exhibited significant positive association with number of branches per plant (0.115), number of clusters per plant (0.204), number of pods per cluster (0.099), number of pods per plant (0.264), pod length (0.146), number of seeds per pod (0.294), test weight (0.099) and seed yield per plant (0.288). In contrast, a significant negative correlation was exhibited with the days to 50 *per cent* flowering (-0.104).

4.3.3 Number of branches per plant

Number of branche*s* per plant exhibited significant positive association with days to 50 *per cent* flowering (0.110), plant height (0.115), number of clusters per plant (0.275), number of pods per plant (0.179), pod length (0.165), number of seeds per pod (0.212), test weight (0.186) and seed yield per plant (0.340). In contrast, a significant negative correlation was exhibited with the number of pods per cluster (-0.056).

4.3.4 Number of clusters per plant

Number of clusters per plant exhibited significant positive association with days to 50 *per cent* flowering (0.241), plant height (0.204), number of branches per plant (0.275), number of pods per cluster (0.230), number of pods per plant (0. 558), pod length (0.426), number of seeds per pod (0.561), test weight (0.543) and seed yield per plant (0.746).

Table 6 Phenotypic correlation coefficients for growth, yield, yield contributing traits in F_3M_2 blackgram [*Vigna mungo* (L). Hepper]

	DFF	**PH**	**NB**	**NCP**	**NPC**	**NPP**	**PL**	**NSP**	**TW**	**TSY**
DFF	1	-0.1045*	0.1100*	0.2411**	0.2443**	0.2558**	0.0235	0.1762**	0.1981**	0.2639**
PH		1	0.1154*	0.2043**	0.0995*	0.2643**	0.146**	0.2949**	0.0992*	0.2885**
NB			1	0.2753**	-0.0567	0.1799**	0.1653**	0.2128**	0.1865**	0.3407**
NCP				1	0.2305**	0.5581**	0.4266**	0.5616**	0.5433**	0.7461**
NPC					1	0.3931**	-0.0469	0.1695**	0.0417	0.2671**
NPP						1	-0.0269	0.1201*	0.2972**	0.6324**
PL							1	0.478**	0.4088**	0.3305**
NSP								1	0.401**	0.6404**
TW									1	0.6823**
TSY										1

**Significance at 0.01 probability level *Significance at 0.05 probability level

DFF = Days to 50% flowering
PH = Plant height (cm)
NB = Number of branches plant $^{-1}$
NCP = Number of clusters plant^{-1}
NPC = Number of pods cluster^{-1}
NPP = Number of pods plant^{-1}
PL = Pod length (cm)
NSP = Number of seeds pod^{-1}
TW = Test weight (g)
TSY = Total seed yield (g)

4.3.5 Number of pods per cluster

Number of pods per cluster exhibited significant positive association with days to 50 *per cent* flowering (0.244), plant height (0.99), number of clusters per plant (0.230), number of pods per plant (0.393), number of seeds per pod (0.169), seed yield per plant (0.267) and non-significantly with the test weight (0.042). In contrast, negative non-significant correlation was exhibited with the number of branches per plant (-0.057) and pod length (-0.047).

4.3.6 Number of pods per plant

Number of pods per plant exhibited significant positive association with days to 50 *per cent* flowering (0.255), plant height (0.264), number of branches per plant (0.179), number of clusters per plant (0.558), number of pods per cluster (0.393), number of seeds per pod (0.120), test weight (0.297) and seed yield per plant (0.632). In contrast, a significant negative non-significant correlation was exhibited with the pod length (-0.026).

4.3.7 Pod length (cm)

Pod length exhibited significant positive association with plant height (0.146), number of branches per plant (0.165), number of clusters per plant (0.426), number of seeds per pod (0.478), test weight (0.408) and seed yield per plant (0.330) and positive association non-significantly with the days to 50 *per cent* flowering (0.023), In contrast, a significant negative non-significant correlation was exhibited with number of pods per cluster (-0.046), number of pods per plant (-0.026).

4.3.8 Number of seeds per pod

Number of seeds per pod exhibited significant positive association with days to 50 *per cent* flowering (0.176), plant height (0.294), number of branches per plant (0.212), number of clusters plant (0.561), number of pods per cluster (0.169), number of pods per plant (0.120), pod length (0.478), test weight (0.401) and seed yield per plant (0.640).

4.3.9 100 seed weight (g)

100 seed weight exhibited significant positive association with days to 50 *per cent* flowering (0.198), plant height (0.099), number of branches per plant (0.186), number of clusters per plant (0.543), number of pods per cluster (0.417), number of pods per plant (0.297), pod length (0.408), number of seeds per pod (0.401) and seed yield per plant (0.682).

4.3.10 Total seed yield per plant (g)

Total seed yield per plant exhibited significant positive association with days to 50 *per cent* flowering (0.263), plant height (0.288), number of branches per plant

(0.340), number of clusters per plant (0.746), number of pods per cluster (0.267), number of pods per plant (0.632), pod length (0.330), number of seeds per pod (0.640) and test weight (0.682).

4.4 Path coefficient analysis

Seed yield is generally under the polygenic control, selecting for economic yield directly for enhancement in yield level will not be fruitful as it affects the other associated traits and vice versa. To understand the influence of different agro-morphological traits on seed yield, the association of these traits with seed yield were divided into direct and indirect effects. This gives more clarity while selecting for essential traits, which may contribute towards increased seed yield per plant. The path analysis between yield and yield related traits were estimated and the results are depicted in Table 7.

4.4.1 Days to 50 per cent flowering

The number of days to 50 *per cent* flowering showed a negative direct effect on seed yield per plant (-0.0156) through positive indirect effect of the plant height (0.0016) and negative indirect effects of the number of branches per plant (-0.0017), number of clusters per plant (-0.0038), number of pods per cluster (-0.0038), number of pods per plant (-0.004), pod length (0.004), number of seeds per pod (-0.0028) and test weight (-0.0031).

4.4.2 Plant height (cm)

Plant height showed a positive direct effect on seed yield per plant (0.0026) through positive indirect effects of the number of branches per plant (0.0003), number of clusters plant per plant (-0.0005), number of pods per cluster (0.0003), number of pods per plant (0.0007), pod length (0.0004), number of seeds per pod (0.0008), test weight (0.0003) and negative indirect effects of the days to 50 *per cent* flowering (-0.0003).

4.4.3 Number of branches per plant

Number of branches per plant showed a positive direct effect on seed yield per plant (0.1005), through positive indirect effects of the days to 50 *per cent* flowering (0.0111), plant height (0.0116), number of clusters per plant (0.0277), number of pods per plant (0.0181), pod length (0.0166), number of seeds per pod (0.0214), test weight (0.0187) and negative indirect effects of the number of pods per cluster (-0.0057).

4.4.4 Number of clusters per plant

Number of clusters per plant showed a positive direct effect on seed yield per plant (0.1023), through positive indirect effects of the days to 50 *per cent*

Table 7 Phenotypic path coefficient analysis showing direct (diagonal) and indirect effects of different traits on seed yield per plant in F$_3$M$_2$ blackgram [*Vigna mungo* (L). Hepper] genotypes evaluated at Shivamogga during Rabi-2020

Effect of trait	*Via* Character								
	DFF	**PH**	**NB**	**NCP**	**NPC**	**NPP**	**PL**	**NSP**	**TW**
DFF	**-0.0156**	0.0016	-0.0017	-0.0038	-0.0038	-0.004	-0.0004	-0.0028	-0.0031
PH	-0.0003	**0.0026**	0.0003	0.0005	0.0003	0.0007	0.0004	0.0008	0.0003
NB	0.0111	0.0116	**0.1005**	0.0277	-0.0057	0.0181	0.0166	0.0214	0.0187
NCP	0.0247	0.0209	0.0282	**0.1023**	0.0236	0.0571	0.0436	0.0574	0.0556
NPC	0.0025	0.001	-0.0006	0.0023	**0.0101**	0.004	-0.0005	0.0017	0.0004
NPP	0.103	0.1064	0.0724	0.2247	0.1583	**0.4026**	-0.0108	0.0484	0.1196
PL	-0.0012	-0.0077	-0.0087	-0.0224	0.0025	0.0014	**-0.0525**	-0.0251	-0.0214
NSP	0.07	0.1171	0.0845	0.223	0.0673	0.0477	0.1898	**0.3971**	0.1592
TW	0.0699	0.035	0.0658	0.1918	0.0147	0.1049	0.1443	0.1415	**0.353**
r values	**0.2639****	**0.2885****	**0.3407****	**0.7461****	**0.2671****	**0.6324****	**0.3305****	**0.6404****	**0.6823****

* Significant at 0.05 level of probability; ** Significant at 0.01 level of probability; r: Correlation coefficient with seed yield plant^{-1}
Residual effect: 0.3972

DFF = Days to 50% flowering
PH = Plant height (cm)
NB = Number of branches $^{-1}$
NCP = Number of clusters plant^{-1}

NPC = Number of pods cluster^{-1}
NPP = Number of pods plant^{-1}
PL = Pod length (cm)
NSP = Number of seeds pod^{-1}

TW = Test weight (g)
TSY = Total seed yield (g)

flowering (0.0247), plant height (0.0209), number of branches per plant (0.0282), number of pods per cluster (0.0236), number of pods per plant (0.0571), pod length (0.0436), number of seeds per pod (0.0574) and test weight (0.0556).

4.4.5 Number of pods per cluster

Number of pods per cluster showed a positive direct effect on seed yield per plant (0.010), through positive indirect effects of the days to 50 *per cent* flowering (0.0025), plant height (0.001), number of clusters per plant (0.0023), number of pods per plant (0.004), number of seeds per pod (0.0017), test weight (0.0004) and negative indirect effects of the number of branches per plant (-0.0006) and pod length (-0.0005).

4.4.6 Number of pods per plant

Number of pods per plant showed a positive direct effect on seed yield per plant (0.4026), through positive indirect effects of the days to 50 *per cent* flowering (0.103), plant height (0.1064), number of branches per plant (0.724), number of clusters per plant (0.2247), number of pods per cluster (0.1583), number of seeds per pod (0.0484) test weight (0.1196) and negative indirect effects of the pod length (-0.0108).

4.4.7 Pod length (cm)

Pod length showed a negative direct effect on seed yield per plant (-0.0525), through positive indirect effects of the number of pods per cluster (0.0025), number of pods per plant (0.0014) and negative indirect effects of the days to 50 *per cent* flowering (-0.0012), plant height (-0.0077), number of branches per plant (-0.0087), number of clusters per plant (-0.0224), number of seeds per pod (-0.0251) test weight (-0.0214).

4.4.8 Number of seeds per pod

Number of seeds per pod showed a positive direct effect on seed yield per plant (0.3971), through positive indirect effects of the days to 50 *per cent* flowering (0.07), plant height (0.1171), number of branches per plant (0.0845), number of clusters per plant (0.223), number of pods per cluster (0.0673), number of pods per plant (0.0477), pod length (0.1898) and test weight (0.1592).

4.4.9 100 seed weight (g)

100 seed weight showed a positive direct effect on seed yield per plant (0.353), through positive indirect effects of the days to 50 *per cent* flowering (0.0699), plant height (0.035), number of branches per plant (0.0658), number of clusters per plant (0.1918), number of pods per cluster (0.0147), number of pods per plant (0.1049), pod length (0.1443) and number of seeds per pod (0.1415).

4.5 Transgressive segregants for yield and its attributing traits in black gram

Many plant breeders have reported transgressive segregants in segregating population and suggested transgressive segregation may be used as a positive tool in plant breeding. Success in obtaining desired transgressive segregants depends on obtaining genetic recombination between both linked and unlinked alleles.

