GENETIC ANALYSIS OF GRAIN YIELD AND PHYSIOLOGICAL ATTRIBUTES IN F_3 GENERATION OF BLACKGRAM [*Vigna mungo* (L.) Hepper]

BY

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B.Sc. (Ag.)

THESIS SUBMITTED TO THE
ACHARYA N.G. RANGA AGRICULTURAL UNIVERSITY
IN PARTIAL FULFILMENT OF THE REQUIREMENTS
FOR THE AWARD OF THE DEGREE OF

MASTER OF SCIENCE IN AGRICULTURE

(GENETICS AND PLANT BREEDING)

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2019

DECLARATION

I, **Ms. MUKKU SARVANI,** hereby declare that the thesis entitled **"GENETIC ANALYSIS OF GRAIN YIELD AND PHYSIOLOGICAL ATTRIBUTES IN F_3 GENERATION OF BLACKGRAM [*Vigna mungo* (L.) Hepper]"** submitted to the Acharya N.G. Ranga Agricultural University for the degree of Master of Science in Agriculture is the result of original research work done by me. I also declare that no material contained in the thesis has been published earlier in any manner.

Place : Tirupati

Date :

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CERTIFICATE

Ms. MUKKU SARVANI has satisfactorily prosecuted the course of research and that thesis entitled **"GENETIC ANALYSIS OF GRAIN YIELD AND PHYSIOLOGICAL ATTRIBUTES IN F_3 GENERATION OF BLACKGRAM [*Vigna mungo* (L.) Hepper]"** submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that neither the thesis nor its part thereof has been previously submitted by her for a degree of any University.

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This is to certify that the thesis entitled **"GENETIC ANALYSIS OF GRAIN YIELD AND PHYSIOLOGICAL ATTRIBUTES IN F_3 GENERATION OF BLACKGRAM [*Vigna mungo* (L.) Hepper]"** submitted in partial fulfilment of the requirements for the degree of 'Master of Science in Agriculture of the Acharya N.G. Ranga Agricultural University, Guntur is a record of the bonafide research work carried out by **MUKKU SARVANI** under our guidance and supervision.

No part of the thesis has been submitted by the student for any other degree or diploma. The published part and all assistance received during the course of investigations have been duly acknowledged by the author of the thesis.

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ACKNOWLEDGEMENTS

It gives me immense gratification to place on records my profound gratitude and sincere appreciation to each and every one of those who have helped me this endeavor.

*At the outset, I submit that it is by the blessings of the **"Almighty",** I have been able to complete my studies successfully and present this humble piece of work, for which I am eternally indebted.*

*With deep sense of gratitude, honorable respect and immense pleasure, I bestow my earnest and sincere thanks to the Chairman of the advisory committee **Dr. P. Shanthi,** Assistant Professor, Department of Genetics and Plant Breeding, S. V. Agricultural College, Tirupati for her valuable peerless guidance, unflinching support, expert counsel, diligent efforts, kind treatment, sustained help and constant encouragement throughout the course of the investigation. Her keen interest and patient hearing have installed in me the spirit of confidence to successfully complete the task.*

*I humbly place on record my respect and gratitude to **Dr. M. Reddi Sekhar,** Professor, Department of Genetics and Plant Breeding, S. V. Agricultural College, Tirupati for his amenable and stupendous guidance and valuable suggestions during the period of my study.*

*I sincerely accentuate my everlasting gratitude to the revered member of my Advisory Committee **Dr. P. Latha**, Senior Scientist, Department of Crop Physiology, S. V. Agricultural College, Tirupati for her valuable guidance and cooperation throughout my period of thesis.*

*I deem it privilege in expressing my fidelity to **Dr. K. Hariprasad Reddy**, Professor and Head, **Dr. D. Mohan Reddy**, Professor, **Dr. V.L.N Reddy**, Associate Professor, **Smt. D. Bharathi,** Assistant Professor and **Smt. Sreevalli Devi,** Assistant Professor for their help and guidance during the period of my study which enabled the successful completion of my work.*

*I wish to express my sincere thanks to **Smt. D. Bharathi**, Assistant Professor for her kind cooperation and keen interest in providing the seed material.*

*I extend my unfeigned obligation to **Dr. K. Devaki**, Assistant Professor, Department of Entomology, **Dr. K. Vishwanath,** Scientist, RARS, Tirupati and **Dr. B. Ravindra Reddy**, Associate Professor, Department of Statistics and Computer Applications for their valuable suggestions and guidance during my research study.*

I express my heartfelt thanks to ***Dr. G. Prabhkar Reddy****, Farm Superintendent,* ***Mr. Parthasarathy****, Farm Manager,* ***Mr. Govindaiah****, A.E.O, other field staff and* ***farm labour*** *for their timely co-operation in the farming operations.*

Diction is not enough to express my regards from the inner core of my heart to my ever loved Parents, ***Sri. Suryanarayana and Smt. Sudha*** *who have taught the concepts of life and their dedicated efforts to educate me to this level helped me a lot in shaping myself. I am profoundly indebted to my. uncle* ***Sri. Kamalnath*** *and aunt* ***Smt. Udaya Lakshmi*** *for their constant encouragement, affection and cooperation throughout my career.*

With boundless affection, I owe an encompassing debt to my beloved sister ***Swathi,*** *my brother-in-law* ***Swamy*** *and all my family members for their encouragement during the study.*

I express my heartfelt gratitude and thanks to my seniors ***Saritha, Kavitha*** *and* ***Sofia*** *for their valuable guidance and encouragement.*

I cordially concede my gratitude to my colleagues ***Reshmi, Venkatratnam, Swaminathan, Priyanka, Sailaja, Aruna, Sowjanya and Mustaq*** *for their cooperation and help during study.*

Diction is my predilection to express my heartful thanks to my joyful friend's gallery ***Sri vidya, Prasanna, Revathi, Surya teja, Sadik, Anuhya, Pravalika and Ragamallika*** *for their extreme help during the course of my study.*

I have immense pleasure to extend my whole hearted thanks to my juniors ***Prasindu, Geetha, Hima bindu, Maha Lakshmi, Bhargavi, Sukrutha, Nagendra Naidu, Maneesha, Prashanth, Sai and Suvarna.***

It is a pleasure to acknowledge the affection and help rendered by, ***Munirathnam, Venkata Lakshmi, Munirathnam*** *and* ***Tygarajula Naidu,*** *non-teaching staff of Department of Genetics and Plant Breeding, S.V. Agricultural College, Tirupati. I also extend my heartfelt thanks to the* ***library*** *staff for their kind and timely help.*

I am highly thankful to Acharya N.G. Ranga Agricultural University, Guntur for all the facilities extended during the period of my post-graduation programme.

Sarvani….

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LIST OF SYMBOLS AND ABBREVIATIONS

%	Per cent
ANOVA	Analysis of Variance
CD	Critical difference
CFBD	Compact Family Block Design
$cm^2 g^{-1}$	Centimeter square per gram
cm	Centimeter
cm^2	Square Centimeter
cm^{-2}	Per centimeter square
CV	Coefficient of Variation
DAS	Days After Sowing
df	Degrees of freedom
et al.	And others
Fig.	Figure
G	Genotypic
g	Gram
GA	Genetic Advance
GAM	Genetic Advance as per cent of Mean
GCV	Genotypic Coefficient of Variation
h^2(bs)	Heritability in broad sense
i.e.	Which is to say in other words
kg	Kilogram
kg ha^{-1}	Kilogram per hectare
m ha	Million hectares
m t	Million tonnes
m	Metre
No.	Number
PCV	Phenotypic Coefficient of Variation
per se	As such with mean

r_g	Genotypic correlation coefficient
r_p	Phenotypic correlation coefficient
S. No.	Serial Number
SCMR	SPAD Chlorophyll Meter Reading
$S.E_m$	Standard Error of mean
SPAD	Soil Plant Analysis Development
t ha^{-1}	Tonnes per hectare
via	Through
viz.,	Namely
V_p	Phenotypic variance
V_g	Genotypic variance
$\overline{X}$	Grand mean
q ha^{-1}	Quintals per hectare

ABSTRACT

Author of the thesis	:	**MUKKU SARVANI**
Title of the thesis	:	**"GENETIC ANALYSIS OF GRAIN YIELD AND PHYSIOLOGICAL ATTRIBUTES IN F_3 GENERATION OF BLACKGRAM [*Vigna mungo* (L.) Hepper]"**
Degree to which submitted	:	**MASTER OF SCIENCE IN AGRICULTURE**
Faculty	:	**AGRICULTURE**
Discipline	:	**GENETICS AND PLANT BREEDING**
Major Advisor	:	**Dr. P. SHANTHI**
University	:	**ACHARYA N.G. RANGA AGRICULTURAL UNIVERSITY**
Year of submission	:	**2019**

The present investigation entitled "Genetic analysis of grain yield and physiological attributes in F_3 generation of blackgram [*Vigna mungo* (L.) Hepper]" was carried out during *kharif,* 2018 at dry land farm, S. V. Agricultural College, Tirupati in a Compact Family Block Design with four replications. The objectives were to study the variability, heritability, genetic advance as per cent of mean, character association among different yield, yield related and physiological attributes as well as their direct and indirect effects on seed yield per plant and to identify transgressive segregants for yield and physiological attributes. The experimental material consisted of three F_3 populations generated from LBG-787 x LBG-752, TU-94-02 x LBG-752, TU-94-02 x KU-1006 and their parents *i.e.,* LBG-787, TU-94-02, LBG-752 and KU-1006.

The analysis of variance between families revealed significant differences between crosses for all the 19 characters studied viz., days to 50% flowering, days to maturity, plant height, 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, test weight, Specific Leaf Area (30 DAS), Specific Leaf Area (45 DAS), Specific Leaf Weight (30 DAS), Specific Leaf Weight (45 DAS), SPAD Chlorophyll Meter Reading (30 DAS), SPAD Chlorophyll Meter Reading (45 DAS), biomass per plant, harvest index and seed yield per plant. The analysis of variance among progenies within each family indicated significant difference

between progeny means for all the characters studied in cross, LBG-787 x LBG-752, except for test weight in TU-94-02 x LBG-752 and SLW(45 DAS) in TU-94-02 x KU-1006.

Heritability and genetic advance as per cent of mean were high for plant height, number of clusters per plant, number of pods per cluster, number of pods per plant, SLA (30 DAS) and seed yield in cross LBG-787 x LBG-752, plant height, number of clusters per plant, number of pods per plant, biomass per plant and seed yield in cross TU-94-02 x KU-1006 and SLA (45 DAS) in cross TU-94-02 x LBG-752. This suggests that these traits had sufficient amount of variability indicating the presence of additive gene action and least influence of environment. Thus, direct selection for these traits in respective crosses results in further improvement of seed yield and physiological traits.

In all the crosses, seed yield has shown significant positive association with plant height, 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, biomass per plant and harvest index. Path analysis revealed that plant height, number of pods per cluster, test weight, harvest index and biomass per plant in cross LBG-787 x LBG-752, plant height and number of clusters per plant in cross TU-94-02 x KU-1006 and number of clusters per plant, number of seeds per pod, SLA (45 DAS) and harvest index in cross TU-94-02 x LBG-752 exerted high positive direct effects on seed yield per plant. Hence, these traits can be used in selection criterion for the development of high yielding genotypes in their respective crosses.

Good number of positive transgressive segregants were propelled for plant height, number of clusters per plant, SLA (30 DAS), SLW (45 DAS), SCMR (30 DAS) and seed yield in cross LBG-787 x LBG-752; for plant height, number of clusters per plant, number of seeds per pod, test weight, SLA (30 DAS), SLA (45 DAS), SLW (30 DAS) and seed yield in cross TU-94-02 x KU-1006, for plant height, test weight, SLA (30 DAS), SLA (45 DAS), SLW (30 DAS), SLW (45 DAS) and seed yield in cross TU-94-02 x LBG-752. Hence forwarding these transgressive segregants to further generation contributes to the development of most promising genotypes.

Among all the three crosses studied, cross TU-94-02 x KU-1006 can be considered for breeding high yielding varieties along with good physiological characters through selection in further generations.

Chapter –I

Introduction

Chapter I

INTRODUCTION

Blackgram [*Vigna mungo* (L.) Hepper] (2n= 22) belongs to the family *Fabaceae* and the genus *Vigna.* Among the seven species of Vigna cultivated as pulse crops, blackgram (*Vigna mungo* (L.) Hepper) is the member of the Asian *Vigna* crop group under subgenus Ceratotropics (Verdcourt, 1970).

Blackgram is native to India (Vavilov, 1926). The progenitor of blackgram is believed to be *Vigna mungo* var. *silvestris* which grows wild in India (Lukoki *et al*., 1980). It is a staple crop in the 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 and subtropics (Delic *et al*., 2009).

Blackgram is one of the most highly priced pulse crop cultivated in almost all parts of India. It has inevitably marked itself as the most popular pulse and can be most appropriately referred as the “king of the pulses” due to its mouthwatering taste and numerous other nutritional qualities. Blackgram is a perfect combination of all nutrients which includes proteins (25-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins (Karamany, 2006). It stands next to soybean in its dietary protein content. It is rich in vitamin A, B_1, B_3 and has small amount of thiamine, riboflavin, niacin and vitamin C in it. It contains 78% to 80% nitrogen in the form of albumin and globulin (Das *et al*., 2002). The dry seeds are good source of phosphorus. It also has very high calorie content *i.e.* 347 calories per 100 gm of blackgram. Therefore, blackgram is the cheapest available source of protein for the poor and vegetarians (Tharanathan and Mahadevamma, 2003).

The biological value of blackgram improves greatly, when wheat or rice is combined with it because of the complementary relationship of 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 nutritive fodder, especially for milch animals. Blackgram also has medicinal properties like curing diabetes, sexual dysfunction, nervous disorder, hair disorders, digestive system disorders and rheumatic afflictions. It is valued for its high digestibility and freedom from flatulence effect (Fary, 2002).

Being a leguminous crop, it has unique characteristics of maintaining and restoring soil fertility through fixing atmospheric nitrogen in symbiotic association with *Rhizobium* bacteria present in the root nodules (Ahmad *et al.,* 2001). It proves to be a great rotation crop enhancing the yield of main crop as well. It is mainly cultivated in a cereal-pulse cropping system primarily to conserve soil nutrients and utilize the left over soil moisture particularly after rice cultivation. It is a short duration pulse crop (Delic *et al.,* 2009), usually flowering within 30-60 days of sowing and maturing within 60-90 days. It is generally cultivated as *kharif* crop but also does well in summer season as a catch crop.