Keeping the importance of transgressive segregants in view, an analysis of transgressive segregation for yield contributing attributes was carried out in the present investigation. The plants which had values exceeding the mean value of the higher parent or lagging behind the mean value of the lower parent were identified as transgressive segregants.

The number of such plants that fit this definition and the percentage of the transgressive segregants in F_3M_2 population is presented in Table 8. F_3M_2 plants that surpassed the parental limits were observed for days to first flowering, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100 seed weight (g) and seed yield per plant (g). Highest proportion of transgressive segregants were recorded for plant height followed by number of clusters per plant, seed yield per plant, number of pods per plant, 100 seed weight, number of branches per plant, pod length, days to 50 *per cent* flowering, number of seeds per pod and number of pods per cluster.

4.5.1 Days to 50 per cent flowering

The number of desirable transgressive segregants for days to 50 *per cent* flowering were 12, whereas the number of undesirable transgressive segregants were 15. Total 27 transgressive segregants identified for days to 50 *per cent* flowering.

4.5.2 Plant height (cm)

The number of desirable transgressive segregants for plant height were 20, which were greater than superior parent, whereas the number of undesirable transgressive segregants were 39, which are lower than the inferior parent. Total 59 transgressive segregants identified for plant height.

4.5.3 Number of branches per plant

The number of desirable transgressive segregants for number of branches per plant were 15, whereas the number of undesirable transgressive segregants were 20. Total 35 transgressive segregants identified for number of branches per plant.

4.5.4 Number of clusters per plant

The number of desirable transgressive segregants for number of clusters per plant were 11 which are greater than superior parent, whereas the number undesirable transgressive segregants were 47, which are lower than the inferior parent. Total 58 transgressive segregants identified for number of clusters per plant.

4.5.5 Number of pods per cluster

The number of desirable transgressive segregants for number of pods per cluster were 12, whereas the number undesirable transgressive segregants were 4. Total 16 transgressive segregants identified for number of pods per cluster.

4.5.6 Number of pods per plant

The number of desirable transgressive segregants for number of pods per plant were 12, whereas the number undesirable transgressive segregants were 30. Total 42 transgressive segregants identified for number of pods per plant.

4.5.7 Pod length (cm)

The number of desirable transgressive segregants for pod length were 13, whereas the number of undesirable transgressive segregants were 16. Total 29 transgressive segregants identified for pod length.

4.5.8 Number of seeds per pod

The number of desirable transgressive segregants for number of seeds per pod were 16, whereas the number undesirable transgressive segregants were 2. Total 18 transgressive segregants identified for number of seeds per pod.

4.5.9 Test weight (g)

The number of desirable transgressive segregants for test weight were 17, whereas the number of undesirable transgressive segregants were 22. Total 39 transgressive segregants identified for test weight.

4.5.10 Total seed yield per plant (g)

The number of desirable transgressive segregants for total seed yield per plant were 12, which were greater than superior parent. In contrast, the number of undesirable transgressive segregants were 44, which were lower than the inferior parent. Total 56 transgressive segregants identified for seed yield per plant.

Table 8 Transgressive segregants for yield and its component traits in F_3M_2 population of the cross between PU31 X Rashmi.

Trait	PU31 × Rashmi			Parents		No. Transgressive Segregants	
	Mean	Highest Plant Value	Lowest Plant Value	PU31	Rashmi	Superior than better parent	Lower than the Lowest Parent
DFF	42.16	47	37	42.40	40.60	12	15
PH	30.82	37	24	32.05	28.60	20	39
NB	3.33	4.12	2.4	3.59	3.74	15	20
NCP	15.72	19	11	13.72	15.06	11	47
NPC	3.70	4.7	2.8	3.44	3.57	12	4
NPP	45.16	58	31	44.20	49.30	12	30
PL	4.86	6	3.8	4.63	4.73	13	16
NSP	5.39	7	4.1	5.17	5.61	16	2
TW	4.61	5.3	2.98	4.66	4.62	17	22
TSY	10.48	16.4	5.2	10.46	10.31	12	44

DFF = Days to 50% flowering
PH = Plant height (cm)
NB = Number of branches $^{-1}$
NCP = Number of clusters plant^{-1}
NPC = Number of pods cluster^{-1}
NPP = Number of pods plant^{-1}
PL = Pod length (cm)
NSP = Number of seeds pod^{-1}
TW = Test weight (g)
TSY = Total seed yield (g)

DISCUSSION

V DISCUSSION

The present research work entitled "Assessment of genetic variability by combined hybridization and mutation in Black gram [*Vigna mungo* (L.) Hepper.]" was conducted using 400 progeny lines of black gram to evaluate the direct selection parameters (variability, heritability, and genetic advance), indirect selection parameters (correlation and path coefficient) and to identify the transgressive segregants for yield and its attributing traits in black gram. The findings from the field data concerning ten quantitative traits in a set of 400 progeny lines have been discussed in light of earlier researchers explanations in related aspects under the following subheads.

5.1 Analysis of variance (ANOVA)

Analysis of variance (ANOVA) revealed significant mean squares attributable to genotypes for all the characters studied (Table 4.1). Mean squares due to 'genotypes vs. checks' were significant for all the traits. These results are in agreement with those of Singh *et al.* (2014b), Sushmitharaj *et al.* (2018b). ANOVA is the preliminary step that indicates presence of variability among the genotypes under investigation. Significant differences among the genotypes justifies quantification of variability.

5.2 Genetic variability parameters

There are two distinct reasons for making comparisons of genetic variation for quantitative characters. The first is to compare ability to respond to selection, and the second is to make inferences about the forces that maintain genetic variability (Haule, 1991). First degree statistics *viz*., mean, range, standardized range and second degree statistics *viz*., genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV) and broad sense heritability facilitates in deciphering genetic variability. Unit dependent nature of mean and range do not facilitate comparison across traits. While GCV and PCV estimates are unit independent and enable comparison across traits. However, information on heritable variability is more relevant than total variability for crop improvement. This is measured by broad-sense heritability which is the ratio of genetic variance to the total variance expressed in *per cent*. Estimate of heritability serves as indicator for effective selection. The utility of estimates of heritability is increased when they are used in conjunction with the selection differential (Johnson *et al.,* 1955a).

The variability available in segregating population is one of the key for any crop improvement programs. Accordingly, utility of the segregating population evaluation can be assessed based on the knowledge of mean, range and variance suggesting the extent of variation and studies on association of the characters. Direct and indirect effect of various characters on yield provides guidelines for effective selection.

5.2.1 Range, skewness and kurtosis in the F_3M_2 generation

The F_3M_2 generation of cross (PU31 × Rashmi) exhibited a considerable amount of variability for all ten characters individually (Table 4.2). The range is 37 to 47 for days to 50 *per cent* flowering, 24 cm to 37 cm for plant height, 2.40 to 4.12 for number of branches, 11 to 19 for number of clusters per plant, 2.80 to 4.70 for number of pods per cluster, 31 to 58 for number of pods per plant, 3.8 cm to 6 cm for pod length, 4.10 to 7 for number of seeds per pod, 2.98 g to 5.30 g for 100 seed weight and 5.2 g to 16.40 g for total seed yield per plant.

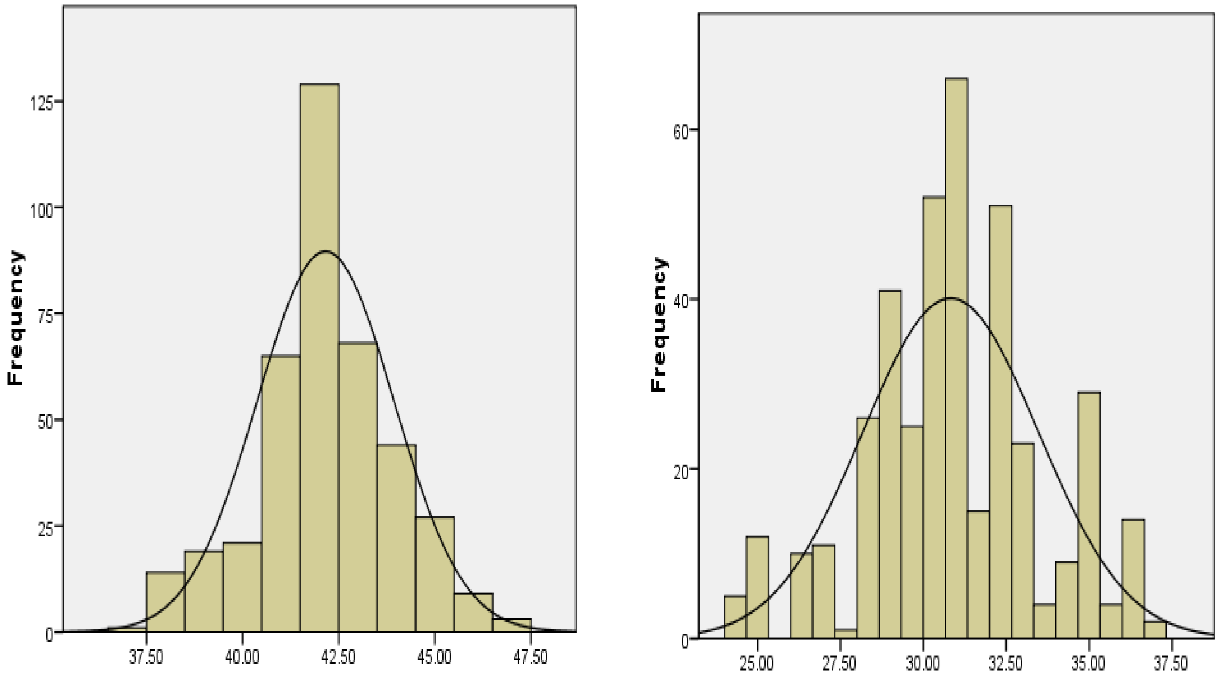
The progeny lines under present investigation showcased wide range of variation suggesting ample amount of scope for selection of elite lines for further improvement in black gram.

The study of distribution properties such as coefficients of skewness (third- degree statistic) and kurtosis (fourth-degree statistic) provides insight about the nature of gene action and number of genes controlling the traits (Robson.,1956), respectively. The skewed distribution of a trait, in general, suggests that the trait is under the control of non-additive gene action, especially epistasis and influenced by environmental variables (Pooni *et al.*, 1977b; Kimberg and Bingham., 1998 and Roy., 2000).

Traits showing skewed distribution indicates that genes controlling the character are predominantly dominant irrespective of enhancing or inhibiting effects on the expression of the trait. In general, the distribution pattern of F_3M_2 generation suggested dominance and dominance based epistasis as the major causes for significant variation and asymmetrical distribution of the majority of the traits investigated in the present study.

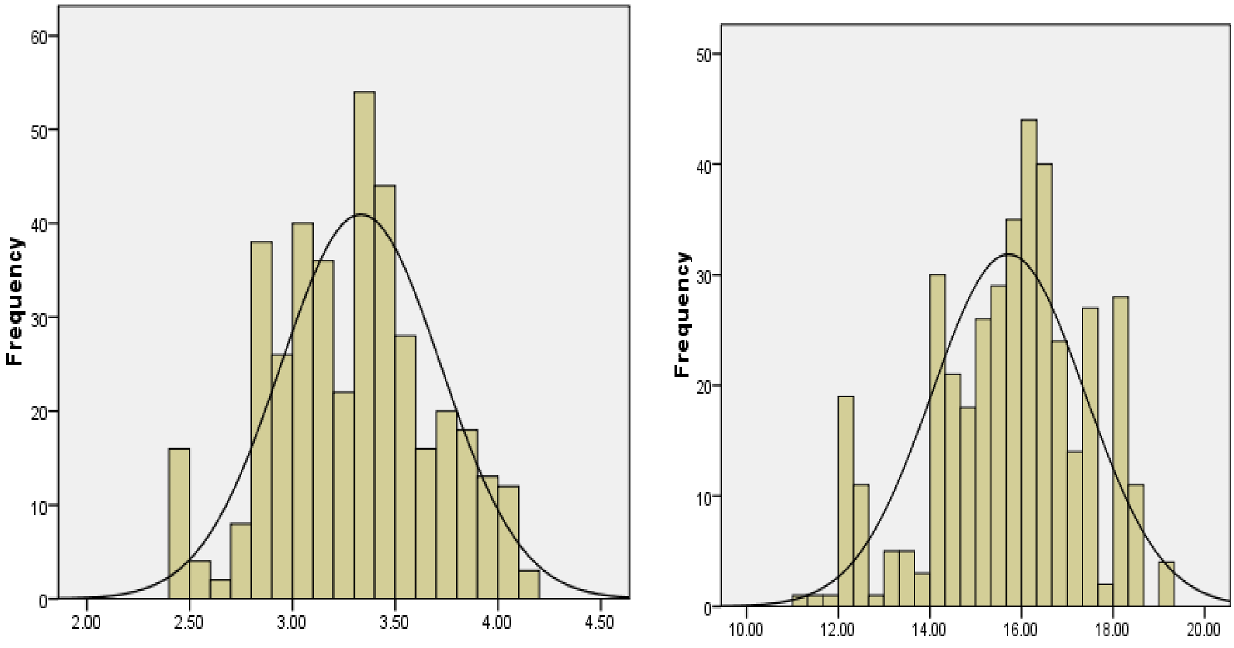
The traits with platykurtic distribution are controlled by fewer and a large number of genes, respectively. Kurtosis is negative or close to zero in the absence of gene interactions and is positive in the presence of gene interactions (Pooni *et al.*, 1977b; Choo and Reinbergs 1982). The inferences on the relative number of genes and nature of genetic control of different traits in F_3M_2 generation of blackgram are discussed below.

Out of ten yield and yield attributing traits evaluated, three characters *viz,* number of pods per cluster, pod length and seed yield per plant showed positive skewness with platykurtic distribution which is an evidence for involvement of moderate number of genes among which equal frequency of genes had increasing and decreasing effects with complementary type of epistasis on the expression of the traits. Similar findings were obtained by the previous studies conducted by Vadivel. (2019), Kuralarasan and Jayamani. (2021b).



Days to 50% flowering

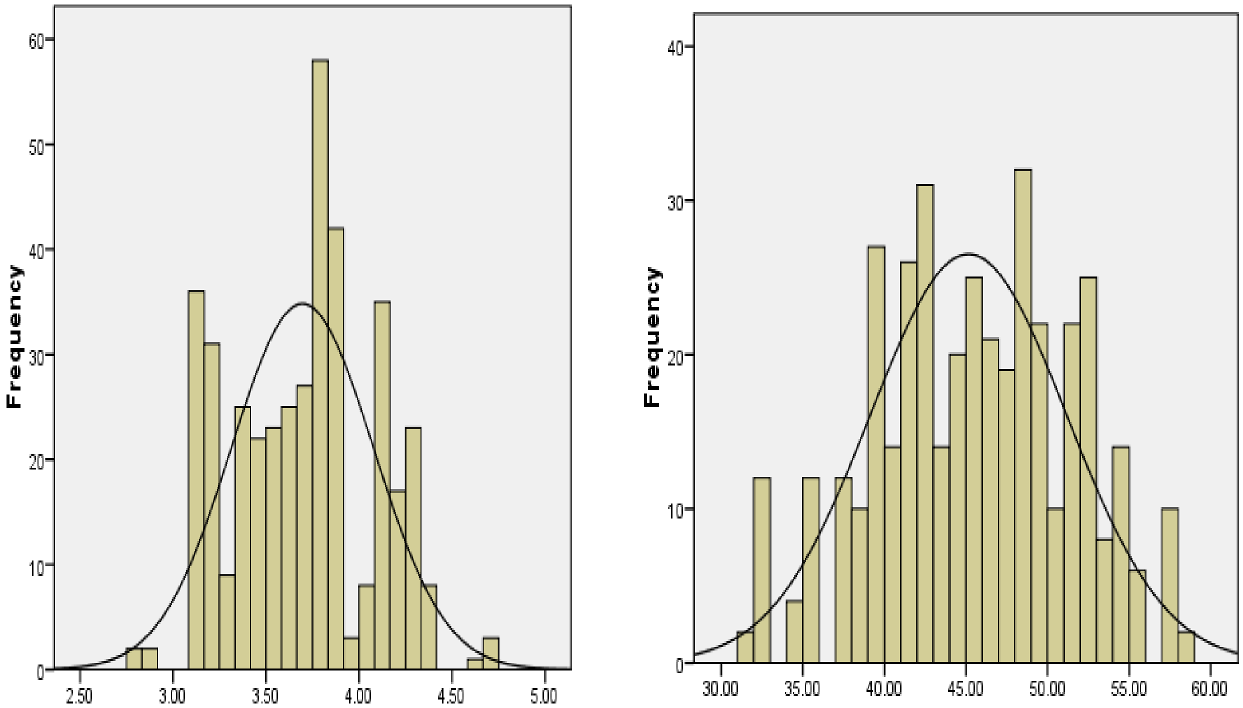
Plant height



Number of branches

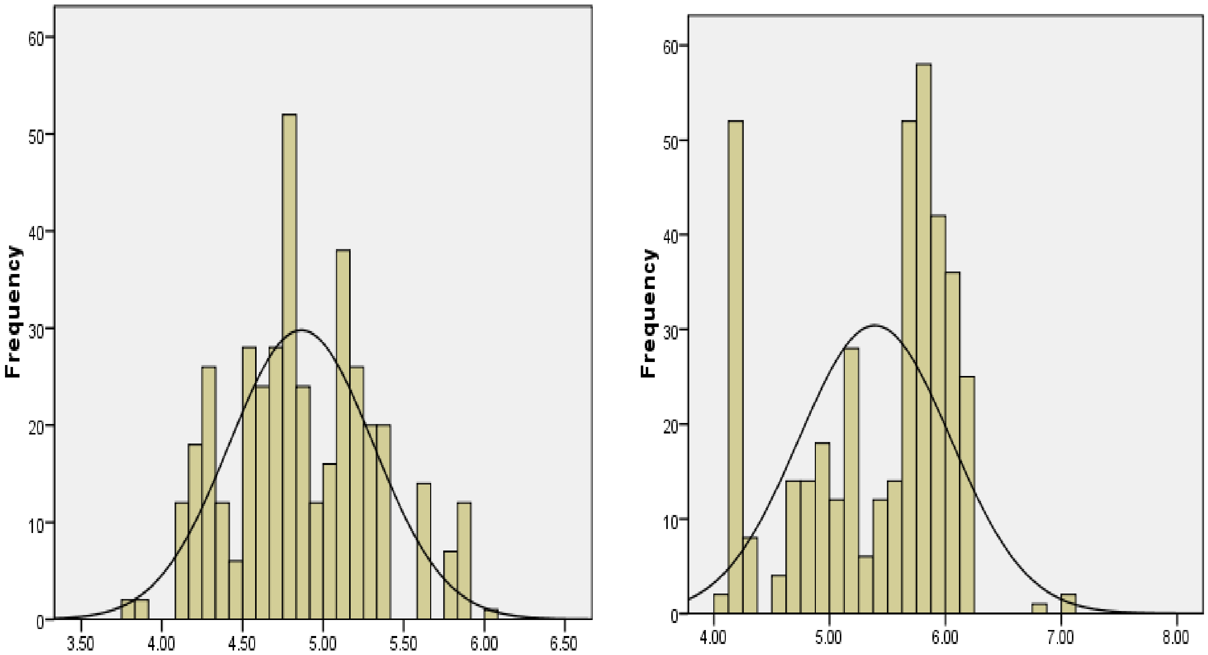
Number of clusters per plant

Fig 1: Frequency distribution of the days to 50% flowering, plant height, number of branches and number of clusters per plant in F_3M_2 blackgram



Number of pods per cluster

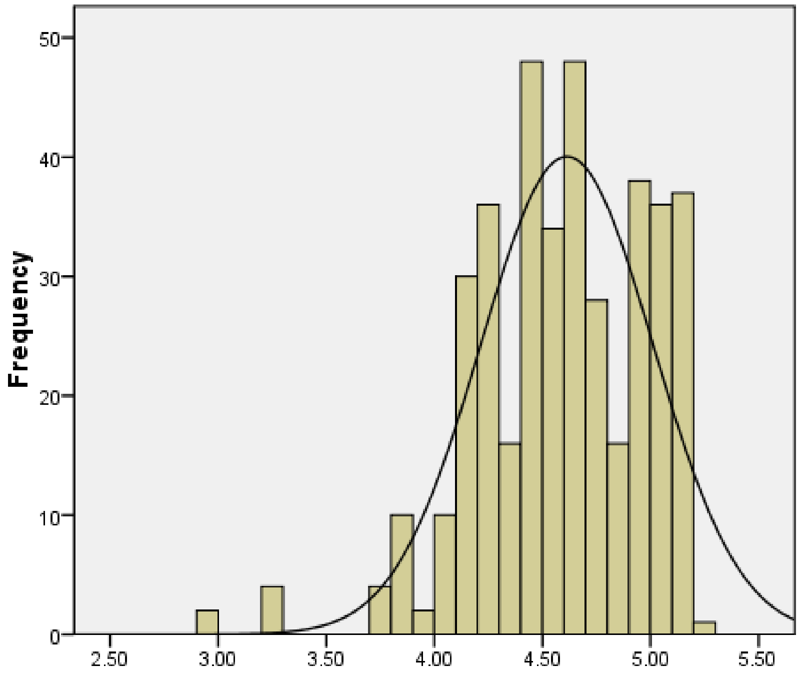
Number of pods per plant



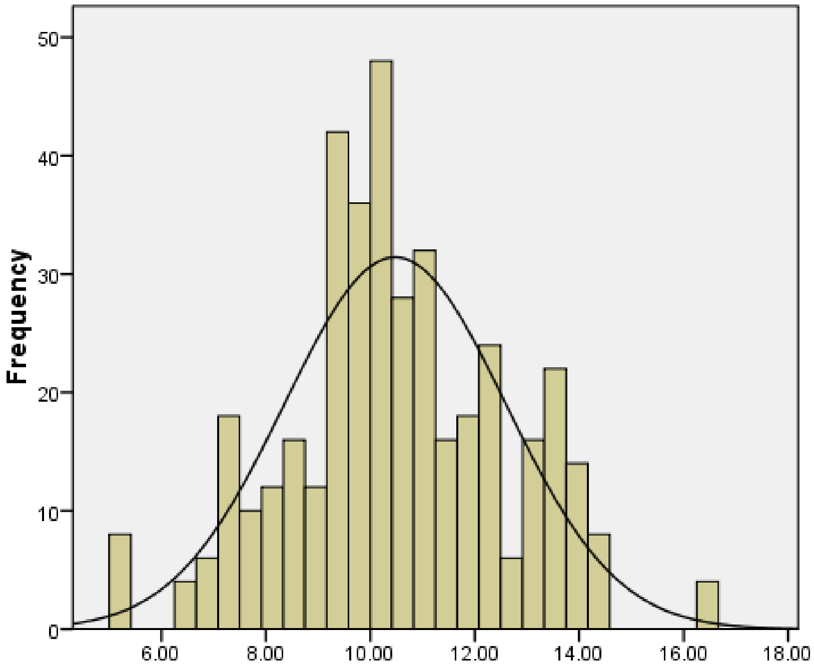
Pod length

Number of seeds per pod

Fig 2: Frequency distribution of the number pods per cluster, number of pods per plant, pod length and number of seeds per pod in F_3M_2 blackgram



100 seed weight



Total seed weight

Fig 3: Frequency distribution of the 100 seed weight and total seed yield per plant in F_3M_2 blackgram.