Blackgram is an annual trailing or erect plant with a height of 30-90 cm and profuse branching. The stem is slightly ridged and covered with brown hairs. The leaves are large, trifoliate and hairy, generally with a purplish tinge. The flowers are axillary, racemose, complete, self-pollinated and yellow in color. The inflorescence consists of cluster of 5-6 flowers at the top of long hairy peduncle. Pods are short, erect to suberect, 4-6 cm long, brown to black in color and hairy containing about 6- 10 seeds. The seeds are generally black or dark brown with smooth seed coat and protruding hilum.

It accounts for 13 per cent of 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 m t and productivity of 604 kg ha^{-1}. Andhra Pradesh is one of the major blackgram growing states of India with an area of 3.81 lakh hectares, with a production of 3.13 lakh tonnes and productivity of 821.5 kg ha^{-1} (Anonymous, 2018).

The critical position of pulse production particularly blackgram against the increased population poses a challenge on the part of breeders to develop high yielding, short duration, bold-grained and disease resistant varieties. This can only be achieved through a planned and purposeful 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 percent flowering, days to maturity, 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, grain yield per plant *etc.* in blackgram. Physiological characters such as SPAD Chlorophyll Meter Reding, Specific Leaf Area, Specific Leaf Weight, biomass per plant and harvest index also contribute to gain in grain yield.

Yield can be enhanced by selecting highly heritable and correlated morphological and physiological attributes which contribute to yield advantage in a given environment and combining them to enable further identification of genotypes with desirable combination of traits.

A survey on genetic parameters such as variability, heritability, genetic advance and gene action involved in the inheritance of morphological and physiological 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. Heritability in conjunction with genetic advance is more useful than heritability alone in the prediction of resultant effect of selecting the best individual (Johnson *et al.,* 1955a).

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

Path coefficient analysis is a standardized partial regression coefficient, which splits the correlation into the measures of direct and indirect effects. It therefore reveals whether the association of these characters with yield is due to their direct effect on yield or it is a consequence of their indirect effect via some other character. If the correlation between yield and other character is due to direct effect of that 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 transgressive segregation in early generations as high heterotic crosses would result in more productive transgressive segregants in later generations as pointed by Arunachalam (1981). Transgressive segregation creates an opportunity for new hybrids to arise that are more fit than their ancestors. Transgressive segregants are more adaptable and resistant under various environmental conditions. Transgressive segregants can be predicted and observed within progenies of an early segregating generation.

Thorough knowledge on the genetic parameters such as variability, heritability, genetic advance and gene action in the segregating population will provide a systematic approach for identifying the high yielding genotypes. Keeping all these in view, the present study in blackgram was undertaken with 30 progenies of three F_3 populations derived from three crosses LBG-787 x LBG-752, TU-94-02 x KU-1006 and TU-94-02 x LBG-752, which were selected based on high mean performance for seed yield (previous studies carried by Bharathi, 2017) with the following objectives:

1. To estimate variability, heritability and genetic advance for both morphological and physiological attributes.
2. To assess the magnitude of association of morphological and physiological attributes on yield.
3. To ascertain the relative contribution of direct and indirect effects of component characters towards yield.
4. To identify transgressive segregants for morphological and physiological attributes.

Chapter – II

Review of Literature

Chapter II

REVIEW OF LITERATURE

Blackgram 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 blackgram is seed and the yield of this crop is very low because of the non-availability of high yielding and stable 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 subheads.

2.1 Variability, heritability and genetic advance as per cent of mean

2.2 Character association

2.3 Path coefficient analysis

2.4 Transgressive segregation

2.1 VARIABILITY, HERETABILITY 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 presence of wide spectrum of variability will enhance the chance of selecting desired genotypes. The yield and yield components of a breeding population are highly influenced by the environment which renders it difficult to conclude whether the observed variability is heritable or not. It therefore becomes essential to partition the observed variability into heritable and non-heritable components by studying genotypic and phenotypic coefficients of variation.

To have the knowledge of the heritable portion of variability it is necessary to estimate the heritability of each character. The broad sense heritability gives an idea about the portion of observed variability attributable to genetic differences and indicates the accuracy with which a genotype can be identified by phenotypic performance. An estimate of heritability gives information on the magnitude of inheritance of quantitative traits but does not provide the amount of genetic progress that will result from selecting the best individuals.

Heritability along with genetic advance is useful in estimating the influence of environment. Genetic advance refers to the improvement in the mean genotypic value of selected plants over the base population. Estimates of heritability along with estimates of genetic advance are more useful in choice of selection method rather than heritability or genetic advance alone. Hence, the knowledge on nature and extent of genetic variation, heritability and genetic advance as percent of mean in the population of parents and hybrids is essential for planning sound breeding programmes.

Mishra (1983) observed that heritability estimates were high for 100 seed weight and plant height whereas moderate for pods per plant in 18 varieties of blackgram having diverse origin. Plant height, pods per plant and clusters per plant had high predicted genetic advance accompanied by high variability and moderate heritability.

Byregowda *et al.* (1997) reported that sufficient variability was recorded for grain yield per plant, pods per plant, branches per plant and plant height in 18 blackgram genotypes of diverse origin. The germplasm also showed high heritability values associated with high genetic advance for grain yield per plant and pods per plant. High heritability in conjugation with medium genetic advance was obtained for 100-seed weight and branches per plant.

Isaacs *et al.* (2000) assessed thirty two blackgram genotypes for phenotypic and genotypic coefficients of variability, heritability and genetic advance. High heritability associated with high genetic advance was obtained for single plant yield, pods per plant and other yield attributing traits, except for number of seeds per pod. High heritability with medium genetic advance was obtained for 100-seed weight.

Parameswarappa and Lamani (2005) reported significant differences among forty blackgram genotypes for days to 50% flowering, plant height, number of branches per plant, number of pods per plant, test weight and yield per plant.

Priti *et al.* (2006) reported existence of considerable amount of variability for all the characters studied among fifty blackgram genotypes except for pod length, no. of seeds per pod, 100-seed weight and protein content. The yield per plant exhibited highest values of genotypic and phenotypic coefficient of variation (GCV and PCV). High estimates of heritability, genotypic coefficient of variation and genetic advance was observed for number of branches per plant, number of clusters per plant, number of pods per plant and yield per plant.

Singh and Singh (2006) evaluated 10 parents, 45 F_1's and 45 F_2's of blackgram for genetic variability and the results revealed that high estimates of heritability were recorded for days to 50% flowering, days to maturity and plant height in both F_1 and F_2. Moderate heritability estimates has been observed for pod length, seeds per pod and harvest index. The genetic advance over the mean of respective traits were maximum for plant height followed by days to 50% flowering, harvest index and days to maturity.

A significant variability was recorded for pod length, plant height, seed yield, seeds per pod and 100 seed weight in mungbean (Gul *et al.,* 2007). Highest PCV and GCV was recorded for pod weight, seed yield, pods per plant when evaluated 24 lines of blackgram were evaluated in four different environments. A wide range of variability in five quantitative traits is also reported by Pervin *et al*. (2007). Heritability in the broad sense with genetic advance expressed as percentage of mean was comparatively low.

Faisal *et al*. (2008) stated that leaf area, pods per plant, plant height and biological yield showed high phenotypic and genotypic variances and the magnitude of heritability was high for 100-seed weight, pods per plant, pod length, biological yield, grain yield, days to maturity, harvest index, branches per plant and plant height based on their study on eighteen blackgram genotypes.

Malik *et al.* (2008) observed significant variability for seed yield, harvest index, pods per plant, pod length, seeds per pod, 100 seed weight, days to 50% flowering, plant height and branches per plant in blackgram.

In a study conducted by Konda *et al.* (2009) involving 40 genotypes of blackgram for genetic variability of seed yield and its component traits, it was found that higher estimates of GCV was observed for plant height, crude fiber content and hundred seed weight. Moderate GCV estimates were observed for days to 50% flowering, length of reproductive period and grain yield per plant. Very high heritability was seen for days to 50% flowering, days to maturity, plant height, length of reproductive period, hundred seed weight, protein content and crude fiber content. High genetic advance as per cent of mean was observed for plant height, crude fiber content, hundred seed weight and days to 50% per cent flowering indicating under the control of additive gene effects, may serve as better source for breeding programme to develop high yielding varieties.

In mungbean, Suresh *et al.* (2010) reported higher per cent of GCV for harvest index followed by seed yield, number of branches and number of clusters per plant and concluded that these characters are under the influence of genetic control.

High heritability (broad sense) along with high genetic advance as percent of mean was observed in mungbean by Rahim *et al.* (2010) for plant height, number of pods per plant, number of seeds per pod, test weight and seed yield per plant.

Arulbalachandran *et al.* (2010) observed high variability for plant height, branches per plant, clusters per plant, pods per plant, seeds per pod, seed yield and 100 seed weight of in M_2 generation of blackgram obtained by the effect of mutation by gamma rays.

Genetic variability studies carried out by Meshram *et al.* (2012) among 27 blackgram genotypes revealed that the characters *viz*., plant height, number of pods per plant , pod weight 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) blackgram 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).

In pigeon pea, Visakho Shuny *et al.* (2013) reported a high degree of variability in the selected germplasm as significant differences existed among the genotypes for all the quantitative characters studied. Their estimates of phenotypic coefficient of variation (PCV) were higher than those of genotypic coefficient of variation (GCV) for all these traits, indicating influence of environmental factors on these characters.

Sowmini and Jayamani (2013) by estimating genetic variability among 193 blackgram 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.

Narasimhan *et al.* (2013) recorded higher phenotypic and genotypic coefficients of variation among twelve blackgram genotypes for total seed yield, number of pods per plant and number of bunchs. 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 bunches, number of pods per plant and total seed yield.

Samad *et al.* (2013) concluded that the traits *viz.,* leaf area at 50% flowering and number of nodules at 50% flowering showed high GCV estimates whereas, number of nodules at 50% flowering, number of secondary branches at first flower, leaf area at 50% flowering and number of leaves at 50% flowering exhibited high PCV. The heritability, genetic advance (GA) and genetic advance as percentage of mean (GAM %) were found to be low for these characters.

Ramya *et al.* (2014) reported high estimates of PCV and GCV for primary branches per plant clusters per plant, pods per plant and seed yield in M_2 generation of blackgram.

Panigrahi *et al.* (2014) reported higher PCV than GCV for all the quantitative characters assessed in blackgram 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% flowering, days to maturity and seeds per pod recorded low GCV values.

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 percent 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 blackgram.

Presence of moderate magnitude of heritability in broad sense, genetic advance as percentage of mean, phenotypic and genotypic coefficients of variation in respect of seed per pod, plant height and yield has been reported by Mandal *et al.* (2014) while working with 135 blackgram genotypes.

Panigrahi and Baisakh (2014) concluded that the high magnitudes of genotypic and phenotypic coefficient of variations were recorded for the traits plant height, primary branches per plant and pod per plant. High heritability coupled with genetic advance was observed for plant height, pod per plant and primary branches per plant indicating that heritability is due to additive gene action and selection based on these characters may be effective.

In an experiment carried out by Vijay *et al.* (2015) in blackgram with fourteen lines, three testers and 42 F_1s 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% flowering and clusters per plant respectively. High genetic advance as percent 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 blackgram to assess genetic variability and they recorded highest

GCV for number of branches per plant, seed yield per plant, number of clusters per plant, branch length, number of pods per plant and plant height. High heritability coupled with high genetic advance was observed for branch length, number of branches, plant height, clusters per plant, seed yield per plant and number of pods per plant.

Priyanka *et al.* (2016) conducted variability studies among 24 blackgram lines and revealed that the genotypes were highly variable for number of cluster 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 percent 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 thirty six blackgram 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 index, seed yield per plant, biological yield per plant, pods per plant and harvest index. Estimated of 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 blackgram 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 percent 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 blackgram 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% flowering, harvest index, seed yield per plant. High heritability coupled with high genetic advance as percent of mean was recorded for pods per plant.

Genetic variability studies among fifteen blackgram accessions along with two checks and two local varieties by Jyothi *et al.* (2017) for grain yield and water use efficiency revealed that heritability in broad sense was high for seed yield, test weight of seed and total biomass. High genetic advance as percent 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 twenty six mutant lines of urdbean 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 yield indicated predominance of additive gene action in governing the inheritance of these traits.

Ozukum and Sharma (2017) in their study on five urdbean 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 urdbean lines. High broad sense heritability estimates were recorded for days to 80% maturity, days to 50% flowering and 100 seed weight. The highest genetic advance as percent of mean was recorded for yield per plot (28.92 %) followed by number of pods per plant.

Panda *et al.* (2017) reported that among 50 blackgram genotypes studied the magnitudes of heritability in broad sense was found to be low for number of seeds per pod, pod girth and pod length; moderate for days to maturity, days to 50% flowering and number of branches per plant; high 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. The high heritability in conjunction with high genetic advance was noted in number of seeds per plant and seed yield per plant.

Leaf chlorophyll content is a key indicator of the physiological status of a plant. Chlorophyll content per unit leaf area (chlorophyll density) has been used as an index of photosynthetic capacity and growth of many crop plants and it is most important to enhance crop performance because chlorophyll is a major photosynthetic pigment.

Takabe *et al.* (1990) pointed out the importance of the chlorophyll meter that provides a simple quick and non- destructive method for estimating area-based leaf nitrogen concentration. The major role of this pigment is to absorb and reacts with visible light in the photosynthesis (Bowyer and Leegood 1997).

In peanut, Arunyanark *et al.* (2009) demonstrated that the variation in transpiration efficiency was closely correlated with genotypic variation in chlorophyll density and hence with photosynthetic capacity, such that chlorophyll density could be used as a potential indicator of transpiration efficiency in peanut. The chlorophyll meter or SPAD (Soil Plant Analysis Development) also offers a new strategy for synchronizing nitrogen application with actual crop demand in rice (Peng *et al.,* 1996). It indicates the need of a nitrogen top dressing that would result greater agronomic efficiency of nitrogen fertilizer than commonly pre-application of nitrogen

(Hussain *et al.,* 2000). SPAD value may also be used directly to monitor leaf nitrogen status in rice (Peng *et al.,* 1996) and determine the time of nitrogen top dressing.