Negatively skewed and platykurtic distribution was exhibited by seven characters *viz.,* days to 50 *per cent* flowering, plant height, number of branches, number of clusters per plant, for number of pods per plant, number of seeds per pod, 100 seed weight. Signifying the involvement of a large number of dominant genes with a majority of them having increasing effects and duplicate type of epistasis in the inheritance of these traits. This kind of distribution of character will help to protect the individual plant from deleterious alleles arising from existing variability.

5.2.2 Phenotypic coefficient of variation

Usually units of character absolute values differ among themselves and variances calculated for them cannot be used for the comparison. Hence, degree of variability for different characters is compared utilizing the estimates of coefficient of variation which expresses variance as *per cent* of mean. The estimated genotypic and phenotypic coefficients of variation (GCV and PCV) depict the level of variability. Estimation of high values of GCV and PCV for the characters indicates greater variability and lower values indicate lesser variability and the narrow difference between GCV and PCV which implies lesser influence of the environmental effects on the trait expression.

In the results of the current experiment, the PCV values were higher than their corresponding GCV values for all the component traits studied. These findings were in close agreement with the reports of Panigrahi *et al.* (2014); Gandi *et al.* (2018) and Surekha *et al.* (2020).

In the F_3M_2 segregating lines studied, The PCV estimates were relatively high for seed yield per plant and moderate PCV values were observed for number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods plant and number of seeds per pod and low PCV values were recorded for days to 50 *per cent* flowering, plant height, pod length and test weight. These findings were in close agreement with the reports of Punia *et al.* (2013); Deepshikha *et al.* (2014); Kumar *et al.* (2015) and Singh *et al.* (2016).

5.2.2 Genotypic coefficient of variation

Moderate values of GCV were observed for number of branches per plant, number of pods plant, number of seeds per pod and seed yield per plant. Low were recorded for days to 50 *per cent* flowering, plant height, number of clusters per plant, number of pods per cluster, pod length and test weight. Similar findings were obtained by the previous studies conducted by Sushmitharaj *et al.* (2018) and Teja *et al.* (2021).

Number of branches per plant, number of pods per plant, number of seeds per pod showed moderate GCV and PCV. These findings were in close agreement with the reports of Reni *et al.* (2013); Deepshikha *et al.* (2014); Singh *et al.* (2014), Sushmitharaj *et al.* (2018) and Patidar *et al.* (2018).

Days to 50 per cent flowering, plant height, pod length and 100 seed weight showed low GCV and PCV. These findings were in close agreement with the reports of Singh *et al*. (2016); Priyanka *et al*. (2016); Gowsalya *et al*. (2016) and Teja *et al*. (2021).

Number of clusters per plant and number of pods per cluster showed low GCV and moderate PCV. These findings were in close agreement with the reports of Konda *et al*. (2008); Chouhan *et al*. (2018); Tank *et al*. (2018) and Sathees *et al*. (2019).

5.2.3 Heritability and Genetic advance

The difference between the estimates of PCV and GCV was small for almost all the traits specifying less influence of environment in expression of these characters implying phenotypic differences among the genotypes may be given due consideration for selection. However, in the case of the number of clusters per plant and hundred seed weight, the difference was relatively higher, indicating a relatively more significant effect of the environment on these traits. So that in these traits, other variability parameters like heritability may also be considered for selection.

The predictions from the GCV gives a measure of variability and explain the validity of the selection for the traits. Nevertheless, it does not provide a precise picture of the degree of genetic gain predicted from phenotypic selection, unless there is a known heritable fraction of variance (heritability). The broad sense heritability is the ratio of genotypic and phenotypic variances for the traits and therefore it is highly reliable in deciding selection procedures.

Greater heritability values were noticed for the Days to 50 *per* cent flowering, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and 100 seed weight. This indicates that effective selection can be made for these traits.

Heritability estimates indicate both additive and non-additive gene action. So high heritability does not always imply high genetic gain. Heritability, along with genetic advance, can be used as efficient selection parameters instead of heritability alone as both together implies the heritability due to additive gene effects.

In the present F_3M_2 segregating population, high heritability associated with more genetic advance as *per cent* of mean was documented for days to 50 *per cent* flowering, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, 100 seed weight, pod length, number of seeds per pod, seed yield per plant. Parallel results were obtained by Chaithanya *et al*. (2019); Chowdhury *et al*. (2020); Singh *et al*. (2020) and Rehman *et al*. (2021).

It is very clear from the findings of the present field experiment that the Number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and seed yield per plant exhibited the greater values of PCV, GCV, heritability and genetic advance. It is highly insisted to select these traits to attain increased yield.

5.3 Correlation coefficient analysis

Correlation coefficient analysis provides the idea about the mutual relationship between the various component traits and seed yield. Traits exhibit association due to linkage or pleiotropy. If the linkage is between two desirable traits, it will be helpful as the selection for such traits leads to the simultaneous improvement of both the traits. As seed yield is the complex trait controlled by minor genes and depends on many factors for its expression, selection for seed yield directly is not always fruitful. Therefore, it is more desirable to select the yield attributing traits that show significant positive relation with seed yield for the yield improvement.

Seed yield per plant exhibited a positive association with the days to 50 per cent flowering, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, 100 seed weight and number of seeds per pod. The results obtained by Arya *et al*. (2017); Gopinath *et al*. (2018); Hadimani *et al*. (2019) and Chowdhury *et al*. (2020) were in close agreement with the results of the present findings.

The outcomes of present investigation revealed that, the traits *viz*., days to 50 per cent flowering, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, 100 seed weight, pod length and number of seeds per pod were correlated with seed yield per plant positively and significantly in turn indicating their major role in increasing seed yield per plant through improvement performed upon them. Consequently, yield can be upgraded utilizing these yield attributing traits for direct selection.

5.4 Path coefficient analysis

An efficient selection criterion for crop improvement requires a thorough knowledge of association among seed yield and its component characters and between themselves. To obtain meaningful interpretation of dependent and independent variables cause of association, separating correlation into direct and indirect effects of cause is necessary especially when a trait is affected by many other traits like yield (Wright., 1921).

To interpret the results of path analysis following points are taken as guidelines (Singh and Chaudhari, 1977).

1. If the correlation coefficient between a causal factor and the effect is almost equal to its direct effect, then correlation explains the true relationship and a direct selection through this trait will be effective.
2. If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects seem to be the cause of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection.
3. Correlation coefficient may be negative, but the direct effect is positive and high. Under these circumstances, a restricted simultaneous selection model is to be followed *i.e.,* restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect.
4. If correlation coefficient is negative and direct effect is also negative, then we must drop the selection based on that character.

Path coefficient analysis was developed by Wright (1921) and later elaborated by Dewey and Leu (1959). It is a form of standardized partial regression coefficient analysis which reflects the association among dependent and independent characters and measures the relative importance of each trait involved in contributing to the final product of correlation among dependent and independent characters arise due to direct effect of the characters. In the present study, path coefficient analysis was carried out by choosing pod yield per plant as dependent character.

The traits such as plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, 100 seed weight and number of seeds per pod exerted a positive direct effect on seed yield per plant. The traits days to 50 *per cent* flowering and pod length exerted negative direct effects. Selection would be rewarding if these traits were considered accordingly. Similar findings were obtained by the previous studies conducted by Shivade *et al*. (2011), Partap *et al*. (2019); Shanti *et al*. (2019) and Shridhar *et al*. (2020).

Plant height, number of pods per cluster and number of branches per plant exhibited low and positive direct effect on seed yield per plant and their contribution towards seed yield was through number of pods per plant indirectly.

Number of pods per plant and number of seeds per pod exerted the highest positive direct effects on seed yield per plant. The number of clusters per plant exerted the highest positive indirect effect through the number of clusters per plant on seed yield per plant, considering these traits while selecting the genotype for the breeding program would be rewarding. Hence, priority should be given to these traits while selecting genotypes for high yield in black gram.

5.5 Transgressive segregants identified for yield and yield attributing traits

In self pollinated crops, the success of selection depends on the extent to which breeders can fix transgressive segregation in the early generations. Appearance of individuals, in the progeny from a hybrid, which exceed either of the two parents of the hybrid with respect to one or more characters is known as transgressive segregation and the individual is called transgressive segregant. Transgressive segregation can be exploited for development of genotypes with positive characters from both the parents. These plants are produced by accumulation of favorable genes from both the parents as a consequence of segregation and recombination.

The studies on transgressive segregation in the segregating generation suggest that parents do not represent the extremes in terms of intensities of desired characters. If some genes for enhanced expression of a character are lacking in the genotype of the increasing parent but are present in donar parent, some individuals among the hybrid derivatives, emanating from the cross of these parents might receive a fortuitous gene combination showing a larger effect than produced by either of the parents (Gardner, 1968).

In brief, transgressive individuals with values exceeding the better parent were observed in F_3M_2 population for all the ten characters studied. This indicates that the parents possess different alleles and genes governing respective characters from which it could be inferred that there is a lot of scope of bringing the beneficial alleles into a single genotype through rigorous selection. Hence, from this study it is suggested that after evaluating the segregants for different characters along with yield, handling of selected segregants in later generations through selection could result in arriving desirable plant type along with high yield. The percentage of transgressive segregants for seed yield

Highest number of transgressive segregants identified for plant height and number of clusters per plant. The results suggested the existence of large count of transgressive segregants in early segregating generations for almost all the traits which provides a wide scope for the meticulous selection of these genotypes. Similar findings were obtained by the previous studies conducted by Shivakumar *et al.* (2013); Baliram (2014); Chouhan *et al.* (2018) and Guindon *et al.* (2019).

Several superior transgressive segregants were identified for seed yield per plant 42 (10.5 %). Progeny line 47 & progeny line 63 were shown highest seed yield per plant in F_3M_2 popultion. Progeny line 43 and progeny line 47 recorded highest number of pods per plant and was superior for yield. Similarly, progeny line 123 and progeny line159 recorded highest number of seeds per pod. Hence, these five progenies stand superior against others with respect to yield and its attributing traits and can be considered by the breeder for their utility in further breeding program.

Conclusion

- The evaluated F_3M_2 population recorded higher GCV, PCV, heritability and genetic advance as *per cent* of mean for majority of yield attributes indicating wide variation for these traits which are amenable for selection of elite genotypes.
- Number of clusters per plant and number of pods per plant had the maximum positive significant correlation and direct effect with total seed yield per plant.
- Progeny line 47 and progeny line 63 were found to be high yielding among the population.
- Superior transgressive segregants were identified for traits *viz*., number of clusters per plant. Which stands superior against other yield attributing traits.

Future line of work

- The present F_3M_2 material had wide genetic variability for most of the traits which can be exploited for selection program for yield improvement.
- The traits which have shown high heritability and more genetic advance could be further improved through simple selection procedures.
- Seed yield per plant had strong positive association with various yield attributing traits. Hence it is helpful to figure out the selection indices by considering more than one character at the time of selection to get the desired selection response.
- Progeny line 47 and progeny line 63 had high mean performance for seed yield per plant among the population. Therefore, selecting these progenies and promoting them to future generations will help in developing superior and high yielding genotypes.

SUMMARY

VI SUMMARY

The present investigation entitled "Assessment of genetic variability by combined hybridization and mutation in black gram [*Vigna mungo* (L.) Hepper.]" was carried out during *Rabi* 2020 at Zonal Agricultural and Horticultural Research Station (ZAHRS), Navile, Shivamogga, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga, Karnataka, India. The experimental material consisted of 400 F_3M_2 progeny lines along with four checks (PU31, Rashmi, DBGV5 and DU1).

The experiment was laid out in an augmented experimental design with ten blocks, each block with 40 lines and a total of 400 progeny lines. The genotypes were unreplicated, while checks were replicated twice in all the blocks, for the selection parameters such as variability, heritability, genetic advance and association studies for yield and yield attributing traits and to identify the transgressive segregants for yield and its attributing traits in black gram.

The objectives of the investigation were to study the variability, heritability, genetic advance as *per cent* of mean, character association for different yield related traits along with their direct and indirect effects on seed yield per plant and identification of transgressive segregants for yield and yield attributing traits *viz.*, days to 50 *per cent* flowering, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, 100 seed weight, number of seeds per pod and total seed yield per plant.

It is apparent from the analysis of variance that the genotypes varied significantly for several traits examined. The F_3M_2 population had an ample amount of variability for nearly all of the studied attributes.

Results of genetic variability studies revealed higher GCV and PCV for the trait seed yield per plant. Moderate level of GCV and PCV was found for number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and traits like days to 50 *per cent* flowering, plant height, pod length, 100 seed weight exhibited low GCV and PCV. High heritability along with high genetic advance as *per cent* of mean was recorded for number of pods per plant and seed yield per plant.

By taking into consideration of the above mentioned selection parameters, it is evident that the traits like the number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod has the highest values of PCV, GCV, broad-sense heritability and genetic advance. Selecting certain attributes is extremely suggested to achieve enhanced production.

Association studies displayed that, traits such as days to 50 *per cent* flowering, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, 100 seed weight and number of seeds per pod were positively and significantly correlated with seed yield per plant. Number of clusters per plant had the maximum positive significant correlation with seed yield per plant.

Results obtained through path coefficient analysis showed highest positive direct effect of number of pods per plant and number of seeds per pod exerted the highest positive direct effects on seed yield per plant. Among the remaining traits studied, plant height, number of branches per plant, number of clusters per plant and number of pods per cluster exhibited low and positive direct effect on seed yield per plant and their contribution towards seed yield was through number of pods per plant indirectly.

Therefore, there is incredible opportunity to find good potential genotypes from the existing population set for the successful breeding program. Based on mean performance, progeny line 47 and progeny line 63 documented maximum seed yield. Progeny line 161 showed early flowering and possibly earlier development, reflecting the capabilities of this progeny variant to be used for the evolution of early maturing cultivars.

Highest number of transgressive segregants identified for plant height and number of clusters per plant. The results suggested the existence of large amount of transgressive segregants in early segregating generations for almost all the traits which provides a wide scope for the meticulous selection of these genotypes.

Progeny line 43 and progeny line 47 recorded highest number of pods per plant and was superior for yield. Similarly, progeny line 123 and progeny line 159 recorded highest number of seeds per pod. Hence, these five progenies stand superior against others with respect to yield and its attributing traits and can be considered by the breeder for their utility in further breeding program.

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VII REFERENCES

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VIII APPENDIX

Performance of F_3M_2 population of cross (PU31 × Rashmi) for quantitative traits

Progeny line no.	DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
1	42.00	30.60	3.40	14.20	3.90	48.00	4.70	5.20	4.35	10.10
2	41.00	31.00	3.00	15.20	3.50	42.00	4.20	4.70	3.90	9.68
3	40.00	30.33	2.90	12.00	3.60	38.00	4.80	4.20	4.26	9.10
4	42.00	31.00	3.20	14.50	3.70	41.00	5.10	5.80	4.76	10.29
5	43.00	32.33	2.41	15.00	4.10	45.00	4.70	5.10	5.10	10.80
6	39.00	28.90	4.10	12.60	3.19	38.00	3.80	4.20	4.65	7.50
7	42.00	28.67	3.20	14.30	3.45	37.00	4.30	4.30	4.36	7.31
8	43.00	35.00	2.90	15.80	3.80	54.00	4.70	4.70	4.85	10.01
9	42.00	29.67	3.40	13.00	3.40	41.80	4.60	5.10	4.71	9.80
10	44.00	30.67	3.60	16.70	4.70	52.00	4.90	4.80	4.96	11.00
11	39.00	30.60	2.60	13.80	3.60	41.00	4.30	5.20	3.95	7.30
12	42.00	31.00	3.67	15.26	4.25	51.00	4.80	5.30	4.96	11.02
13	40.00	30.15	3.50	13.40	3.80	46.00	4.20	4.70	4.28	9.85
14	39.00	30.00	3.67	12.90	3.60	42.00	4.60	4.90	4.20	9.20
15	42.00	32.00	4.00	15.00	3.95	54.00	4.70	5.20	4.60	11.30
16	41.00	30.60	3.90	16.00	3.56	44.00	4.70	4.70	4.20	9.20
17	39.00	28.50	2.90	12.60	3.20	35.00	4.15	4.30	4.10	7.10
18	41.00	30.67	3.50	16.00	3.60	48.00	5.10	5.10	4.40	10.40
19	39.00	29.67	3.10	14.90	3.40	47.00	4.10	4.60	4.30	9.30
20	43.00	32.33	4.10	16.12	4.12	52.00	5.30	5.90	4.50	11.00
21	43.00	31.60	2.42	15.00	3.90	45.00	4.70	5.10	5.10	10.80
22	40.00	29.30	4.10	12.00	3.45	39.00	3.80	4.20	4.65	7.50

APPENDICES

Progeny line no.	DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
23	39.00	28.67	3.20	11.75	3.19	37.00	4.30	4.30	4.36	7.31
24	43.00	31.50	2.90	14.04	3.70	42.00	4.70	4.70	4.85	10.01
25	42.00	29.67	3.40	13.70	3.40	41.80	4.60	5.10	4.71	9.80
26	44.00	32.00	3.60	16.70	4.20	52.00	4.90	4.80	4.96	11.00
27	41.00	30.00	3.20	13.90	3.60	49.00	4.20	4.20	4.36	9.50
28	43.00	33.00	3.00	16.00	4.70	51.00	4.50	5.90	5.12	12.06
29	45.00	35.00	3.80	16.50	4.60	55.00	4.40	5.90	5.20	13.20
30	38.00	29.00	3.20	13.40	3.50	35.00	4.20	4.90	4.16	7.00
31	42.00	32.00	4.00	17.40	3.80	54.00	4.70	5.20	4.60	11.30
32	42.00	31.00	3.90	13.00	3.70	47.00	4.70	4.70	4.20	9.20
33	40.00	27.00	2.90	12.60	3.19	35.00	4.15	4.30	4.10	7.10
34	43.00	30.67	3.50	16.00	3.80	48.00	5.10	5.10	4.40	10.40
35	42.00	29.67	3.10	13.20	3.40	47.00	4.10	4.60	4.30	9.30
36	43.00	32.33	4.10	16.12	3.90	49.00	5.30	5.90	4.50	11.00
37	42.00	30.00	3.40	14.00	3.80	48.00	4.70	5.20	4.35	10.10
38	41.00	29.00	3.00	12.25	3.50	45.00	4.20	4.70	3.90	9.68
39	39.00	28.60	2.80	11.00	3.40	41.00	4.60	4.16	4.30	9.16
40	42.00	30.15	3.20	14.50	3.86	46.00	5.10	5.80	4.76	10.29
41	41.00	35.40	3.20	12.50	3.24	37.30	4.40	4.80	4.20	7.80
42	44.00	35.00	3.20	18.00	3.80	51.90	5.10	6.20	4.20	13.40
43	42.00	33.00	3.00	19.00	3.30	58.00	4.10	5.50	4.90	13.80
44	39.00	28.00	3.10	15.40	3.35	48.00	4.53	4.20	5.10	10.00
45	41.00	31.33	3.40	16.60	3.90	49.00	4.90	5.70	4.43	12.34
46	47.00	30.62	3.30	18.25	4.00	54.00	4.40	5.70	5.00	14.40
47	45.00	25.00	4.00	17.26	4.30	58.00	4.50	5.90	5.20	16.40

Progeny line no.	DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
48	40.00	37.00	3.70	16.60	3.46	44.00	4.86	5.70	4.50	12.40
49	42.00	26.00	3.50	18.20	3.80	49.00	4.90	5.74	5.20	14.50
50	41.00	35.60	2.46	14.80	4.00	46.00	4.60	5.60	4.87	13.50
51	41.00	32.00	3.10	14.60	4.30	32.00	4.20	4.80	4.30	7.20
52	44.00	35.90	3.46	18.40	3.72	50.30	5.00	5.80	4.90	13.60
53	42.00	32.00	3.40	15.20	3.90	41.00	4.47	4.90	4.36	8.40
54	43.00	25.00	2.60	14.80	3.85	48.60	4.50	4.20	4.23	8.20
55	44.00	30.00	3.90	14.60	3.60	43.00	5.20	5.97	4.90	13.68
56	45.00	31.67	2.90	15.10	4.10	49.60	4.30	4.80	4.20	9.60
57	41.00	33.33	3.70	16.50	3.80	52.50	4.63	6.10	4.80	13.60
58	44.00	28.00	2.90	12.40	3.86	39.50	4.10	4.20	3.90	6.26
59	42.00	35.00	2.80	15.25	3.40	48.00	4.90	5.80	5.10	11.80
60	45.00	30.00	3.80	14.60	3.10	39.00	4.96	5.65	4.98	11.16
61	41.00	31.33	3.40	16.60	3.90	49.00	4.90	5.70	4.43	12.34
62	47.00	30.65	3.30	18.30	4.20	53.00	4.20	5.40	4.90	13.80
63	44.00	25.00	4.00	17.24	4.25	57.00	4.40	5.70	5.10	16.40
64	40.00	37.00	3.40	16.50	3.30	47.00	4.86	5.70	4.46	11.96
65	42.00	26.00	3.50	18.20	3.80	49.00	4.90	5.74	5.20	14.50
66	40.00	36.00	2.50	15.00	4.10	49.00	4.80	5.80	4.87	13.60
67	42.00	29.53	2.70	14.20	3.20	44.00	4.20	5.70	2.98	7.20
68	43.00	26.27	2.90	16.00	2.90	39.00	4.53	5.85	4.65	10.40
69	43.00	35.00	3.80	16.20	2.80	47.00	4.80	5.90	4.63	12.40
70	44.00	29.23	3.90	18.10	4.10	52.00	4.60	5.95	4.80	13.40
71	44.00	30.00	3.90	14.60	3.60	43.00	5.20	5.97	4.90	13.68
72	43.00	31.67	2.90	15.10	4.10	49.60	4.30	4.80	4.20	9.60