SPAD chlorophyll meter is an indicator of the photo-synthetically active light- transmittance characteristics of the leaf, which is dependent on the unit amount of chlorophyll per unit leaf area (chlorophyll density) (Richardson *et al*., 2002).

A direct close relationship of transpiration efficiency with SPAD Chlorophyll Meter Readings was reported in groundnut (Nageswara Rao *et al*., 2001) and it is a direct linear relationship through extracted leaf chlorophyll (Yadava 1986) and also related leaf nitrogen concentration (Kantety *et al*., 1996).

2.2 CHARACTER ASSOCIATION

Correlation is the process through which we can measure the phenotypic and genotypic relation. It also provides us the information about relationship about dependent and independent variables. Correlation analysis informs us about the relative importance of the breeding traits. Therefore, information on association between characters is quite useful to plant breeders to formulate their breeding and selection strategies. As the yield of plant is a complex, polygenically inherited trait, direct selection is not effective. But, it could be improved through a number of component characters, which are simple in inheritance and less subjected to environmental influences. Hence, the knowledge of association of yield components with yield and among themselves would be of great help to the breeder in obtaining improved yields. A brief review of literature on the association of characters in blackgram is presented here under.

Patil and Deshmukh (1989) reported that seed yield was significantly correlated with plant height, pods per plant, seeds per pod, pod length and 100- seed weight while days to 50% flowering and days to maturity were negatively correlated with seed yield.

Verma *et al.* (1992) concluded that seed yield has significant positive correlation with 100-seed weight, number of days to maturity, number of primary branches and plant height both at genotypic and phenotypic levels in blackgram.

Character association studies were carried out by Mahto and Mahto (1997) among 11 cultivars of blackgram. They reported that seed yield was positively correlated with 100-seed weight, days to 50 per cent flowering, plant height, number of branches per plant, number of seeds per pod and days to maturity.

A study conducted by Savithramma *et al.* (1999) in 19 diverse genotypes of blackgram revealed that seed yield had significant positive association with plant height, number of clusters per plant, number of pods per cluster and number of seeds per pod.

Ghafoor *et al.* (2000) from correlation studies on 484 blackgram genotypes found that grain yield had high correlation with number of branches, pods per plant, pods per branch, seeds per pod, seed weight and biological yield. Among some selected genotypes it was observed that grain yield had significant positive correlation with days to 50% flowering and days to maturity.

Yadav and Dahiya (2000) carried out correlation studies in 160 blackgram germplasm lines and found that seed yield had a high positive correlation with number of pods, test weight, primary branches and seeds per pod. Some other traits that exhibited a positive correlation were plant height-test weight, plant height-maturity, primary branches per plant and pods per plant.

Vaithiyalingan *et al.* (2002) by conducting association studies involving 30 hybrids and 11 parents in blackgram determined that seed yield has significant positive association with branches per plant, clusters per plant, pods per plant, seeds per pod, dry matter production and harvest index.

Srividhya *et al.* (2005) carried out correlation analysis in 15 F_2 crosses derived from 6 x 6 diallel cross in urdbean and revealed that seed yield per plant was positively and significantly associated with pods per plant, clusters per plant, seeds per pod, 100-seed weight and biomass and concluded that the selection based on these characters would be helpful for yield improvement in urdbean.

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 blackgram 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.

Seed yield in blackgram 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 significant correlated with each other.

The correlation analysis conducted by Sharma *et al.* (2006) in 14 blackgram genotypes indicated that seed yield per plant was positively and significantly correlated with pods per plant, branches per plant and 1000-seed weight.

Sudhakar *et al.* (2006) evaluated greengram and blackgram genotypes and reported the significant inverse relationship between SCMR and SLA in blackgram and no correlation in greengram genotypes. Further they noticed that there is a significant positive correlation between SCMR and seed yield in both blackgram and greengram under moisture stress indicating that SCMR could be used as a screening tool for grain yield under drought conditions.

A study conducted by Singh *et al.* (2007) revealed that seed yield had significant positive association with number of pods per plant, plant height pod length, number of seeds per pod, days to flower and days to maturity, while negative correlation was observed with primary branches per plant. Number of pods per plant with plant height and pod length, number of seeds per pod and plant height had positive and significant correlations.

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 mungbean 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. Harvest index had significant positive correlation with seed yield per plant while it had significant negative correlation with seeds per pod, plant height and dry weight per plot. 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.

Younis *et al.* (2008) noticed that the days to flowering had negative correlation with all the traits except pods per plant in 24 lentil genotypes.

Negative and significant correlation of days to flower with harvest index has also been observed. Plant height had positive correlation with biological yield and seed yield. Number of primary branches had positive correlation with biological yield, 100-seed weight and harvest index. Positive and significant correlation of pods per plant with biological yield and seed yield has been observed. Pods per plant also had positive correlation with hundred seed weight and harvest index.

Konda *et al*. (2008) observed that the branches per plant, clusters per plant, pods per plant, seeds per pod, pod length and hundred seed weight exhibited significant and positive correlation with yield per plant and concluded that clusters per plant is an important component influencing yield in blackgram.

Kadam *et al.* (2008) stated that yield in blackgram had a high significant and positive correlation with plant height, leaf area, total dry weight, number of pods per plant, number of grains per pod and 1000-grain weight and negatively correlated with flowers shedded.

Malik *et al.* (2008) evaluated 18 genotypes of blackgram 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.

Examination of moisture stress effects on three mungbean genotypes by Omid *et al*. (2009) revealed that seed yield was positively correlated with harvest index, biomass and plant height.

Ashok *et al.* (2010) evaluated six mungbean x blackgram hybrids for differences in plant growth, dry matter partitioning, and yield under rainfed conditions and found that biomass was positively related to total moisture use and seed yield to daily crop transpiration.

Isha Parveen *et al.* (2011) reported that the pods per plant, harvest index and clusters per plant were significantly and positively correlated with seed yield in blackgram. 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. On contrary, 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 contrary, highly significant negative association of clusters per plant with number of seeds per pod.

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

Shivade *et al.* (2011) carried out a study among 36 genotypes of blackgram 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.

Baroowa and Gogoi (2012) observed positive correlations of soil moisture with leaf chlorophyll, chlorophyll stability index, plant height, leaf area, cell membrane stability and yield. Blackgram variety PU19 was found to be more resistant than greengram variety pratap against drought stress.

Pushpa *et al.* (2012) analysed two blackgram cultivars (Mash-1and Mash 338) and stated that the characters pods per plant and seeds per pod possess high positive correlation with yield.

Srivastava and Singh (2012) reported that the seed yield per plant possessed highly significant positive correlation with number of pods per plant, 100-seed weight, primary branches per plant in mungbean during *kharif*. Pushpa Reni *et al.* (2013) reported that the pods per plant, 100-seed weight and days to 50% flowering had positive direct effect on grain yield in blackgram genotypes. 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% flowering and days to maturity. They suggested that these traits could be used for the improvement of grain yield resulting in the evolution of high yielding varieties of blackgram.

Suresh *et al.* (2013) observed that the seed yield per plant had highly significant positive correlation with pods per plant in mungbean. The trait, plant height had high positive significant correlation with pods per plant and seeds per pod. Likewise the days to 50 per cent flowering had highly 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% flowering, pods per cluster and 100-seed weight showed highly 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 mungbean.

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 mungbean during *kharif*. It was also observed that pods per plant exhibited positive and significant correlation with 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 mungbean.

Pushpa reni *et al.* (2013) reported that pods per plant and plant height had highly significant genotypic and phenotypic correlation with grain yield hence these traits could be used for the improvement of grain yield resulting in the evolution of high yielding varieties of blackgram.

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.

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

Correlation studies by Singh *et al.* (2014) among 128 urdbean 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.

Anitha *et al.* (2015) evaluated 17 blackgram genotypes under both irrigated and water deficit conditions to assess impact of moisture stress on physiological parameters like SLA, SCMR, yield and yield component traits. They concluded that water deficit at flowering stage resulted in reduction of physiological and yield parameters. There is a wide diversity among blackgram genotypes in their physiological and yield related parameters under both moisture levels.

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, total dry matter production has been recorded by Kanimoli *et al.* (2015)

Correlation coefficient analysis involving 35 genotypes of urdbean 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.

Baroowa and Gogoi (2016) assessed response pattern of blackgram (T9, KU 301) and greengram (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 relative leaf water content, plant height, leaf number, leaf area and shoot:root biomass.

Mehra *et al.* (2016) concluded that seeds per plant, 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 seeds per plant followed by pods per plant, biological yield per plant, plant height and 100-seed weight.

Monika *et al.* (2016) estimated genotypic and phenotypic correlations in all possible combinations for 75 accessions of blackgram. 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. Sateesh *et al.* (2016) observed significant positive correlation of number of branches per plant and negative correlation of plant height with seed yield both at phenotypic and genotypic level.

Sohel *et al.* (2016) revealed that yield per plant in blackgram 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.

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

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

Correlation between chlorophyll Stability index (CSI) and soil moisture was found to be positively significant in both greengram and blackgram by Pandiyan *et al.* (2017). They also stated that VBN (Bg) 4 and VBN (Bg) 6 in blackgram have physiological and biochemical capability for drought tolerance in water stress condition.

The association studies carried out by Suguna *et al.* (2017) among 12 hybrids and four parents of blackgram 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 blackgram 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% flowering, days to maturity exhibited negative and significant association with grain yield per plant.

2.3 PATH COEFFICIENT ANALYSIS:

As yield is a complex character controlled by polygenes and greatly influenced by environment, selection based on yield is not effective, hence selection for yield components, which are less prone to environmental influences is very valuable. Therefore it is essential to measure the contribution of various traits towards the yield through correlation and partitioning the correlation coefficient into the components of direct and indirect effects (Ramana and Singh, 1987). The quantity and direction of influence *ie.,* both direct and indirect effects are estimated by path coefficient analysis. The available literature on path coefficient analysis carried out in blackgram was furnished here under.

Parameshwarappa *et al.* (1991) revealed that days to 30 percent flowering and plant height have maximum positive direct effect on yield and days to first podding and number of pod bearing clusters per plant exhibit a high negative direct effect on yield based on his analysis on 225 blackgram genotypes.

Shanmugasundaram and Sreerangaswamy (1995) stated that pod number followed by days to maturity had positive direct effect on seed yield while plant height had negative effect on seed yield.

Sajikumar *et al.* (1996) found that pod weight had positive direct effect on seed yield whereas seeds per pod had the highest negative direct effect followed by pods per plant and 100-seed weight in urdbean.

Ghafoor *et al.* (2000) tested 77 blackgram genotypes by path analysis for their suitability to organic farming under rain-fed conditions. They stated that maximum direct effect on seed yield was contributed by biological yield.

Twenty blackgram genotypes were examined under rice fallow conditions by Kingshlin and Vanniarajan (2000) for path analysis and revealed that maximum direct effect on seed yield was recorded through days to 50% flowering, followed by pods per plant and seeds per pod.

Ninety three urdbean 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 blackgram 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.

Pods per plant had the highest positive direct effect on seed yield followed by test weight and number of branches per plant as reported by Parameswarappa and Lamani (2005) based on their experiment with 40 blackgram genotypes.

Path coefficient analysis by Sharma *et al.* (2005) using ten blackgram genotypes revealed that number of pods per plant and 1000-seed weight had positive direct effects on grain yield per plant. Days to maturity, plant height, number of pods per plant, and 1000-seed weight showed positive indirect effects on grain yield per plant.

Umadevi and Meenakshi (2005) assessed 60 genotypes of blackgram and concluded that number of clusters per plant showed the highest positive direct effect on yield (1.468) followed by number of pods per plant and pod length. The estimates of residual effect (0.121) reflect the adequacy and appropriateness of the characters chosen for path analysis

Makeen *et al.* (2009) based on their studies on 22 micromutants of T9 blackgram 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.* (2011) conducted a study to know direct and indirect effects of various yield component characters on yield among 36 genotypes of blackgram and revealed that the characters days to first 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, branch height, 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 urdbean 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 urdbean

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% flowering and pod length showed direct negative effect on seed yield as reported by Singh *et al.* (2014) among 28 promising urdbean genotypes.

Jyothsna *et al.* (2016) examined 12 blackgram 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.

Rasel *et al.* (2016) by assessing ten blackgram 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.* (2017) assessed 30 blackgram 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% flowering revealed negative direct effect of given magnitudes towards seed yield per plant.

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

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

Path analysis by Rekha and Reddy (2017) among 31 mungbean 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.* (2017) evaluated 21 blackgram 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.

Ragul *et al.,* (2018) subjected 52 progenies in F_5 generation derived from an interspecific cross between greengram (*Vigna radiata* cv. VBN(Gg)2) and blackgram (*Vigna mungo* cv. Mash 114) to path analysis and concluded 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.

2.4 TRANSGRESSIVE SEGREGATION:

Transgressive segregation refers to the phenomenon through which we get variation in F_2 or later segregating generations outside the range of both the parents. No much published information is available on this aspect in blackgram. Hence research report on pulses and oilseed crops are also reviewed herewith.

Langham (1961) reported high-low method of crop improvement in which he explained the basis of transgressive segregation. According to him there are upper (high) and lower (low) limits for the expression of character, the highest frequency of individuals having average expression which are favored by natural selection. It is postulated that the genes responsible for high performance are associated with modifiers or buffers which will not allow the expression of characters beyond a certain higher limit. When crosses were made between high performing lines, they would be associated with negative buffer only and hence could not transgress a threshold limit.

Similar situation would occur when crosses made between low performing lines. However, when cross made between high and low performing parents, there is a maximum possibility of getting transgressive segregation from F_2 generation onwards, since the segregating high genes will be buffered or linked with positive modifiers. Similar procedure can be continued in future generations also for accumulation of more positive buffers with more high genes. Improvement has been shown by him in sesamum for certain characters by this procedure.

Auckland and Singh (1976) reported transgressive segregation in respect of plant height, seed size, pod number and seed yield in F_2 generation of Kabuli x Deshi cross in chickpea.

Bahl (1979) initiated the work on Kabuli-Deshi introgression in 1976 and reported the encouraging results from this line of work. He could isolate early maturing types with determinant in growth habit and better harvest index as compared to standard check variety. He also suggested that three ways instead of single crosses are more useful for introgression of new germplasm into the breeding population.

Ugale (1980) studied three crosses in chickpea and recorded transgressive segregants in all the crosses for nine characters. In case of plant spread, the highest proportion of individuals (30.77%) transgressed the increasing parent. He observed transgressive segregants in respect of days to flowering, pod number, fruiting branches, seed yield per plant, seeds per pod, 100-seed weight and plant height in descending order.