Progeny line no.	DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
73	41.00	33.33	3.70	16.50	3.80	52.50	4.63	6.10	4.80	13.60
74	44.00	28.00	2.90	12.40	3.86	39.50	4.10	4.20	3.90	6.26
75	42.00	35.00	2.80	15.25	3.40	48.00	4.90	5.80	5.10	11.80
76	45.00	30.00	3.80	14.60	3.10	39.00	4.96	5.65	4.98	11.16
77	41.00	36.00	3.10	12.00	3.26	37.40	4.50	4.90	4.30	7.50
78	44.00	35.00	3.20	18.00	3.80	51.90	5.10	6.20	4.20	13.40
79	42.00	33.00	3.00	19.00	3.45	57.00	4.40	5.60	5.00	14.00
80	39.00	28.00	3.10	15.40	3.35	48.00	4.53	4.20	5.10	10.00
81	43.00	29.73	3.10	16.20	4.30	52.00	4.80	5.40	4.60	11.40
82	42.00	30.87	3.50	14.00	4.40	45.00	4.76	5.60	4.20	11.20
83	43.00	30.00	3.40	18.40	3.85	47.00	5.40	5.70	5.10	13.80
84	42.00	32.00	3.45	15.60	3.10	46.00	4.60	5.20	4.16	9.20
85	41.00	33.00	3.16	17.00	3.80	51.00	4.80	6.10	4.69	12.10
86	39.00	34.00	3.30	15.70	3.90	52.00	4.76	4.90	4.67	10.80
87	41.00	32.00	3.90	16.00	4.30	50.60	4.80	4.20	4.26	10.00
88	43.00	30.20	2.90	18.20	4.00	51.90	5.30	5.80	5.10	13.50
89	42.00	33.00	3.80	14.00	3.19	41.80	5.14	4.80	4.50	9.00
90	44.00	31.00	3.49	17.60	3.90	53.10	4.80	5.70	4.80	12.30
91	45.00	32.00	3.36	16.80	3.90	46.00	4.80	5.35	4.39	10.60
92	42.00	30.63	3.60	17.20	3.80	50.20	5.16	5.70	5.20	12.06
93	44.00	29.83	3.40	14.80	3.60	42.00	4.26	4.20	4.53	7.80
94	42.00	32.60	3.70	17.96	3.50	45.60	5.00	5.98	4.95	13.20
95	42.00	33.67	3.46	16.40	3.70	51.00	4.30	5.74	4.69	12.80
96	44.00	30.97	3.60	18.00	3.80	54.33	5.30	5.95	4.90	13.00
97	43.00	31.07	3.00	16.30	4.30	57.00	5.20	5.80	4.80	12.40

Progeny line no.	DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
98	40.00	28.40	4.12	16.30	3.12	40.00	5.20	5.10	4.80	10.40
99	41.00	32.00	3.46	14.67	3.90	53.00	4.20	4.20	3.26	7.00
100	43.00	31.00	3.60	18.10	4.10	50.00	5.20	5.64	5.14	13.00
101	41.00	33.00	3.16	17.00	3.80	51.00	4.80	6.10	4.69	12.10
102	39.00	34.00	3.30	15.70	3.90	52.00	4.76	4.90	4.67	10.80
103	41.00	32.00	3.90	16.00	4.30	50.60	4.80	4.20	4.26	10.00
104	43.00	30.20	2.90	18.20	4.00	51.90	5.30	5.80	5.10	13.50
105	42.00	33.00	3.80	14.00	3.19	41.80	5.14	4.80	4.50	9.00
106	44.00	31.00	3.49	17.60	3.90	53.10	4.80	5.70	4.80	12.30
107	42.00	24.00	3.00	17.40	3.62	46.00	4.80	5.68	4.90	11.80
108	45.00	34.00	3.50	16.80	3.80	54.90	5.26	5.26	5.20	12.80
109	43.00	31.03	3.40	17.64	3.90	46.00	4.40	5.67	4.90	12.40
110	41.00	29.67	3.20	14.00	3.16	32.00	4.80	5.60	4.65	8.00
111	42.00	33.67	3.46	16.40	3.70	51.00	4.30	5.74	4.69	12.80
112	44.00	30.97	3.60	18.00	3.80	54.33	5.30	5.95	4.90	13.00
113	43.00	31.07	3.00	16.30	4.30	57.00	5.20	5.80	4.80	12.40
114	41.00	29.20	4.12	16.30	3.14	43.00	5.30	5.40	4.76	10.80
115	41.00	32.00	3.46	14.67	3.90	53.00	4.20	4.20	3.26	7.00
116	43.00	31.00	3.60	18.10	4.10	50.00	5.20	5.64	5.20	13.00
117	43.00	29.73	3.10	16.20	4.30	52.00	4.80	5.40	4.60	11.40
118	42.00	30.87	3.50	14.00	4.40	45.00	4.76	5.60	4.20	11.20
119	43.00	30.00	3.40	18.40	3.85	47.00	5.40	5.70	5.10	13.80
120	42.00	32.00	3.45	15.60	3.10	46.00	4.60	5.20	4.16	9.20
121	40.00	32.00	3.10	15.00	3.40	41.00	4.90	5.40	5.10	9.80
122	42.00	29.63	3.40	14.26	3.76	39.10	4.80	4.90	4.57	8.60

Progeny line no.	DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
123	39.00	35.00	4.00	18.30	3.67	43.00	5.80	7.00	5.14	14.20
124	42.00	25.00	3.10	14.00	3.10	42.80	4.50	4.20	4.63	8.20
125	45.00	30.10	3.50	16.00	3.60	45.00	5.20	5.80	4.56	10.10
126	42.00	26.00	2.90	12.01	3.20	37.60	4.60	4.20	4.40	5.40
127	43.00	29.00	3.60	16.40	3.68	38.00	5.24	6.10	4.63	10.60
128	42.00	31.00	3.50	16.80	3.16	39.33	5.10	5.90	4.68	10.70
129	44.00	30.60	3.30	16.40	4.10	42.00	5.06	5.80	4.40	10.20
130	42.00	24.70	2.96	12.20	3.48	32.00	4.60	4.20	3.80	5.20
131	42.00	28.00	3.10	16.00	3.85	40.30	4.30	5.95	4.20	10.02
132	38.00	29.00	3.70	16.30	3.80	40.30	5.40	6.10	4.30	10.50
133	43.00	34.00	3.40	15.60	4.15	43.60	5.10	5.75	3.90	9.60
134	42.00	29.00	3.10	15.70	3.10	46.00	4.80	6.00	4.10	9.70
135	43.00	28.00	3.00	17.60	3.70	47.00	5.30	5.60	5.15	12.30
136	42.00	31.33	2.50	16.80	4.20	46.00	5.10	6.00	5.10	11.20
137	45.00	29.00	3.70	18.10	3.80	47.00	5.40	6.20	5.20	13.10
138	38.00	35.00	3.60	16.60	4.10	45.00	4.90	5.70	4.50	11.30
139	41.00	28.00	3.40	15.40	4.20	44.00	4.70	5.40	4.30	8.40
140	40.00	31.10	4.10	16.84	3.50	42.42	5.12	5.70	4.76	11.30
141	45.00	30.10	3.50	16.00	3.60	45.00	5.20	5.80	4.56	10.10
142	42.00	26.00	2.90	12.01	3.20	37.60	4.60	4.20	4.40	5.40
143	43.00	29.00	3.60	16.40	3.68	38.00	5.24	6.10	4.63	10.60
144	42.00	31.00	3.50	16.80	3.16	39.33	5.10	5.90	4.68	10.70
145	44.00	30.60	3.30	16.40	4.10	42.00	5.06	5.80	4.40	10.20
146	42.00	24.80	2.96	12.20	3.48	32.00	4.60	4.20	3.80	5.20
147	41.00	30.00	3.40	16.40	3.10	41.67	6.00	5.70	4.60	10.50

Progeny line no.	DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
148	42.00	28.00	3.20	14.60	3.39	34.00	5.60	5.70	4.45	8.40
149	45.00	34.67	3.30	14.00	4.15	39.80	5.80	6.00	4.57	10.60
150	44.00	35.00	3.10	15.00	3.90	42.00	4.50	5.80	4.60	9.60
151	43.00	28.00	3.00	17.60	3.70	47.00	5.30	5.60	5.20	12.30
152	42.00	31.33	2.50	16.80	4.20	46.00	5.10	6.00	5.10	11.20
153	45.00	29.00	3.70	18.10	3.80	47.00	5.40	6.20	5.30	13.10
154	38.00	35.00	3.60	16.60	4.10	45.00	4.90	5.70	4.50	11.30
155	41.00	28.00	3.40	15.40	4.20	44.00	4.70	5.40	4.30	8.40
156	43.00	31.20	4.10	16.96	3.80	42.33	5.16	5.80	4.83	11.40
157	40.00	32.00	3.10	15.00	3.40	41.00	4.90	5.40	5.10	9.80
158	42.00	29.63	3.40	14.26	3.76	39.10	4.80	4.90	4.57	8.60
159	39.00	35.00	4.00	18.00	3.67	43.00	5.80	7.00	5.20	14.20
160	42.00	25.00	3.10	14.00	3.10	42.80	4.50	4.20	4.63	8.20
161	37.00	30.00	3.20	15.60	3.25	33.00	5.70	5.96	4.84	9.70
162	42.00	27.00	3.80	17.40	3.50	48.00	5.40	5.93	5.14	12.05
163	42.00	29.00	3.60	17.60	3.10	41.68	5.90	5.80	4.95	11.00
164	45.00	33.00	3.25	16.60	4.36	45.00	5.60	6.15	5.10	10.30
165	42.00	27.00	3.35	15.80	3.45	46.00	5.00	4.20	4.60	9.50
166	44.00	32.00	3.25	15.46	3.80	40.00	4.30	5.23	4.50	9.40
167	41.00	32.00	3.30	15.50	3.59	39.00	4.70	5.75	4.25	9.40
168	43.00	35.00	3.40	15.67	3.25	44.60	4.80	5.70	4.67	10.26
169	42.00	29.00	2.90	14.86	4.30	32.00	4.96	6.15	4.20	8.00
170	41.00	36.00	3.15	17.40	4.23	52.00	4.30	5.20	4.45	8.60
171	43.00	30.00	3.10	15.60	4.20	45.00	5.20	5.80	4.60	9.20
172	45.00	27.00	3.34	17.00	3.20	40.30	4.80	6.16	5.00	10.10

Progeny line no.	DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
173	42.00	25.00	3.40	15.50	3.35	39.00	4.50	5.80	4.59	9.40
174	42.00	35.00	3.20	12.00	3.45	34.00	4.57	6.24	4.50	9.30
175	42.00	27.00	2.80	15.80	3.80	40.67	5.00	6.00	4.23	9.20
176	44.00	32.17	3.90	16.60	3.50	43.33	5.20	5.89	4.43	11.00
177	41.00	33.33	2.89	15.86	4.00	44.00	5.60	6.00	4.10	9.00
178	42.00	35.67	3.00	15.95	3.60	44.00	5.85	4.20	4.80	9.20
179	43.00	32.00	3.20	16.00	3.50	41.00	4.40	5.78	4.65	9.70
180	42.00	29.00	2.40	13.60	3.16	37.00	5.20	4.30	4.50	7.60
181	42.00	27.00	3.35	15.80	3.45	46.00	5.00	4.20	4.60	9.50
182	44.00	32.00	3.25	15.46	3.80	40.00	4.30	5.23	4.50	9.40
183	41.00	32.00	3.30	15.50	3.59	39.00	4.70	5.75	4.25	9.40
184	43.00	35.00	3.40	15.67	3.25	44.60	4.80	5.70	4.67	10.26
185	42.00	29.00	2.90	14.86	4.30	31.00	4.96	6.15	4.20	8.00
186	41.00	36.00	3.15	17.40	4.23	52.00	4.30	5.20	4.45	8.60
187	43.00	31.60	3.40	12.40	3.50	48.00	5.30	6.15	4.60	9.80
188	41.00	32.17	3.50	16.10	3.75	42.00	5.15	5.90	4.70	10.10
189	42.00	33.33	3.20	15.80	3.15	42.00	5.40	5.20	4.31	9.70
190	41.00	35.67	3.60	17.00	3.40	42.00	5.10	6.15	4.96	11.10
191	42.00	27.00	2.80	15.80	3.80	40.67	5.00	6.00	4.23	9.20
192	44.00	32.17	3.90	16.60	3.50	43.33	5.20	5.89	4.43	11.00
193	41.00	33.33	2.89	15.86	4.00	44.00	5.60	6.00	4.10	9.00
194	42.00	35.67	3.00	15.95	3.60	44.00	5.85	4.20	4.80	9.20
195	43.00	32.00	3.20	16.00	3.50	41.00	4.40	5.78	4.65	9.70
196	42.00	29.00	2.45	14.60	3.20	38.00	5.40	4.20	4.70	7.40
197	38.00	31.00	3.10	15.98	3.15	35.00	5.85	6.00	4.86	9.80

Progeny line no.	DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
198	42.00	27.00	3.80	17.40	3.50	48.00	5.40	5.93	5.13	12.05
199	42.00	29.00	3.60	17.60	3.10	41.68	5.90	5.80	4.95	11.00
200	45.00	33.00	3.25	16.60	4.36	45.00	5.60	6.15	5.10	10.30
201	42.00	32.00	4.00	17.40	3.80	54.00	4.70	5.20	4.60	11.30
202	41.00	31.00	3.90	16.00	3.19	48.00	4.70	4.70	4.20	9.20
203	43.00	27.00	2.90	12.60	3.70	35.00	4.15	4.30	4.10	7.10
204	38.00	30.67	3.50	16.00	3.19	48.00	5.10	5.10	4.40	10.40
205	42.00	29.67	3.10	14.90	4.10	47.00	4.10	4.60	4.30	9.30
206	43.00	32.33	4.10	16.12	3.20	49.00	5.30	5.90	4.50	11.00
207	42.00	30.00	3.40	14.20	3.90	48.00	4.70	5.20	4.35	10.10
208	40.00	29.00	3.00	12.25	3.50	32.00	4.20	4.70	3.90	9.68
209	41.00	28.70	2.90	15.40	3.96	52.00	4.80	4.20	4.26	9.10
210	38.00	30.15	3.20	14.50	3.70	35.00	5.10	5.80	4.76	10.29
211	40.00	31.60	2.43	16.20	3.20	45.00	4.70	5.10	5.10	10.80
212	41.00	29.30	4.10	13.60	3.19	42.30	3.90	4.20	4.65	7.50
213	42.00	28.67	3.20	14.30	3.45	37.00	4.30	4.30	4.36	7.31
214	43.00	31.50	2.90	15.80	3.80	54.00	4.70	4.70	4.85	10.01
215	42.00	29.67	3.40	13.00	3.40	41.80	4.60	5.10	4.71	9.80
216	44.00	32.00	3.60	16.70	4.20	52.00	4.90	4.80	4.96	11.00
217	41.00	30.00	3.20	14.96	3.60	55.00	4.20	4.20	4.36	9.50
218	40.00	33.00	3.00	11.40	4.70	49.00	4.50	5.90	5.12	12.06
219	45.00	35.00	3.80	15.60	3.50	51.00	4.40	5.90	5.15	13.20
220	41.00	29.00	3.20	13.40	4.10	35.00	4.20	4.90	4.16	7.00
221	39.00	30.60	2.60	14.68	3.30	49.56	4.30	5.20	3.95	7.30
222	40.00	31.00	3.67	15.26	3.20	46.00	4.80	5.30	4.96	11.02

Progeny line no.	DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
223	42.00	30.15	3.50	14.80	3.80	51.00	4.20	4.70	4.28	9.85
224	44.00	30.00	3.67	14.46	3.60	54.00	4.60	4.90	4.20	9.20
225	42.00	32.00	4.00	17.40	3.80	54.00	4.70	5.20	4.60	11.30
226	41.00	30.60	3.90	16.00	3.19	48.00	4.70	4.70	4.20	9.20
227	43.00	28.50	2.90	12.60	3.70	35.00	4.15	4.30	4.10	7.10
228	38.00	30.67	3.50	16.00	3.19	48.00	5.10	5.10	4.40	10.40
229	42.00	29.67	3.10	14.90	4.10	47.00	4.10	4.60	4.30	9.30
230	43.00	32.33	4.10	16.12	3.20	49.00	5.30	5.90	4.50	11.00
231	42.00	30.60	3.40	14.20	3.90	48.00	4.70	5.20	4.35	10.10
232	40.00	31.00	3.00	12.25	3.50	32.00	4.20	4.70	3.90	9.68
233	41.00	30.33	2.90	15.40	3.96	52.00	4.80	4.20	4.26	9.10
234	38.00	31.00	3.20	14.50	3.70	35.00	5.10	5.80	4.76	10.29
235	40.00	32.33	2.42	16.20	3.20	45.00	4.70	5.10	5.10	10.80
236	41.00	28.90	4.10	13.60	3.19	42.30	3.90	4.20	4.65	7.50
237	42.00	28.67	3.20	14.30	3.45	37.00	4.30	4.30	4.36	7.31
238	43.00	35.00	2.90	15.80	3.80	54.00	4.70	4.70	4.85	10.01
239	42.00	29.67	3.40	13.00	3.40	41.80	4.60	5.10	4.71	9.80
240	44.00	30.67	3.60	16.70	4.20	52.00	4.90	4.80	4.96	11.00
241	44.00	30.00	3.90	14.60	3.60	43.00	5.20	5.97	4.90	13.68
242	44.00	31.67	2.90	15.10	4.10	49.60	4.30	4.80	4.20	9.60
243	41.00	33.33	3.70	16.50	3.80	52.50	4.63	6.10	4.80	13.60
244	44.00	28.00	2.90	12.40	3.86	39.50	4.10	4.20	3.90	6.26
245	42.00	35.00	2.80	15.25	3.40	48.00	4.90	5.80	5.10	11.80
246	45.00	30.00	3.80	14.60	3.10	39.00	4.96	5.65	4.98	11.16
247	41.00	36.00	3.10	12.00	3.26	37.40	4.50	4.90	4.30	7.50

Progeny line no.	DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
248	44.00	35.00	3.20	18.00	3.80	51.90	5.10	6.20	4.20	13.40
249	42.00	33.00	3.00	15.40	3.45	57.00	4.40	5.60	5.00	14.00
250	39.00	28.00	3.10	19.00	3.20	45.00	4.40	4.30	5.00	10.60
251	41.00	31.33	3.40	16.60	3.90	49.00	4.90	5.70	4.43	12.34
252	47.00	30.67	3.40	18.20	4.10	55.00	4.43	5.80	5.10	14.00
253	45.00	25.00	4.00	17.26	4.30	57.00	4.50	5.90	5.20	16.30
254	40.00	36.00	3.80	16.80	3.45	48.00	4.98	5.68	4.43	12.00
255	42.00	26.00	3.50	18.20	3.80	49.00	4.90	5.74	5.20	14.50
256	41.00	36.00	2.50	15.00	4.10	49.00	4.80	5.80	4.87	13.60
257	42.00	29.53	2.70	14.20	3.20	44.00	4.20	5.70	2.98	7.20
258	43.00	26.27	2.90	16.00	2.90	39.00	4.53	5.85	4.65	10.40
259	43.00	35.00	3.80	16.20	4.10	47.00	4.80	5.90	4.63	12.40
260	44.00	29.23	3.90	18.10	2.80	52.00	4.60	5.95	4.80	13.40
261	41.00	32.00	3.10	14.60	4.30	31.00	4.20	4.80	4.30	7.20
262	44.00	36.00	3.50	18.30	3.69	51.30	5.10	6.00	5.12	13.90
263	42.00	32.00	3.40	15.20	3.90	41.00	4.47	4.90	4.36	8.40
264	43.00	24.00	2.56	14.86	3.85	48.60	4.50	4.24	4.23	8.30
265	44.00	30.00	3.90	14.60	3.60	43.00	5.20	5.97	4.90	13.68
266	45.00	31.67	2.90	15.10	4.10	49.60	4.30	4.80	4.20	9.60
267	41.00	33.33	3.70	16.50	3.80	52.50	4.63	6.10	4.80	13.60
268	44.00	28.00	2.90	12.40	3.86	39.50	4.10	4.20	3.90	6.26
269	42.00	35.00	2.80	15.25	3.40	48.00	4.90	5.80	5.10	11.80
270	45.00	30.00	3.80	14.60	3.10	39.00	4.96	5.65	4.98	11.16
271	41.00	36.00	3.10	12.00	3.26	37.40	4.50	4.90	4.30	7.50
272	45.00	35.00	3.20	18.00	3.80	51.90	5.10	6.20	4.20	13.40

Progeny line no.	DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
273	42.00	33.00	3.00	16.60	3.45	57.00	4.40	5.60	5.00	14.00
274	39.00	28.00	3.10	15.40	3.35	48.00	4.53	4.20	5.10	10.00
275	41.00	31.33	3.40	16.60	3.90	49.00	4.90	5.70	4.43	12.34
276	44.00	30.50	3.20	19.00	4.20	53.00	4.20	5.60	4.86	13.90
277	45.00	25.00	4.00	17.26	4.30	57.00	4.50	5.90	5.15	16.30
278	40.00	36.00	3.80	16.80	3.45	48.00	4.98	5.68	4.43	12.00
279	42.00	26.00	3.50	18.20	3.80	49.00	4.90	5.74	5.15	14.50
280	40.00	36.00	2.50	15.00	4.10	49.00	4.80	5.80	4.87	13.60
281	42.00	33.67	3.46	16.40	3.70	51.00	4.30	5.74	4.69	12.80
282	44.00	30.97	3.60	18.00	3.80	54.33	5.30	5.95	4.90	13.00
283	42.00	29.33	4.12	16.40	3.16	42.00	5.60	5.20	4.95	10.50
284	43.00	31.07	3.00	16.30	4.30	57.00	5.20	5.80	4.80	12.40
285	41.00	32.00	3.46	14.67	3.90	53.00	4.20	4.10	3.26	7.00
286	43.00	31.00	3.60	18.10	4.10	50.00	5.20	5.64	5.20	13.00
287	43.00	29.73	3.10	16.20	4.30	52.00	4.80	5.40	4.60	11.40
288	42.00	30.87	3.50	14.00	4.40	45.00	4.76	5.60	4.20	11.20
289	43.00	30.00	3.40	18.40	3.85	47.00	5.40	5.70	5.10	13.80
290	42.00	32.00	3.45	15.60	3.10	46.00	4.60	5.20	4.16	9.20
291	41.00	33.00	3.16	17.00	3.80	51.00	4.80	6.10	4.69	12.10
292	39.00	34.00	3.30	15.70	3.90	52.00	4.76	4.90	4.67	10.80
293	41.00	32.00	3.90	16.00	4.30	50.60	4.80	4.10	4.26	10.00
294	43.00	30.20	2.90	18.20	4.00	51.90	5.30	5.80	5.10	13.50
295	42.00	33.00	3.80	14.00	3.19	41.80	5.14	4.80	4.50	9.00
296	44.00	31.00	3.49	17.60	3.90	53.10	4.80	5.70	4.80	12.30
297	42.00	24.20	3.10	17.60	3.68	48.00	5.00	5.67	4.80	12.00