Jaiswal and Singh (1986) observed large variation in F_2 generation of four crosses for yield and yield contributing characters. They observed segregants for yield per plant, pods per plant, plant height, branching and 100-seed weight. Further they believed the possibilities of introgressing desirable genes from *C. reticulatum* into cultivated chickpea.

Reddy and Singh (1989) obtained superior transgressive segregants in the B_1F_2 population for all the important character *viz*., pods per plant, pods per cluster, seed weight and yield per plant. This reveals the introgression of wild germplasm created large amount of genetic variability and ultimately the frequency of transgressive segregants for yield increased. These results suggested that only one backcross with the recurrent parent may be enough to achieve higher proportion of transgressive segregation in the wide crosses of blackgram.

Reddy and Singh (1990) reported that high mean and large variance where exhibited in the F_2 generation of T 44 x PLN 15 for yield per plant and pod per plant, in ML 5 x LM 293 (B_1F_2) for pod per plant and in T 44 x ML 5 (F_2) for days to first flowering. The F_2 generation of T 44 x PLN 15 showed transgression for seeds per pod, yield per plant and pods per plant. ML 5 x LM 293 (F_2) and T44 x ML 5 (B_2F_2) expressed significantly higher transgressives for days to first flower and seed weight, respectively.

Singh and Singh (1996) affected interspecific hybrid involving four genotypes of mungbean (*Vigna radiata* L.) as female and three genotypes of urdbean (*Vigna mungo* L.) as male parent. They reported that genotypes influenced cross ability, germination, survival and fertility of F_1s. The crossed seeds were shriveled and the F1s were partially fertile, late maturing and intermediate in morphology. Purple colour of stem was dominant over green color. Only 2 out of 6 hybrids, namely, BHUM 1 x Pant U30 and T44 x T9 resulted in fertile F_1s which reached maturity. Fertility of the progenies improved from F_2 to F_4 generations. Desirable transgressive segregates in case of plant height, numbers of branches per plant, pods per plant, pod length, seeds per pod, yield per plant observed in the advanced generations, open up new avenues for amelioration of these crops.

Mitra and Mehra (1998) advanced F_2 generation of two crosses of grasspea by single seed descent, random bulk and pedigree method of breeding and observed transgressants in F_5 generation. They observed transgressive segregants for pods per plant, seeds per pod, 100-seed weight and yield per plant, more or less by all three methods.

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

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

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 X 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 longbean [*Vigna sesquipedalis* (L.) Fruw]. Trends were different for different crosses. In cross 1, high mean variance and significant transgressive segregation (STS) pattern were 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 STS 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 was exhibited high mean and STS in the BC_2F_1 generation. Pod length, in general did not show good transgressive segregation in the crosses.

Kotzamanidis (2006) studied the thirteen successful crosses in peanut (*Arachis hypogaea* L.) in 1985 belong to the crossing schemes: Virginia x Spanish, Virginia x Valencia, Valencia x Virginia, Virginia x Virginia, Valencia x Valencia, Valencia x Spanish and seven successful crosses in 1986 belong to two crossing scheme : Virginia x Valencia, Virginia x Virginia. Transgressive segregation for yield characters of 100-pod weight and 100-seed weight was studied. Pedigree selection was applied from the 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 x Spanish. Yield and quality of peanut could be improved by exploiting the phenomenon of transgressive variation occurring in cross between Virginia x Spanish.

Dhole and Reddy (2011) reported that total of eight transgressive segregants (2.56%) was recorded in the cross- I of mungbean, 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 F2 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. Transgressive segregants were also reported in mungbean for various characters (Kataraki and Kajjidoni, 2006 and Sarwar *et al.* 2004). Changes in mean value were closely followed by alteration in variances.

Kshirsagar *et al.* (2013) reported transgressive segregation for plant height, days to first flowering, yield per plant and harvesting duration in F_3 generation of two intervarietal crosses of tomato.

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.

Shashikumar *et al.* (2016) observed transgressive segregants for pod yield per plant in the cross KCG-6 x ICGV-9114 cross of groundnut.

Showkath *et al.* (2016) evaluated F_3 population of HA 10-8 x RIL 180 and FPB 21 x RIL 180 and 25 transgressive segregants in FPB 21 x RIL 180 for number of pods per plant.

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 in seeds per plant, number of pods per plant, biological yield and seed yield.

Chapter – III

Material and Methods

Chapter III

MATERIAL AND METHODS

The details of the material utilized, methodologies adopted and statistical analysis followed in the present investigation to fulfil the desired objectives are briefly presented in this chapter under the following headings.

3.1 LOCATION OF THE EXPERIMENTAL SITE

The present investigation entitled "**Genetic analysis of grain yield and physiological attributes in F_3 generation of blackgram [*Vigna mungo* (L.) Hepper.]**" was carried out during *Kharif*, 2018 at dry land farm of Sri Venkateswara Agricultural College, Tirupati situated at an altitude of 182.9 m above mean sea level, 13°N latitude and 79°E longitude in accordance with the objectives.

3.1.1 Environmental Conditions

The weather conditions were moderate during the crop period. The rainfall received from crop seedling to harvesting stage was sufficient for the crop growth. Weekly mean data of meterological parameters during the crop growth period is presented in Table 3.1 and Fig. 3.1.

3.2 MATERIALS

The experimental material consisted of three F_3 populations generated from LBG-787 x LBG-752, TU-94-02 x LBG-752 and TU-94-02 x KU-1006 along with their parents. The F_3 population in each cross was derived from raising seeds obtained from single plants in F_2 population selected based on high mean performance for seed yield per plant. The parents and F_3 material were made available by the Department of Genetics and Plant Breeding, S. V. Agricultural College, Tirupati.

Table 3.2 Weekly mean meteorological data during the period of crop growth

Standard week	Date	Temperature (^{0}C)				Mean relative humidity (RH %)		Rain fall (mm)		No. of rainy days	
	From To	Max		Min							
		A	DN	A	DN	A	DN	A	DN	A	DN
31	29 July - 04 Aug.	37.2	2.47	28.0	2.2	50.1	-7.6	0.0	-7.44	0	-0.8
32	05 Aug. - 11 Aug.	35.7	0.4	26.0	0.41	57.7	0.16	10.6	-13.69	2	0.5
33	12 Aug. - 18 Aug.	32.0	-1.94	25.0	0.45	62.7	-1.28	14	-35.17	2	-1.1
34	19 Aug. - 25 Aug.	35.8	2.03	27.1	2.39	51.0	-14.43	0.0	-52.67	0	-2.5
35	26 Aug. - 01 Sep.	35.8	2.15	24.9	0.55	59.5	-5.8	44.6	9.95	2	0.2
36	02 Sep. - 08 Sep.	36.2	2.83	25.5	1.23	55.2	-9.16	12.0	-27.66	1	-0.8
37	09 Sep. - 15 Sep.	35.2	1.92	25.3	1.02	67.6	1.16	56.8	30.62	3	1.4
38	16 Sep. - 22 Sep.	32.0	-1.9	22.8	-1.75	73.0	9.06	96.6	69.8	4	2.3
39	23 Sep. - 29 Sep.	34.8	0.67	24.6	0.05	65.2	0.08	4.0	-21.09	1	-0.2
40	30 Sep. - 06 Oct.	32.0	-1.26	24.5	0.77	73.6	7.29	16.4	-28.44	2	-0.2
41	07 Oct. – 13 Oct	35.1	1.59	22.2	-1.05	64.3	5.49	3.60	-25.62	1	-0.8
42	14 Oct. – 20 Oct.	33.3	0.17	23.2	0.70	72.2	1.20	73.6	48.13	2	0.4
43	21 Oct. – 27 Oct.	32.6	0.25	20.0	-1.91	65.5	-1.01	00.0	-31.19	0	-1.7
44	28 Oct. – 03 Nov.	32.3	1.49	22.7	0.91	69.3	4.20	14.0	-38.68	1	-2.0

A: Actual **DN**: Deviation from decimal mean

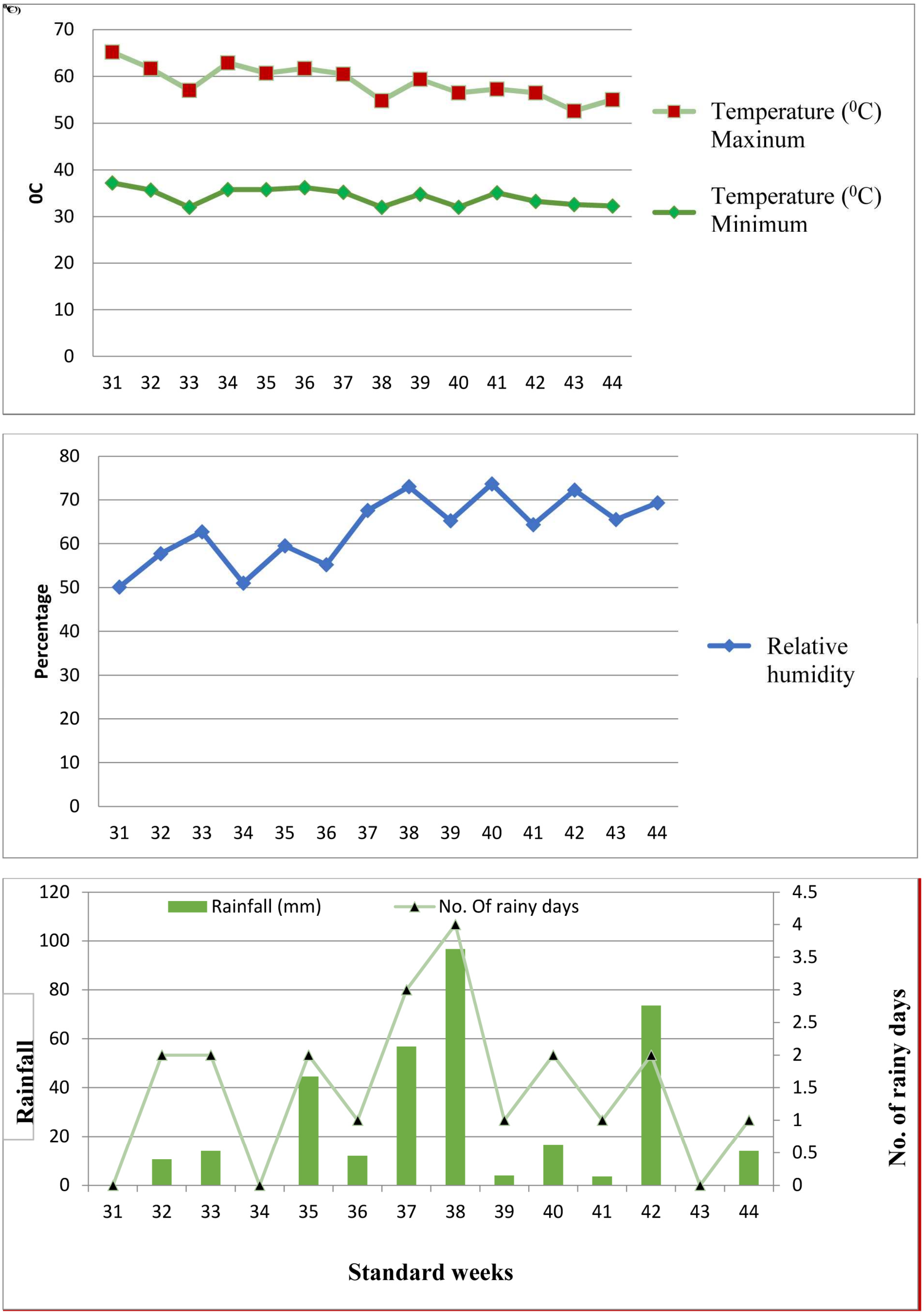

Fig. 3.1 Standard week wise meteorological data during the crop period

Parents – 1. LBG-787
2. TU-94-02
3. LBG-752
4. KU-1006

Crosses – 1. LBG-787 x LBG-752
2. TU-94-02 x KU-1006
3. TU-94-02 x LBG-752

The characteristics of the four parental genotypes were presented in Table 3.1 and they are shown in Plate 3.2.

Table 3.1 Important characteristics of parental genotypes:

S. No.	Genotype	Characteristics
1	LBG-787	It yields up to 13-14 q ha^{-1}. It comes to maturity within 70-75 DAS. It is resistant to powdery mildew.
2	TU-94-02	It yields up to 15 q ha^{-1}. It comes to maturity within 70 DAS. It is high yielding and resistant to Yellow Vein Mosaic Virus. It is mostly suitable for rabi season.
3	LBG-752	It yields up to 18-20 q ha^{-1}. It comes to maturity within 75-80 DAS. It is photo insensitive and resistant to Yellow Vein Mosaic Virus.
4	KU-1006	It yields up to 12-13 q ha^{-1}. It comes to maturity within 75-80 DAS. It is suitable for both kharif and rabi season.

Plate 3.1 Overall view of experimental field layout

LBG-787

TU-94-02

LBG-752

KU-1006

Plate 3.2 Parental genotypes

3.3 METHODS

3.3.1 Field Layout

Three F_3 populations along with their parents were grown during *Kharif*, 2018 in a Compact Family Block Design with four replications. The crop was sown on 30th July, 2018. Each family consisted of 10 progenies and 2 parents of respective cross. The families were randomly allotted in each replication and the progenies were randomly allotted within each family. In each replication, every progeny was sown in two rows of 3 m length with a spacing of 30 cm between the rows and 10 cm between the plants within the row. To eliminate border effect, on either side of the plot, border rows were planted. Thinning was done to have single seedling per hill. The overall view of the experimental field was presented in Plate 3.1.

3.3.2 Crop Husbandry

Recommended dose of chemical fertilizers (20 kg N, 50 kg P_2O_5 per hectare) were broadcasted in the form of urea and single super phosphate before sowing. For the control of sucking pests, Monocrotophos @ 1.6 ml l^{-1} and Imidacloprid @ 0.3 ml l^{-1}were applied at 15 and 35 DAS respectively. For the control of leaf eating and pod boring caterpillars, Larvin @ 1g l^{-1} and Spinosad @ 0.3 ml l^{-1} was sprayed at 45 and 60 DAS.

Cultural practices like weeding and irrigation were followed regularly to maintain good crop growth.