Progeny line no.	DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
298	45.00	34.00	3.50	16.80	3.80	54.90	5.26	5.26	5.20	12.80
299	43.00	31.03	3.40	17.64	3.90	46.00	4.40	5.67	4.90	12.40
300	41.00	29.67	3.20	14.00	3.16	32.00	4.80	5.60	4.65	8.00
301	45.00	32.00	3.36	16.80	3.90	46.00	4.80	5.35	4.39	10.60
302	42.00	30.63	3.60	17.20	3.80	50.20	5.16	5.70	5.20	12.06
303	44.00	29.83	3.40	14.80	3.60	42.00	4.26	4.20	4.53	7.80
304	42.00	32.60	3.70	17.96	3.50	45.60	5.00	5.98	4.95	13.20
305	42.00	33.67	3.46	16.40	3.70	51.00	4.30	5.74	4.69	12.80
306	44.00	30.97	3.60	18.00	3.80	54.33	5.30	5.95	4.90	13.00
307	43.00	31.07	3.00	16.30	4.30	57.00	5.20	5.80	4.80	12.40
308	42.00	29.33	4.00	16.40	3.16	42.00	5.60	5.20	4.95	10.50
309	41.00	32.00	3.46	14.67	3.90	53.00	4.20	4.20	3.26	7.00
310	43.00	31.00	3.60	18.10	4.10	50.00	5.20	5.64	5.14	13.00
311	43.00	29.73	3.10	16.20	4.30	52.00	4.80	5.40	4.60	11.40
312	42.00	30.87	3.50	14.00	4.40	45.00	4.76	5.60	4.20	11.20
313	43.00	30.00	3.40	18.40	3.85	47.00	5.40	5.70	5.10	13.80
314	42.00	32.00	3.45	15.60	3.10	46.00	4.60	5.20	4.16	9.20
315	41.00	33.00	3.16	17.00	3.80	51.00	4.80	6.10	4.69	12.10
316	39.00	34.00	3.30	15.70	3.90	52.00	4.76	4.90	4.67	10.80
317	41.00	32.00	3.90	16.00	4.30	50.60	4.80	4.20	4.26	10.00
318	43.00	30.20	2.90	18.20	4.00	51.90	5.30	5.80	5.10	13.50
319	42.00	33.00	3.80	14.00	3.19	41.80	5.14	4.80	4.50	9.00
320	44.00	31.00	3.49	17.60	3.90	53.10	4.80	5.70	4.80	12.30
321	43.00	28.00	3.00	17.60	3.70	47.00	5.30	5.60	5.14	12.30
322	42.00	31.33	2.50	16.80	4.20	46.00	5.10	6.00	5.10	11.20

Progeny line no.	DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
323	45.00	29.00	3.70	18.10	3.80	47.00	5.40	6.20	5.13	13.10
324	38.00	35.00	3.60	16.60	4.10	45.00	4.90	5.70	4.50	11.30
325	41.00	28.00	3.40	15.40	4.20	44.00	4.70	5.40	4.30	8.40
326	43.00	31.20	4.10	16.96	3.80	42.33	5.16	5.80	4.83	11.40
327	40.00	32.00	3.10	15.00	3.40	41.00	4.90	5.40	5.10	9.80
328	42.00	29.63	3.40	14.26	3.76	39.10	4.80	4.90	4.57	8.60
329	39.00	35.00	4.00	18.60	3.58	41.00	5.90	6.30	5.10	14.50
330	42.00	25.00	3.10	14.00	3.10	42.80	4.50	4.20	4.63	8.20
331	45.00	30.10	3.50	16.00	3.60	45.00	5.20	5.80	4.56	10.10
332	42.00	26.00	2.90	12.01	3.20	37.60	4.60	4.20	4.40	5.40
333	43.00	29.00	3.60	16.40	3.68	38.00	5.24	6.10	4.63	10.60
334	42.00	31.00	3.50	16.80	3.16	39.33	5.10	5.90	4.68	10.70
335	44.00	30.60	3.30	16.40	4.10	42.00	5.06	5.80	4.40	10.20
336	42.00	24.50	2.96	12.20	3.48	32.00	4.60	4.20	3.80	5.30
337	41.00	30.00	3.40	16.40	3.10	41.67	5.80	5.70	4.60	10.50
338	42.00	28.00	3.20	14.60	3.39	34.00	5.60	5.70	4.45	8.40
339	45.00	34.67	3.30	14.00	4.15	39.80	5.80	6.00	4.57	10.60
340	44.00	35.00	3.10	15.00	3.90	42.00	4.50	5.80	4.60	9.60
341	42.00	28.00	3.10	16.00	3.85	40.30	4.30	5.95	4.20	10.02
342	38.00	29.00	3.70	16.30	3.80	40.30	5.40	6.10	4.30	10.50
343	43.00	34.00	3.40	15.60	4.15	43.60	5.10	5.75	3.90	9.60
344	42.00	29.00	3.10	15.70	3.10	46.00	4.80	6.00	4.10	9.70
345	43.00	28.00	3.00	17.60	3.70	47.00	5.30	5.60	5.14	12.30
346	42.00	31.33	2.50	16.80	4.20	46.00	5.10	6.00	5.10	11.20
347	45.00	29.00	3.70	18.10	3.80	47.00	5.40	6.20	5.13	13.10

Progeny line no.	DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
348	38.00	35.00	3.60	16.60	4.10	45.00	4.90	5.70	4.50	11.30
349	41.00	28.00	3.40	15.40	4.20	44.00	4.70	5.40	4.30	8.40
350	43.00	31.20	4.10	16.96	3.80	42.33	5.16	5.80	4.83	11.40
351	40.00	32.00	3.10	15.00	3.40	41.00	4.90	5.40	5.10	9.80
352	42.00	29.63	3.40	14.26	3.76	39.10	4.80	4.90	4.57	8.60
353	39.00	35.00	4.00	18.60	3.67	43.00	5.80	6.80	5.14	14.20
354	42.00	25.00	3.10	14.00	3.10	42.80	4.50	4.20	4.63	8.20
355	45.00	30.10	3.50	16.00	3.60	45.00	5.20	5.80	4.56	10.10
356	42.00	26.00	2.90	12.01	3.20	37.60	4.60	4.20	4.40	5.40
357	43.00	29.00	3.60	16.40	3.68	38.00	5.24	6.10	4.63	10.60
358	42.00	31.00	3.50	16.80	3.16	39.33	5.10	5.90	4.68	10.70
359	44.00	30.60	3.30	16.40	4.10	42.00	5.06	5.80	4.40	10.20
360	42.00	24.60	2.96	12.20	3.48	32.00	4.60	4.20	3.80	5.30
361	42.00	27.00	2.80	15.80	3.80	40.67	5.00	6.00	4.23	9.20
362	44.00	32.17	3.90	16.60	3.50	43.33	5.20	5.89	4.43	11.00
363	41.00	30.00	2.89	15.86	4.00	44.00	5.60	6.00	4.10	9.00
364	42.00	31.00	3.00	15.95	3.60	44.00	5.85	4.20	4.80	9.20
365	43.00	31.60	3.20	16.00	3.50	41.00	4.40	5.78	4.65	9.70
366	42.00	29.00	2.45	14.60	3.20	38.00	5.40	4.20	4.70	7.40
367	38.00	31.90	3.10	15.98	3.15	35.00	5.85	6.00	4.86	9.80
368	42.00	34.00	3.80	17.40	3.50	48.00	5.40	5.93	5.13	12.05
369	42.00	32.00	3.60	17.60	3.10	41.68	5.90	5.80	4.95	11.00
370	45.00	30.80	3.25	16.60	4.36	45.00	5.60	6.15	5.10	10.30
371	42.00	30.00	3.35	15.80	3.45	46.00	5.00	4.20	4.60	9.50
372	44.00	29.00	3.25	15.46	3.80	40.00	4.30	5.23	4.50	9.40

Progeny line no.	DFF	PH	NB	NCP	NPC	NPP	PL	NSP	TW	TSY
373	41.00	29.60	3.30	15.50	3.59	39.00	4.70	5.75	4.25	9.40
374	43.00	32.00	3.40	15.67	3.25	44.60	4.80	5.70	4.67	10.26
375	42.00	28.00	2.90	14.86	4.30	32.00	4.96	6.15	4.20	8.00
376	41.00	29.60	3.15	17.40	4.23	52.00	4.30	5.20	4.45	8.60
377	43.00	31.60	3.40	12.40	3.50	48.00	5.30	6.15	4.60	9.80
378	41.00	32.17	3.50	16.10	3.75	42.00	5.15	5.90	4.70	10.10
379	42.00	31.50	3.20	15.80	3.15	42.00	5.40	5.20	4.31	9.70
380	41.00	35.67	3.60	17.00	3.40	42.00	5.10	6.15	4.96	11.10
381	43.00	31.00	3.10	15.60	4.20	45.00	5.20	5.80	4.60	9.20
382	45.00	31.50	3.34	17.00	3.20	40.30	4.80	6.16	5.00	10.10
383	42.00	31.20	3.40	15.50	3.35	39.00	4.50	5.80	4.59	9.40
384	42.00	30.00	3.20	12.00	3.45	34.00	4.57	6.24	4.50	9.30
385	42.00	29.80	2.80	15.80	3.80	40.67	5.00	6.00	4.23	9.20
386	44.00	32.17	3.90	16.60	3.50	43.33	5.20	5.89	4.43	11.00
387	41.00	30.00	2.89	15.86	4.00	44.00	5.60	6.00	4.10	9.00
388	42.00	31.00	3.00	15.95	3.60	44.00	5.85	4.20	4.80	9.20
389	43.00	31.80	3.20	16.00	3.50	41.00	4.40	5.78	4.65	9.70
390	42.00	28.00	2.50	14.60	3.20	38.00	5.40	4.20	4.70	7.40
391	38.00	31.00	3.10	15.98	3.15	35.00	5.85	6.00	4.86	9.80
392	42.00	32.00	3.80	17.40	3.50	48.00	5.40	5.93	5.14	12.05
393	42.00	31.00	3.60	17.60	3.10	41.68	5.90	5.80	4.95	11.00
394	45.00	30.60	3.25	16.60	4.36	45.00	5.60	6.15	5.10	10.30
395	42.00	28.00	3.35	15.80	3.45	46.00	5.00	4.20	4.60	9.50
396	44.00	27.00	3.25	15.46	3.80	40.00	4.30	5.23	4.50	9.40
397	41.00	27.60	3.30	15.50	3.59	39.00	4.70	5.75	4.25	9.40

Progeny line no.	**DFF**	**PH**	**NB**	**NCP**	**NPC**	**NPP**	**PL**	**NSP**	**TW**	**TSY**
398	43.00	31.00	3.40	15.67	3.25	44.60	4.80	5.70	4.67	10.26
399	42.00	28.00	2.90	14.86	4.30	32.00	4.96	6.15	4.20	8.00
400	41.00	28.90	3.15	17.40	4.23	52.00	4.30	5.20	4.45	8.60

DFF = Days to 50% flowering
PH = Plant height (cm)
NB = Number of branches $^{-1}$
NCP = Number of clusters plant^{-1}
NPC = Number of pods cluster^{-1}
NPP = Number of pods plant^{-1}
PL = Pod length (cm)
NSP = Number of seeds pod^{-1}
TW = Test weight (g)
TSY = Total seed yield (g)