3.3.3 Data Recording

Morphological Attributes: Observations were recorded for the following morphological characters on randomly selected 20 plants in each entry (parent or progeny) in each replication. In total data is collected from 800 F_3 plants and 20 plants of each parental genotype.

3.3.3.1 Days to 50 % flowering: Number of days taken from the date of sowing to the date on which the plants attained 50% of the flowering was recorded.

3.3.3.2 Days to maturity: It was recorded by counting the number of days taken from the date of sowing to the date on which 75% of the pods attained physiological maturity.

3.3.3.3 Plant height (cm): Plant height was measured in centimetres using a scale as the vertical distance of the main axis from ground level to the tip of main raceme at maturity.

3.3.3.4 Number of branches per plant: Total number of branches originating from the main axis were counted at harvest and recorded.

3.3.3.5 Number of clusters per plant: The number of pod bearing clusters were counted at maturity stage on each randomly selected plants.

3.3.3.6 Number of pods per cluster: The number of pods in each cluster was counted and the average was calculated.

3.3.3.7 Number of pods per plant: Number of pods in each sample plant was counted at harvest stage.

3.3.3.8 Pod length (cm): The length of the pod was measured from the base to the tip of the pod on five randomly selected pods from each plant at harvest. The mean value of the sample was recorded as the length of pod in centimetres.

3.3.3.9 Number of seeds per pod: The seeds from five randomly selected pods of each sample plant were counted and averaged to obtain the number of seeds per pod.

3.3.3.10 Hundred seed weight (g): One hundred seeds from each sample plant were counted and weighed on an electronic balance and expressed in grams.

3.3.3.11 Seed yield per plant (g): The pods collected from each sample plants were threshed separately, cleaned, weighed and mean seed yield per plant was expressed in grams.

Physiological attributes: Observations were recorded on 10 randomly selected plants in each entry (parent or progeny) in each replication at 30 and 45 days after sowing (DAS). In total data is collected from 800 F_3 plants and 20 plants of each parental genotype.

3.3.3.12 Specific leaf area (SLA) (cm^2 g^{-1}): Leaf area readings were taken for estimating Specific Leaf Area using leaf area meter (LICOR model -3100). The leaves were cleaned and leaf area is estimated. They are then dried in hot air oven at 80°C for 48 h and dry weight was recorded. Third leaf from the apex of each sampled plant was used to estimate SLA.

$$\text{SLA} = \frac{\text{Leaf area (cm}^2\text{)}}{\text{Leaf dry weight (g)}}$$

3.3.3.13 Specific Leaf Weight (SLW) (g cm^{-2}):

Leaf area readings were taken for estimating Specific Leaf Weight using leaf area meter (LICOR model -3100). The leaves were cleaned and leaf area is estimated. They are then dried in hot air oven at 80°C for 48 h and dry weight was recorded. Third leaf from the apex of each sampled plant was used to estimate SLW.

$$\text{SLW} = \frac{\text{Leaf dry weight (mg)}}{\text{Leaf area (cm2)}}$$

3.3.3.14 SPAD chlorophyll meter reading (SCMR): Since blackgram has trifoliate leaf, SCMR was recorded in all the three leaflets of the third leaf from the apex of each sample plant and the average of it is recorded. SCMR was measured using Minolta SPAD-502 chlorophyll meter.

3.3.3.15 Biomass per plant (g): The mean dry weight of the sample plants was expressed as biomass per plant.

3.3.3.16 Harvest Index (HI) (%): Harvest Index was estimated after harvest using the formula:

$$\mathrm{HI} = \frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

3.4 STATISTICAL ANALYSIS

The data recorded for various characters from each sample plant in parents and F_3 population were subjected to the following statistical analysis.

1. Analysis of variance (Chandel, 1964).
2. Coefficients of variation: PCV and GCV (Burton, 1952).
3. Heritability in broad sense (Allard, 1960).
4. Genetic advance (Johnson *et al.*, 1955a).
5. Character association (Johnson *et al.*, 1955b).
6. Path coefficient analysis (Dewey and Lu, 1959).

3.4.1 Analysis of Variance

The mean values for each character recorded in each progeny lines of three crosses in F_3 generation were subjected to the analysis of variance for Compact Family Block Design, as described by Chandel (1964). The analysis was carried out in two stages.

(a) First from the data of main plots, the variance between crosses and the corresponding pooled error were calculated by treating the experiment as one in simple randomized blocks. The structure of ANOVA for families is given below:

Source	**Degrees of freedom**	**Mean Squares**	**Expected mean squares**
Replications	(r-1)	M_1	$\sigma^{2}{}_{e}{}^{1} + \sigma^{2}{}_{r}$
Families	(f-1)	M_2	$\sigma^{2}{}_{e}{}^{1} + \sigma^{2}{}_{f}$
Error	(r-1) (f-1)	M_3	$\sigma^{2}{}_{e}{}^{1}$

Where,

r = Number of replications

f = Number of families

p = Number of progenies within each family

M_1 = Mean sum of squares due to replications

M_2 = Mean sum of squares due to families

M_3 = Mean sum of squares due to main plot error

$\sigma^{2}{}_{e}{}^{1}$ = Error variance for families

$\sigma^{2}{}_{r}$ = Variance between replications

$\sigma^{2}{}_{f}$ = Variance between families

(b) The analysis for the progenies under each family was done separately for each character using the data of sub plots to give the variance between different selection procedures and corresponding error. The structure of ANOVA for progenies within family is given below:

Source	**Degrees of freedom**	**Mean Squares**	**Expected mean squares**
Replications	(r-1)	M_4	$\sigma^{2}{}_{e}{}^{2} + p\,\sigma^{2}{}_{r}$
Progenies within families	(p-1)	M_5	$\sigma^{2}{}_{e}{}^{2} + r\,\sigma^{2}{}_{p}$
Error	(r-1) (p-1)	M_6	$\sigma^{2}{}_{e}{}^{2}$

Where,

r = Number of replications

f = Number of families

p = Number of progenies within each family

M_4 = Mean sum of squares due to replications

M_5 = Mean sum of squares due to progenies within families

M_6 = Mean sum of squares due to error

σ^2_{e1} = Error variance for families

σ^2_{e2} = Error variance for progenies

σ^2_r = Variance between replications

σ^2_p = Progeny variance within family

Before making comparison, a test of homogeneity of error variance was carried out for each character by applying Bartlett's test of homogeneity (Bartlett, 1964).

Bartlett's test is calculated by the following procedure,

In the first step, the pooled variance is calculated using the formula,

$$S_p^2 = \sum \frac{(n_i - 1)s_i^2}{N - a}$$

Where,

s_p^2 = pooled variance

n_i = number of samples for the ith treatment

s_i^2 = variance of the ith treatment

N = total number of samples

A = total number of treatments

Using the pooled variance, the ‘q’ value is calculated with the help of the following formula,

$$q = (N - a)\log S_p^2 - \sum (n_i - 1)\log(s_i^2)$$

With the help of ‘q’ value, ‘c’ value is calculated by inserting q value in the following formula,

$$c = 1 + \frac{1}{3(a-1)}\left(\sum(n_i - 1)^{-1} - (N - a)^{-1}\right)$$

By using ‘c’ value, bartlett test statistic is calculated using the formula,

$$\chi_0^2 = 2.3026\frac{q}{c}$$

After calculating the Bartlett test statistic, it is compared with the critical value of χ^2 at required degrees of freedom. If the Bartlett test statistic is greater than this critical value, there is a significant difference in the variances. If the Bartlett test statistic is less than this critical value, there is no significant difference in the variances.

From the above ANOVA tables, following statistics were computed

(1) Standard error of mean (S.E$_m$) = $\sqrt{M_6/r}$

(2) Critical difference (C.D.) = S.E$_m$ x $\sqrt{2}$ x t (0.05) at error degree of freedom

(3) Coefficient of variation (C.V.) % = $\frac{\sqrt{\frac{M_6}{r}}\times 100}{\text{Mean of progenies}}$

3.4.2 Estimation of Genetic Parameters

The estimates of mean sum of squares from the above ANOVA were utilized for calculation of following parameters.

3.4.2.1 Variance

The genotypic and phenotypic variances were calculated as per the formulae proposed by Burton (1952).

Phenotypic variance of F$_3$ population = (σ_p^2)

$$\text{Environmental variance } (\sigma^2_e) = \frac{\text{Varianceof parent1} + \text{Varianceof parent2}}{2}$$

$$\text{Genotypic variance } (\sigma^2_g) = \sigma^2_p - \sigma^2_e$$

3.4.2.2 Genotypic and phenotypic coefficient of variation

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by the formulae given by Burton (1952).

$$\text{(i) GCV (\%)} = \frac{\sigma_g}{\overline{X}} \text{ x } 100$$

$$\text{(ii) PCV (\%)} = \frac{\sigma_p}{\overline{X}} \text{ x } 100$$

Where, σ_g, σ_p and $\overline{X}$ were genotypic standard deviation, phenotypic standard deviation and general mean of the character respectively.

Categorization of the range of variation was done as proposed by Sivasubramanian and Madhava menon (1973)

Less than 10%	-	Low
10 – 20 %	-	Moderate
More than 20%	-	High

3.4.2.3 Broad sense heritability

Heritability in broad sense refers to the proportion of genotypic variance to the total variance of the population. Heritability in broad sense [$h^2_{(b)}$] was calculated by the formula given by Lush (1940).

$$\text{Broad sense Heritability} = \frac{\sigma^2_g}{\sigma^2_p} \text{ x } 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

As suggested by Johnson *et al.* (1955), heritability estimates were categorized as

Less than 30%	-	Low
30 – 60 %	-	Moderate
More than 60%	-	High

3.4.2.4 Genetic advance

Genetic advance refers to the expected genetic gain in the next generation by selecting the superior individuals under certain amount of selection pressure. From the heritability estimates, the genetic advance was estimated by following the formula given by Johnson *et al.* (1955a).

$$GA = k\,\sigma_p\,H$$

Where,

GA = Genetic advance

σ_p = Phenotypic standard deviation

H = Heritability (broad sense)

k = Selection differential at 5% selection intensity

3.4.2.5 Genetic advance as per cent of mean (GA as per cent mean)

Genetic advance as per cent of mean was calculated as per the formula.

$$\text{GA as percent of mean} = \frac{GA}{\overline{X}} \times 100$$

Where,

GA = Genetic advance

$\overline{X}$ = Grand mean of the character

The range of genetic advance as percent of mean was classified as suggested by Johnson *et al.* (1955).

Less than 10%	-	Low
10 – 20 %	-	Moderate
More than 20%	-	High

3.4.3 Character Association Analysis

Genotypic and phenotypic correlation coefficients were calculated using the method given by Johnson *et al.* (1955b).

3.4.3.1 Genotypic correlation coefficient (r_g)

$$r_g\,(x_ix_j) = \frac{CoV_g\ (x_ix_j)}{\sqrt{V_g(x_i)\,V_g(x_j)}}$$

Where,

$r_g\,(x_ix_j)$ = Genotypic correlation between 'ith' and 'jth' characters

$V_g\,(x_i)$ = Genotypic variance of ith character

$V_g\,(x_j)$ = Genotypic variance of jth character

$Cov_{(g)}\,(x_ix_j)$= Genotypic covariance between ith and jth characters.

3.4.3.2 Phenotypic correlation coefficient (r_p)

$$r_p\,(x_ix_j) = \frac{CoV_p\ (x_ix_j)}{\sqrt{V_p(x_i).V_p(x_j)}}$$

Where,

$V_p\,(x_i)$ = Phenotypic variance of 'ith' character

$V_p\,(x_j)$ = Phenotypic variance of 'jth' character

$Cov\,(x_ix_j)$= Phenotypic covariance between 'ith' and 'jth' characters.

The significance of correlation coefficients was tested by comparing the genotypic and phenotypic correlation coefficients with table value [Fisher and Yates (1963)] at (n-2) degrees of freedom at 5% and 1% level where, 'n' denotes the number of treatments used in the calculations.

3.4.4 Path Coefficient Analysis

Path coefficient analysis was carried out by the procedure originally proposed by Wright (1921) which was subsequently elaborated by Dewey and

Lu (1959) to estimate the direct and indirect effects of the individual characters on yield.

The following set of simultaneous equations were formulated and solved for estimating various direct and indirect effects.

$$
\begin{array}{ll}
r_{1y} = & p_{1y} + r_{12}p_{2y} + r_{13}p_{3y} + \ldots\ldots\ldots\ldots\ldots + r_{1i}p_{iy} \\
r_{2y} = & r_{21}p_{1y} + p_{2y} + r_{23}p_{3y} + \ldots\ldots\ldots\ldots\ldots + r_{2i}p_{iy} \\
. & . \quad . \quad . \quad . \\
. & . \quad . \quad . \quad . \\
. & . \quad . \quad . \quad . \\
r_{iy} = & r_{i1}p_{1y} + r_{i2}p_{2y} + r_{i3}p_{3y} + \ldots\ldots\ldots\ldots\ldots + p_{iy}
\end{array}
$$

Where,

r_{12} to r_{i-1} = Coefficient of correlation among causal factors.

p_{1y} to p_{iy} = Direct effects of characters '1' to i on character 'y'.

The above equations were written in matrix forms as under:

$$
\begin{array}{ccccc}
A & & C & & B \\
\begin{pmatrix} r_{1y} \\ r_{2y} \\ r_{3y} \\ . \\ . \\ . \\ . \\ . \\ r_{iy} \end{pmatrix}
& = &
\begin{pmatrix}
1 & r_{12} & r_{13} \ldots\ldots\ldots\ldots & r_{1i} \\
r_{21} & 1 & r_{23} \ldots\ldots\ldots\ldots & r_{2i} \\
r_{31} & r_{32} & 1 \ldots\ldots\ldots\ldots & r_{3i} \\
. & . & . & . \\
. & . & . & . \\
. & . & . & . \\
. & . & . & . \\
. & . & . & . \\
r_{i1} & r_{i2} & r_{i3} \ldots\ldots\ldots & 1
\end{pmatrix}
& &
\begin{pmatrix} p_{1y} \\ p_{2y} \\ p_{3y} \\ . \\ . \\ . \\ . \\ . \\ p_{iy} \end{pmatrix}
\end{array}
$$

Then $B = [C]^{-1}A$

Where,

$$[C]^{-1} = \begin{pmatrix} C_{11} & C_{12} & C_{13} \ldots\ldots\ldots\ldots & C_{1i} \\ C_{21} & C_{22} & C_{23} \ldots\ldots\ldots\ldots & C_{2i} \\ . & . & . & . \\ . & . & . & . \\ . & . & . & . \\ C_{i1} & C_{i2} & C_{i3} \ldots\ldots\ldots\ldots & C_{ii} \end{pmatrix}$$

Then, direct effects were calculated as follows:

$$P_{1y} = \sum_{i=1}^{I} C_{1i}\, r_{1y}$$

$$P_{2y} = \sum_{i=1}^{I} C_{2i}\, r_{2y}$$

$$P_{iy} = \sum_{i=1}^{I} C_{ii}\, r_{iy}$$

Besides the direct and indirect effects, the residual effect which measures the contribution of the characters not considered in the causal scheme was obtained as:

$$\text{Residual effect } (P_{RY}) = \sqrt{1 - [P_{1y}r_{1y} + p_{2y}r_{2y} + \ldots\ldots\ldots\ldots + p_{iy}r_{iy}]^2}$$

Where,

P_{RY} = Residual effect

p_{iy} = Direct effect of ‘x_i’ on ‘y’

r_{iy} = Correlation coefficient of ‘x_i’ with ‘y’.

The scales for path coefficients as proposed by Lenka and Mishra (1973) are as follows:

Value for direct or indirect effect	**Rate or Scale**
0.00-0.09	Negligible
0.10-0.19	Low
0.20-0.29	Moderate
0.30-0.99	High
More than 1.00	Very high

3.4.5 Transgressive Segregation:

In the present study, transgressive segregants were identified by finding the number of plants exceeding the mean value of higher parent or lagging behind the mean value of lower parent by critical difference at 5 per cent level. The data recorded on 800 plants (80 plants from each progeny) from each cross was used for calculating the number of transgressive segregants.

Chapter – IV

Results and Discussion

Chapter IV

RESULTS AND DISCUSSION

The experimental results obtained from the present investigation on "Genetic analysis of grain yield and physiological attributes in F_3 generation of blackgram [*Vigna mungo* (L.) Hepper]" are presented under the following sub headings.

4.1 Analysis of variance

4.2 Mean performance of progenies

4.3 Variability, Heritability and Genetic advance as per cent of mean

4.4 Character association analysis

4.5 Path coefficient analysis

4.6 Transgressive segregants

4.1 ANALYSIS OF VARIANCE

The analysis of variance was performed for each character separately and total variation was partitioned into different sources of variation. The results are presented in Table 4.1 and Table 4.2. The analysis of variance between families revealed that the mean sum of squares due to crosses were significant for all the 19 characters studied. The Bartlett's test for homogeneity of error variances for the three crosses indicated that the error variances were homogeneous for all the characters except for number of clusters per plant, number of pods per plant, test weight, Specific Leaf Area (30 DAS), Specific Leaf Area (45 DAS), Specific Leaf Weight (30 DAS) and Specific Leaf Weight (45 DAS).

The analysis of variance between the progenies within each family indicated significant differences between progeny means for all the characters studied in cross LBG-787 x LBG - 752 , except for test weight in cross

Table 4.1 Analysis of variance (mean squares) between families and between progenies within families of three crosses for different grain yield contributing attributes in blackgram

Source of variation	Degrees of freedom	DF	DM	PH	NB	NCP	NPC	NPP	PL	NSP	SY	TW
Analysis of variance between families												
Replications	3	0.10	0.13	5.83*	0.07**	3.93*	0.03	12.6*	0.05**	0.06*	0.78**	0.011
Crosses	2	5.52**	2.66**	51.27**	0.67**	22.67**	0.21**	55.06**	0.12**	0.67**	14.12**	0.11**
Error	6	0.05	0.08	0.90	0.01	0.43	0.01	2.25	0.01	0.01	0.07	0.01
Bartlett's test		NS	NS	NS	NS	S	NS	S	NS	NS	NS	S
Analysis of variance between progenies of different families												
LBG-752 x LBG-787												
Replications	3	0.52	3.02*	63.67**	0.37	34.55**	0.36**	134.39**	0.15	0.07	5.04	0.01**
Progenies	11	11.47**	7.52**	414.58**	2.57**	193.64**	2.32**	796.33**	1.77**	1.90**	43.65**	0.27**
Error	33	0.27	0.79	12.7	0.15	6.19	0.07	25.75	0.03	0.03	2.02	0.01
Bartlett's test		NS	NS	NS	NS	S	NS	S	NS	NS	NS	NS
TU-94-02 x KU-1006												
Replications	3	2.02*	0.29	7.87	0.08	6.92	0.02	21.46*	0.30	0.26	1.04	0.04
Progenies	11	5.27**	9.88**	236.35**	1.87**	121.58**	0.90**	429.06**	1.27**	1.29**	26.79**	0.13
Error	33	0.55	1.91	6.05	0.07	3.81	0.03	7.05	0.22	0.19	0.73	0.05
Bartlett's test		NS	NS	NS	NS	NS	S	S	NS	NS	NS	NS
TU-94-02 x LBG-752												
Replications	3	0.16	0.13	20.18	0.55	1619	0.12	49.33	0.35	0.64	5.18	0.12
Progenies	11	23.81**	15.65**	146.84**	2.21**	63.64*	0.67**	136.75*	1.56**	1.51*	27.72**	0.40**
Error	33	0.22	0.46	30.88	0.56	23.59	0.20	52.54	16.18	0.69	6.36	0.08
Bartlett's test		NS	NS	NS	NS	S	NS	S	NS	NS	NS	NS

*** - Significant at 5 % level; ** - Significant at 1% level** **S - significant; NS - non significant**

DF - Days to 50% flowering
NB - No. of branches
NPP - Number of pods per plant
TW - Test weight (g)
DM - Days to maturity
NCP - No. of clusters per plant
PL - Pod length (cm)
SY - Seed yield per plant (g)
PH - Plant height (cm)
NPC - No. pods per cluster
NSP - No. seeds per pod

Table 4.2 Analysis of variance (mean squares) between families and between progenies within families of three crosses for different physiological attributes in blackgram

Source of variation	Degrees of freedom	SLA (30 DAS)	SLA (45 DAS)	SLW (30 DAS)	SLW (45 DAS)	SCMR (30DAS)	SCMR (45DAS)	BMP	HI
Analysis of variance between families									
Replications	3	0.98	5.90	0.03	0.09*	1.10	0.14	2.64**	1.69
Crosses	2	8166.77**	6927.16**	4.57**	0.32**	215.33**	55.28**	56.41**	35.98**
Error	6	2.01	1.45	0.01	0.01	0.44	0.16	0.06	1.13
Bartlett’s test		S	S	S	S	NS	NS	NS	NS
Analysis of variance between progenies of different families									
LBG-752 x LBG-787									
Replications	3	54.79	58.87	0.04**	0.1	0.68	0.38	9.36*	7.51
Progenies	11	10395.31**	6006.06**	1.36**	2.39**	27.40**	16.22**	66.06**	129.18**
Error	33	26.30	53.28	0.02	0.06	2.23	0.19	3.16	14.47
Bartlett’s test		S	NS	S	NS	NS	NS	NS	NS
TU-94-02 x KU-1006									
Replications	3	1.30	15.22	0.02	0.01	0.7	1.11	10.02	18.85
Progenies	11	187.7**	411.75**	0.61**	0.32**	40.48**	24.01**	135.13**	262.81**
Error	33	12.8	10.20	0.01	0.01	1.26	0.76	5.4	21.41
Bartlett’s test		S	NS	S	NS	NS	NS	NS	NS
TU-94-02 x LBG-752									
Replications	3	4.14	31.72	0.01	0.01	22.65	4.27	13.84	21.33
Progenies	11	324.65**	5894.23**	0.10**	0.03	104.36**	18.21**	57.37*	97.95*
Error	33	12.85	509.08	0.01	0.01	21.88	5.21	22.86	37.90
Bartlett’s test		S	NS	S	NS	NS	NS	NS	NS

*** significant at 5% probability level ; ** significant at 1% probability level** **S - significant; NS - non significant**

SLA (30 DAS) - Specific Leaf Area at 30 DAS (cm^2 g^{-1})
SLW (30 DAS) - Specific Leaf Weight at 30 DAS (g cm^{-2})
SCMR (30DAS) - SPAD Chlorophyll Meter Reading at 30 DAS
BMP - Biomass per plant (g)
SLA (45 DAS) - Specific Leaf Area at 45 DAS (cm^2 g^{-1})
SLW (45DAS) - Specific Leaf Weight at 45 DAS (g cm^{-2})
SCMR (45DAS) - SPAD Chlorophyll Meter Reading at 30 DAS
HI - Harvest Index (%)

TU-94-02 x KU-1006 and for Specific Leaf Weight in cross TU-94-02 x LBG-752. The Bartlett's test for homogeneity of error variances for the progenies within each cross indicated that the error variances were homogeneous for all the characters except for number of clusters per plant, number of pods per plant Specific Leaf Area (30 DAS) and Specific Leaf Weight (30 DAS) in cross LBG-787 x LBG-752; number of pods per cluster, number of pods per plant, Specific Leaf Area (30 DAS) and Specific Leaf Weight (30 DAS) in cross TU-94-02 x KU-1006; number of clusters per plant, number of pods per plant Specific Leaf Area (30 DAS) and Specific Leaf Weight (30 DAS) in cross TU-94-02 x LBG-752.

4.2 MEAN PERFORMANCE OF PROGENIES

The mean performance of thirty F_3 progenies of three crosses along with their parents for seed yield and physiological characters are presented in Table 4.3 and Table 4.4 and are discussed here under:

4.2.1 Days to 50 % Flowering

In the cross LBG-787 x LBG-752, mean of the progenies for days to 50% flowering ranged from 36 days (progeny 1, 2, 4 and 5) to 38 days (progeny 7) whereas, in the cross TU-94-02 x KU-1006 and cross TU-94-02 x LBG-752, it varied between 34 days (progeny 19) and 38 days (progeny 12, 13 and17) and between 33 days (progeny 24) and 35 days (progeny 23, 28 and 30) respectively. Among the three crosses studied, TU-94-02 x LBG-752 has the lowest mean of 35 days and LBG-787 x LBG-752 has shown the highest mean of 37 days.

4.2.2 Days to Maturity

The general mean value for days to maturity ranged from 80 days (progeny 2) to 84 days (progeny 10), 78 days (progeny 15) to 83 days (progeny 14,18 and 20) and 80 days (progeny 21 and 24) to 86 days (progeny 23) in crosses LBG-787 x LBG-752 , TU-94-02 x KU-1006 and TU-94-02 x

LBG-752 respectively. The cross TU-94-02 x KU-1006 has the lowest mean of 81 days and TU-94-02 x LBG-752 has shown the highest mean of 83 days among the three crosses studied.

4.2.3 Plant Height (cm)

In cross LBG-787 x LBG-752, progeny 10 recorded low mean performance for plant height (17.60 cm) whereas, progeny 4 recorded high mean performance (53.41 cm) while in cross TU-94-02 x KU-1006, mean for plant height varied between 25.85 cm (progeny 19) and 52.06 cm (progeny 20). In cross TU-94-02 x LBG-752, it ranged from 23.09 cm (progeny 26) to 43.16 cm (progeny 23). The cross LBG-787 x LBG-752 recorded the lowest mean of 26.51 cm and cross TU-94-02 x KU-1006 has shown the highest mean of 33.41 cm among all the crosses studied.

4.2.4 Number of Branches per Plant

Progenies 10 and 4 showed low (1.90) and high (4.73) mean performance for number of branches per plant in cross LBG-787 x LBG-752. In cross TU-94-02 x KU-1006, the highest mean (4.68) was recorded by progeny 18 and 19 and the lowest mean (3.08) was recorded by progeny 20. In cross TU-94-02 x LBG-752, the mean value ranged between 2.59 (progeny 30) and 4.88 (progeny 23). Cross TU-94-02 x KU-1006 has shown the highest mean of 3.65 whereas cross LBG-787 x LBG-752 has registered the lowest mean of 2.87 for number of branches per plant.

4.2.5 Number of Clusters per Plant

Number of clusters per plant ranged from 12.23 (progeny 9) to 37.63 (progeny 4) in cross LBG-787 x LBG-752, whereas 19.38 (progeny 14) to 34.85 (progeny 17) in cross TU-94-02 x KU-1006 and from 19.50 (progeny 27) to 33.79 (progeny 24) in cross TU-94-02 x LBG-752. Crosses TU-94-02 x LBG-752 and LBG-787 x LBG-752 recorded the highest (23.29) and the lowest mean (18.86) respectively among the crosses studied.

Table 4.3 Mean performance of parents and progenies in F_3 population for different seed yield and its contributing attributes in blackgram

Parent/ Progeny	DF	DM	PH	NB	NCP	NPC	NPP	PL	NSP	SY	TW
LBG - 787 x LBG – 752											
Progeny 1	36	82	20.56	2.37	14.88	1.65	31.72	4.30	5.19	7.23	4.55
Progeny 2	36	80	26.00	2.86	17.76	2.00	37.48	4.50	5.45	8.58	4.62
Progeny 3	37	82	19.03	2.08	12.94	1.35	27.33	4.22	5.13	6.24	4.48
Progeny 4	36	81	53.41	4.73	37.63	2.65	76.45	4.98	5.67	17.90	5.44
Progeny 5	36	81	26.60	2.92	17.93	2.01	38.27	4.47	5.53	8.72	4.61
Progeny 6	37	82	32.95	3.61	22.49	2.48	47.87	6.58	6.22	10.89	4.71
Progeny 7	38	83	34.95	3.72	24.16	4.15	51.65	4.98	5.71	11.68	4.75
Progeny 8	37	81	23.80	2.35	16.43	1.80	34.42	4.32	5.42	7.84	4.61
Progeny 9	37	82	19.48	2.42	12.23	1.49	29.22	4.19	5.20	6.54	4.49
Progeny 10	37	84	17.60	1.90	13.48	1.43	25.96	4.23	5.30	5.89	4.45
LBG – 787	39	79	17.83	2.69	16.45	1.87	30.73	4.75	7.02	8.07	4.80
LBG – 752	42	82	25.93	2.82	20.00	1.91	37.63	4.98	7.15	7.87	4.75
Mean	37	82	26.51	2.87	18.86	2.06	39.06	4.71	5.75	8.95	4.69
C.V.	1.41	1.09	13.45	13.74	13.19	12.98	12.99	3.80	3.15	15.90	1.10
S.E$_m$.	0.26	0.45	1.78	0.20	1.24	0.13	2.54	0.09	0.09	0.71	0.03
C.D. 5%	0.76	1.28	5.13	0.57	3.58	0.39	7.30	0.26	0.26	2.05	0.07
C.D. 1%	1.02	1.72	6.89	0.76	4.81	0.52	9.81	0.35	0.35	2.75	0.10
Range Lowest	36	79	17.60	1.90	12.23	1.35	25.96	4.19	5.13	5.89	4.45
Range Highest	42	84	53.41	4.73	37.63	4.15	76.45	6.58	7.15	17.90	5.44

Cont….

Table 4.3 Contd….

Parent/ Progeny	DF	DM	PH	NB	NCP	NPC	NPP	PL	NSP	SY	TW
TU-94-02 x KU-1006											
Progeny 11	37	81	28.95	3.41	22.23	2.40	46.11	5.04	5.78	9.64	4.78
Progeny 12	38	81	30.35	3.64	22.96	2.56	47.01	5.37	6.08	10.14	4.56
Progeny 13	38	82	31.40	3.76	24.11	2.60	49.26	5.40	6.24	10.39	4.76
Progeny 14	37	83	28.34	3.27	19.38	2.44	43.42	4.74	5.68	9.47	4.86
Progeny 15	35	78	31.44	3.70	23.73	2.64	48.76	5.24	5.73	10.43	4.82
Progeny 16	37	81	28.57	3.38	21.90	2.37	45.48	4.69	5.24	9.53	4.97
Progeny 17	38	82	37.51	4.25	34.85	3.09	57.69	5.85	6.87	12.48	4.99
Progeny 18	36	83	26.47	3.08	19.50	2.07	38.93	4.23	5.27	8.79	4.51
Progeny 19	34	82	25.85	3.08	21.60	2.16	39.57	4.12	5.16	8.61	5.09
Progeny 20	37	83	52.06	4.68	28.55	3.72	68.43	5.79	6.71	17.78	4.55
TU-94-02	36	81	41.80	4.93	20.53	2.03	41.52	4.83	6.52	9.95	4.68
KU-1006	35	79	38.24	2.58	11.68	2.22	25.94	4.51	5.89	7.84	4.63
Mean	36	81	33.41	3.65	22.58	2.52	46.01	4.98	5.93	10.42	4.76
C.V.	2.04	1.70	7.36	7.75	8.65	7.91	5.77	9.43	7.49	8.21	4.79
S.E$_m$.	0.37	0.69	1.23	0.14	0.98	0.10	1.33	0.23	0.22	0.43	0.11
C.D. 5%	1.07	1.99	3.54	0.41	2.81	0.29	3.82	0.68	0.64	1.23	0.33
C.D. 1%	1.43	2.68	4.76	0.55	3.78	0.39	5.13	0.91	0.86	1.65	0.44
Range Lowest	34	78	25.85	2.58	11.68	2.03	25.94	4.12	5.16	7.84	4.51
Range Highest	38	83	52.06	4.93	34.85	3.72	68.43	5.85	6.87	17.78	5.09

Cont….

Table 4.3 contd….

Parent/ Progeny	DF	DM	PH	NB	NCP	NPC	NPP	PL	NSP	SY	TW
TU-94-02 x LBG-752											
Progeny 21	34	80	33.64	3.59	25.55	2.52	44.37	5.44	6.83	13.96	4.94
Progeny 22	34	83	30.45	3.35	22.60	2.29	39.54	5.16	6.27	13.18	4.79
Progeny 23	35	86	43.16	4.88	27.07	3.26	54.80	5.52	7.08	18.27	5.11
Progeny 24	33	80	35.53	3.97	33.79	2.65	45.64	6.60	7.96	15.21	4.63
Progeny 25	34	84	30.01	3.42	23.09	2.28	40.22	5.02	6.36	13.41	4.76
Progeny 26	34	83	23.09	2.95	21.56	1.78	36.42	4.17	5.76	10.64	5.37
Progeny 27	34	85	27.85	3.04	19.50	2.08	31.91	4.55	6.11	12.14	5.48
Progeny 28	35	85	30.28	3.19	22.60	2.25	37.85	4.86	6.30	12.62	4.99
Progeny 29	34	83	30.53	3.36	22.66	2.24	39.63	4.82	6.28	13.21	4.57
Progeny 30	35	85	27.04	2.59	19.59	1.96	35.45	4.46	5.85	11.82	4.96
LBG-752	36	82	41.91	4.83	20.39	1.93	41.20	4.81	6.56	9.90	4.64
TU-94-02	42	81	25.80	2.93	20.13	1.84	37.40	4.79	6.94	7.88	4.80
Mean	35	83	31.61	3.51	23.29	2.25	40.28	5.03	6.53	12.68	5.01
C.V.	1.36	0.82	17.58	21.41	20.85	20.04	17.99	13.92	12.77	19.89	5.66
S.E$_m$	0.24	0.34	2.78	0.38	2.43	0.23	3.62	0.35	0.42	1.26	0.14
C.D. 5%	0.69	0.98	7.99	1.08	6.99	0.65	10.43	1.01	1.20	3.63	0.41
C.D. 1%	0.92	1.32	10.74	1.45	9.39	0.87	14.01	1.35	1.61	4.88	0.55
Range Lowest	33	80	23.09	2.59	19.50	1.78	31.91	4.17	5.76	7.88	4.57
Range Highest	42	86	43.16	4.88	33.79	3.26	54.80	6.60	7.96	18.27	5.48

Cont….

Table 4.3 Contd….

Overall mean performance of three F_3 crosses i.e., LBG - 787 x LBG – 752, TU-94-02 x KU-1006 and TU-94-02 x LBG-752

	DF	**DM**	**PH**	**NB**	**NCP**	**NPC**	**NPP**	**PL**	**NSP**	**SY**	**TW**
Mean	36.20	81.92	30.51	3.34	21.58	2.28	41.78	4.91	6.07	10.68	4.82
C.V.	1.74	1.25	13.83	15.76	16.00	14.65	13.39	10.31	9.29	16.64	4.39
$S.E_m$	0.31	0.51	2.11	0.26	1.73	0.17	2.80	0.25	0.28	0.89	0.11
C.D. 5%	0.88	1.43	5.91	0.74	4.84	0.47	7.85	0.71	0.79	2.49	0.30
C.D. 1%	1.17	1.90	7.83	0.98	6.41	0.62	10.38	0.94	1.05	3.30	0.39
Range Lowest	33	78	17.60	1.90	11.68	1.35	25.94	4.12	5.13	5.89	4.45
Range Highest	42	86	53.41	4.93	37.63	4.15	76.45	6.60	7.96	18.27	5.48

DF - Days to 50% flowering
NB - No. of branches
NPP - Number of pods per plant
TW - Test weight (g)
DM - Days to maturity
NCP - No. of clusters per plant
PL - Pod length (cm)
SY - Seed yield per plant (g)
PH - Plant height (cm)
NPC - No. pods per cluster
NSP - No. seeds per pod

4.2.6 Number of Pods per Cluster

Among all the progenies, progeny 7 registered high mean (4.15) and progeny 3 (1.35) registered low mean for number of clusters per plant in cross LBG-787 x LBG-752. In cross TU-94-02 x KU-1006, the mean value ranged from 2.07 (progeny 18) to 3.72 (progeny 20) while in cross TU-94-02 x LBG-752, it ranged from 1.78 (progeny 26) to 3.26 (progeny 23). Crosses, TU-94-02 x KU-1006 and LBG-787 x LBG-752 registered the highest (2.52) and lowest mean (2.06) respectively.

4.2.7 Number of Pods per Plant

Progeny 10 and 4 recorded low (25.96) and high (76.45) mean performance in cross LBG-787 x LBG-752 respectively for number of pods per plant. Progeny 18 and 20 showed minimum (38.93) and maximum (68.45) mean values for this trait in the cross TU-94-02 x KU-1006 , whereas in cross TU-94-02 x LBG-752, progeny 23 and progeny 27 showed extreme mean values of 54.80 and 31.91. Crosses, TU-94-02 x KU-1006 and LBG-787 x LBG-752 registered the highest and lowest mean value of 46.01 and 39.06 among the three crosses studied.

4.2.8 Pod Length (cm)

Maximum (6.58 cm) and minimum (4.19 cm) mean values for number of pods per cluster was registered by progeny 6 and progeny 9 in cross LBG-787 x LBG-752 , whereas in cross TU-94-02 x KU-1006, it ranged between 4.12 cm (progeny 19) to 5.85 cm (progeny 17). In cross TU-94-02 x LBG-752, mean values varied between 4.17 cm (progeny 26) to 6.60 cm (progeny 24). Among the three crosses studied, TU-94-02 x LBG-752 has the highest mean of 5.03 cm while LBG-787 x LBG-752 noted lowest mean of 4.71 cm.

Table 4.4 Mean performance of parents and progenies in F_3 population for different physiological attributes in blackgram

Parent/ Progeny	SLA (30 DAS)	SLA (45 DAS)	SLW (30 DAS)	SLW (45 DAS)	SCMR (30 DAS)	SCMR (45 DAS)	BMP	HI
				LBG - 787 x LBG – 752				
Progeny 1	266.03	286.14	0.0040	0.0043	38.68	42.68	18.03	37.30
Progeny 2	196.38	223.83	0.0046	0.0059	39.50	43.51	20.69	38.99
Progeny 3	231.33	242.67	0.0042	0.0054	38.72	41.89	17.58	36.81
Progeny 4	205.35	228.26	0.0050	0.0058	45.61	46.73	29.81	53.15
Progeny 5	203.47	266.51	0.0044	0.0049	40.01	43.63	20.55	39.89
Progeny 6	226.54	234.95	0.0049	0.0055	40.95	44.64	21.62	40.78
Progeny 7	205.48	210.67	0.0050	0.0062	41.86	45.26	22.92	40.03
Progeny 8	165.24	234.99	0.0048	0.0060	39.85	42.83	19.41	37.44
Progeny 9	239.44	261.06	0.0043	0.0050	38.87	41.05	17.82	35.83
Progeny 10	263.37	294.03	0.0040	0.0044	35.72	39.05	16.99	34.62
LBG – 787	123.35	165.49	0.0052	0.0062	35.83	43.24	24.89	34.26
LBG – 752	183.40	239.11	0.0049	0.0056	38.81	41.80	27.16	29.19
Mean	209.12	240.64	0.0046	0.0047	39.53	43.02	21.45	38.19
C.V.	2.38	3.24	1.06	5.10	3.78	1.03	8.29	9.96
$S.E_m$	2.56	3.65	0.03	0.13	0.75	0.22	0.89	1.90
C.D. 5%	7.38	10.50	0.07	0.38	2.15	0.64	2.56	5.47
C.D. 1%	9.91	14.11	0.10	0.51	2.89	0.86	3.44	7.35
Range Lowest	123.35	165.49	0.0040	0.0043	35.72	39.05	16.99	29.19
Range Highest	266.03	294.03	0.0050	0.0062	45.61	46.73	29.81	53.15

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Table 4.4 Contd….

Parent/ Progeny	SLA (30 DAS)	SLA (45 DAS)	SLW (30 DAS)	SLW (45 DAS)	SCMR (30 DAS)	SCMR (45 DAS)	BMP	HI
TU-94-02 x KU-1006								
Progeny 11	160.37	183.99	0.0054	0.0062	52.39	37.39	26.02	40.00
Progeny 12	159.06	182.25	0.0055	0.0063	52.89	37.89	27.36	42.74
Progeny 13	158.39	181.37	0.0055	0.0063	53.14	38.14	28.06	44.15
Progeny 14	160.77	184.50	0.0054	0.0062	52.22	37.22	25.55	39.05
Progeny 15	158.31	181.27	0.0055	0.0063	53.18	38.18	28.15	44.34
Progeny 16	160.58	184.26	0.0054	0.0062	52.28	37.28	25.73	39.41
Progeny 17	153.30	174.72	0.0057	0.0065	55.23	40.23	31.21	49.42
Progeny 18	162.51	186.79	0.0054	0.0062	51.36	36.36	23.73	32.69
Progeny 19	163.01	187.46	0.0053	0.0061	51.54	36.54	23.23	31.74
Progeny 20	141.82	159.97	0.0063	0.0071	60.53	45.53	44.46	61.70
TU-94-02	161.30	176.47	0.0057	0.0062	55.24	38.63	25.35	39.37
KU-1006	145.14	156.30	0.0066	0.0074	60.45	38.14	22.67	34.75
Mean	157.05	178.28	0.0057	0.0064	54.20	38.46	27.62	41.61
C.V.	2.28	1.79	1.76	1.89	2.07	2.28	8.42	11.12
S.E$_{m}$.	1.79	1.60	0.06	0.05	0.56	0.44	1.16	2.31
C.D. 5%	5.16	4.59	0.16	0.15	1.62	1.26	3.35	6.66
C.D. 1%	6.93	6.17	0.22	0.21	2.17	1.69	4.49	8.94
Range Lowest	141.82	156.30	0.0053	0.0061	51.36	36.36	22.67	31.74
Range Highest	163.01	187.46	0.0066	0.0074	60.53	45.53	44.46	61.70

Cont….

Table 4.4 Contd….

Parent/ Progeny	SLA (30 DAS)	SLA (45 DAS)	SLW (30 DAS)	SLW (45 DAS)	SCMR (30 DAS)	SCMR (45 DAS)	BMP	HI
TU-94-02 x LBG-752								
Progeny 21	248.71	276.96	0.0057	0.0067	46.56	35.58	38.09	30.42
Progeny 22	249.56	278.02	0.0056	0.0067	45.11	34.88	34.79	27.55
Progeny 23	244.06	271.18	0.0058	0.0069	54.60	39.46	48.22	38.17
Progeny 24	247.29	275.18	0.0057	0.0068	48.91	36.71	40.16	31.79
Progeny 25	249.32	277.71	0.0056	0.0067	45.53	35.08	36.12	28.02
Progeny 26	252.46	281.64	0.0055	0.0066	42.56	33.94	30.58	24.73
Progeny 27	250.73	279.47	0.0056	0.0066	43.17	32.59	32.05	25.37
Progeny 28	250.19	278.80	0.0056	0.0067	44.06	34.37	34.56	27.62
Progeny 29	249.49	277.92	0.0056	0.0067	45.17	34.91	34.87	27.61
Progeny 30	251.08	279.90	0.0056	0.0066	40.36	33.65	31.19	24.70
TU-94-02	169.72	180.88	0.0050	0.0070	54.80	38.14	30.82	25.69
LBG-752	187.73	239.18	0.0047	0.0049	38.30	41.63	26.16	37.33
Mean	237.53	266.40	0.0056	0.0067	47.18	35.66	28.25	35.63
C.V.	1.46	1.50	2.41	2.08	9.92	6.40	17.28	16.93
S.E$_m$	1.79	1.96	0.07	0.07	2.34	1.14	3.08	2.39
C.D. 5%	5.16	5.65	0.20	0.20	6.73	3.28	8.86	6.88
C.D. 1%	6.93	7.59	0.27	0.27	9.04	4.41	11.90	9.24
Range Lowest	169.72	180.88	0.0047	0.0049	40.36	32.59	30.58	24.70
Range Highest	252.46	281.64	0.0058	0.0070	45.60	41.63	48.22	38.17

Cont….

Table 4.4 Contd….

Overall mean performance of three F_3 crosses i.e., LBG - 787 x LBG – 752, TU-94-02 x KU-1006 and TU-94-02 x LBG-752

	SLA (30 DAS)	SLA (45 DAS)	SLW (30 DAS)	SLW (45 DAS)	SCMR (30DAS)	SCMR (45DAS)	BMP	HI
Mean	201.023	228.44	0.0053	0.0061	46.97	39.05	25.78	38.48
C.V.	2.03	2.34	1.88	3.39	6.21	3.71	12.73	12.83
$S.E_m$	2.09	2.59	0.06	0.09	1.46	0.72	1.64	2.47
C.D. 5%	5.87	7.25	0.16	0.26	4.09	2.03	4.60	6.92
C.D. 1%	7.76	9.60	0.21	0.34	5.41	2.69	6.09	9.16
Range Lowest	123.35	156.30	0.0040	0.0043	35.72	32.59	16.99	24.70
Range Highest	266.03	294.03	0.0066	0.0074	60.53	46.73	48.22	61.70

SLA (30 DAS) - Specific Leaf Area at 30 DAS ($cm^2 g^{-1}$)
SLW (30 DAS) - Specific Leaf Weight at 30 DAS ($g cm^{-2}$)
SCMR (30DAS) - SPAD Chlorophyll Meter Reading at 30 DAS
BMP - Biomass per plant (g)

SLA (45 DAS) - Specific Leaf Area at 45 DAS ($cm^2 g^{-1}$)
SLW (45DAS) - Specific Leaf Weight at 45 DAS ($g cm^{-2}$)
SCMR (45DAS) - SPAD Chlorophyll Meter Reading at 30 DAS
HI - Harvest Index (%)

4.2.9 Number of Seeds per Pod

Mean of the progenies for number of seeds per pod ranged from 5.13 (progeny 3) to 6.22 (progeny 6), from 5.16 (progeny 19) to 6.87 (progeny 17) and from 5.76 (progeny 26) to 7.96 (progeny 24) in cross LBG-787 x LBG-752, TU-94-02 x KU-1006 and TU-94-02 x LBG-752 respectively. Among the three crosses studied, cross TU-94-02 x LBG-752 has shown the highest mean of 6.53 and cross LBG-787 x LBG-752 recorded the lowest mean of 5.75 for number of seeds per pod.

4.2.10 Test Weight (g)

Progeny 4 registered the maximum mean performance for test weight (5.44 g) whereas progeny 10 registered the minimum mean performance (4.45 g) in LBG-787 x LBG-752. In the cross TU-94-02 x KU-1006 , mean for test weight ranged from 4.51 g (progeny 18) to 5.09 g (progeny 19) whereas, it varied from 4.57 g (progeny 29) to 5.48 g (progeny 27) in cross. Among the three crosses, TU-94-02 x LBG-752 has shown the highest mean of 5.01 g and LBG-787 x LBG-752 has the lowest mean of 4.69 g among the crosses studied.

4.2.11 Specific Leaf Area (30 DAS) ($cm^2 g^{-1}$)

In cross LBG-787 x LBG-752, the lowest mean value of 165.24 cm^2 g^{-1} was recorded by progeny 8 for SLA taken at 30 DAS and the highest mean value of 266.03 cm^2 g^{-1} was recorded by progeny 1. In cross TU-94-02 x KU-1006, mean values ranged between 141.82 cm^2 g^{-1} (progeny 20) to 163.01 cm^2 g^{-1} (progeny 19) and in cross TU-94-02 x LBG-752, mean value varied between 244.06 cm^2 g^{-1} in progeny 23 to 252.46 cm^2 g^{-1} in progeny 26. Crosses TU-94-02 x LBG-752 and TU-94-02 x KU-1006 registered maximum and minimum values of 237.53 cm^2 g^{-1} and 157.05 cm^2 g^{-1} respectively among the crosses studied.

4.2.12 Specific Leaf Area (45 DAS) ($cm^2 g^{-1}$)

In cross LBG-787 x LBG-752, maximum value of 294.03 cm^2 g^{-1} was registered by progeny 10 for SLA taken at 45 DAS and minimum mean value of 210.67 cm^2 g^{-1} was registered by progeny 7. Similarly, maximum and minimum mean values were recorded by progeny 19 (187.46 cm^2 g^{-1}) and progeny 20 (159.97 cm^2 g^{-1}) in cross TU-94-02 x KU-1006 and by progeny 26 (281.64 cm^2 g^{-1}) and progeny 23 (271.18 cm^2 g^{-1}) in cross TU-94-02 x LBG-752. Highest and the lowest mean values were noted in cross TU-94-02 x LBG-752 (266.40 cm^2 g^{-1}) and cross TU-94-02 x KU-1006 (178.28 cm^2 g^{-1}) respectively among the crosses studied.

4.2.13 Specific Leaf Weight (30 DAS) ($g^{-1} cm^2$)

Mean value of the progenies for SLW taken at 30 DAS varied between 0.0040 g^{-1} cm^2 (progeny 1and 10) and 0.0050 g^{-1} cm^2 (progeny 7), 0.0053 g^{-1} cm^2 (progeny 19) to 0.0063 g^{-1} cm^2 (progeny 20) and from 0.0055 g^{-1} cm^2 (progeny 26) to 0.0058 g^{-1} cm^2 (progeny 23) in crosses LBG-787 x LBG-752, TU-94-02 x KU-1006 and TU-94-02 x LBG-752 respectively. Cross TU-94-02 x KU-1006 has shown the highest mean of 0.0057 g^{-1} cm^2 and cross LBG-787 x LBG-752 has the lowest mean of 0.0046 g^{-1} cm^2 for SLW taken at 30 DAS.

4.2.14 Specific Leaf Weight (45 DAS) ($g^{-1} cm^2$)

In cross, LBG-787 x LBG-752 progeny 1 and progeny 7 exhibited the minimum (0.0043 g^{-1} cm^2) and maximum (0.0062 g^{-1} cm^2) mean values for SLA at 45 DAS. A similar trend was followed by progeny 19 (0.0061 g^{-1} cm^2) and progeny 20 (0.0071 g^{-1} cm^2) in cross TU-94-02 x KU-1006 and by progeny 26 and 30 (0.0066 g^{-1} cm^2) and progeny 23 (0.0069 g^{-1} cm^2) in cross TU-94-02 x KU-1006. Cross TU-94-02 x LBG-752 recorded the highest mean of 0.0067 g^{-1} cm^2 and cross LBG-787 x LBG-752 recorded the lowest mean of 0.0047 g^{-1} cm^2 among three crosses studied.

4.2.15 SPAD Chlorophyll Meter Reading (30 DAS)

In the cross LBG-787 x LBG-752, progeny 10 and progeny 4 registered the lowest (35.72) and the highest (45.61) mean values for SCMR (30 DAS) respectively. In the cross TU-94-02 x KU-1006, mean values varied from 51.36 in progeny 18 to 60.53 in progeny 20. Mean value ranged from 40.36 in progeny 30 to 54.60 in progeny 23 in cross TU-94-02 x LBG-752. In between the crosses, mean value ranged from 54.20 in cross TU-94-02 x KU-1006 to 39.53 in cross LBG-787 x LBG-752.

4.2.16 SPAD Chlorophyll Meter Reading (45 DAS)

Mean values of SCMR (45 DAS) among the progenies varied between 39.05 (progeny 10) and 46.73 (progeny 4) in cross LBG-787 x LBG-752, 36.36 (progeny 18) to 45.53 (progeny 20) in cross TU-94-02 x KU-1006 and 32.59 (progeny 27) to 39.46 (progeny 24) in cross TU-94-02 x LBG-752. Cross LBG-787 x LBG-752 recorded the highest mean of 43.02 while cross TU-94-02 x LBG-752 recorded lowest mean of 35.66 among the three crosses studied.

4.2.17 Biomass per Plant (g)

Mean of the progenies for biomass per plant ranged from 16.99 g (progeny 10) to 29.81 g (progeny 4), 23.23 g (progeny 19) to 44.46 g (progeny 20) and 30.58 g (progeny 26) to 48.22 g (progeny 23) in crosses LBG-787 x LBG-752, TU-94-02 x KU-1006 and TU-94-02 x LBG-752 respectively. Among the crosses studied, cross TU-94-02 x LBG-752 registered the highest mean of 28.25 g and cross LBG-787 x LBG-752 registered the lowest mean of 21.45 g biomass per plant.

4.2.18 Harvest Index (%)

Mean of the progenies for harvest index varied between 34.62% (progeny 10) to 53.15% (progeny 4) in cross LBG-787 x LBG-752, 31.74% (progeny 19) to 61.70% (progeny 20) in cross TU-94-02 x KU-1006 and 24.70% (progeny 30) to 38.17% (progeny 23) in cross TU-94-02 x LBG-752.

TU-94-02 x LBG-752 has the highest mean of 41.61% and TU-94-02 x KU-1006has shown the lowest mean of 35.63% among the three crosses studied.

4.2.1 Seed Yield per Plant (g)

In the cross LBG-787 x LBG-752, mean of the progenies for seed yield per plant ranged from 5.89 g (progeny 10) to 17.90 g (progeny 4) whereas, in cross TU-94-02 x KU-1006 mean ranged from 8.61 g (progeny 19) to 17.78 g (progeny 20) and in cross TU-94-02 x LBG-752, mean ranged from10.64 g (progeny 26) to 18.27 g (progeny 23). Highest mean of 12.68 g and lowest mean of 8.95 g seed yield per plant were recorded by the crosses TU-94-02 x LBG-752, LBG-787 x LBG-752 respectively.

4.3 VARIABILITY, HERITABILITY AND GENETIC ADVANCE AS PER CENT OF MEAN

The variability available in the genotypes is the basic input of plant breeding, as the success of any crop improvement programme depends upon the magnitude and range of variability present within the genotypes. The study of inheritance of various developmental and productive traits through the estimates of genotypic and phenotypic coefficients of variability is helpful for framing an effective breeding programme. The effectiveness of selection for any character depends not only on the amount of phenotypic and genotypic variability but also on estimates of heritability and genetic advance.

Genetic parameters like Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) are useful in detecting the amount of variability present within the germplasm. The GCV measures the magnitude of genetic variability present in the crop. Since, it reflects the heritable portion of variability, it is considered to be more useful than PCV. The difference between PCV and GCV indicates the environmental effect.

The amount of genetic variation alone is not being of much use to the breeder unless it is supplemented with the information on heritability, which gives a measure of the heritable portion of the total variation. Heritability in

Table 4.5 Genetic variability and selection parameters estimated for grain yield and its components in F_3 populations of three blackgram crosses

Character	Cross	Mean	PV	GV	PCV	GCV	h^2(bs)	GA	GAM
Days to 50% flowering	LBG-787 x LBG-752	37.35	3.08	2.80	4.70	4.48	71.0	3.29	8.80
	TU-94-02 x KU-1006	36.31	1.73	1.18	3.63	2.99	68.2	1.85	5.09
	TU-94-02 x LBG-752	35.00	6.13	5.90	7.07	6.94	96.3	4.91	14.03
Days to maturity	LBG-787 x LBG-752	81.52	2.48	1.68	1.93	1.59	47.9	2.20	2.70
	TU-94-02 x KU-1006	81.35	3.91	1.99	2.43	1.73	50.9	2.07	2.55
	TU-94-02 x LBG-752	82.85	4.26	3.80	2.49	2.35	89.1	3.79	4.57
Plant height (cm)	LBG-787 x LBG-752	26.51	113.18	100.47	40.13	37.81	68.8	19.46	73.39
	TU-94-02 x KU-1006	33.41	63.63	57.57	23.87	22.71	90.5	14.87	44.50
	TU-94-02 x LBG-752	31.61	59.88	28.99	24.48	17.04	48.4	7.72	24.42
No. of branches per plant	LBG-787 x LBG-752	2.87	0.76	0.61	30.36	27.07	59.5	1.43	49.73
	TU-94-02 x KU-1006	3.65	0.53	0.45	19.93	18.36	84.9	1.27	34.84
	TU-94-02 x LBG-752	3.51	0.98	0.41	28.19	18.33	42.3	1.86	24.55
No. of clusters per plant	LBG-787 x LBG-752	18.86	53.06	46.86	38.62	36.29	68.3	13.25	70.27
	TU-94-02 x KU-1006	22.58	33.26	29.44	25.54	24.03	88.5	10.52	46.57
	TU-94-02 x LBG-752	23.29	33.61	10.01	24.89	13.58	29.8	3.56	15.27
No. of pods per cluster	LBG-787 x LBG-752	2.06	0.64	0.56	38.61	36.36	68.7	1.46	70.54
	TU-94-02 x KU-1006	2.52	0.26	0.22	20.06	18.44	84.5	1.88	34.92
	TU-94-02 x LBG-752	2.25	0.32	0.12	25.13	15.17	36.4	1.43	18.86

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Table 4.5 Contd….

Character	Cross	Mean	PV	GV	PCV	GCV	h^2(bs)	GA	GAM
No. of pods per plant	LBG-787 x LBG-752	39.06	218.40	192.65	37.84	35.54	68.2	26.85	68.75
	TU-94-02 x KU-1006	46.01	112.56	105.50	23.06	22.32	93.7	20.49	44.52
	TU-94-02 x LBG-752	40.28	73.60	21.05	21.30	11.39	28.6	5.06	12.55
Pod length (cm)	LBG-787 x LBG-752	4.71	0.47	0.44	14.53	14.03	93.2	1.31	17.89
	TU-94-02 x KU-1006	4.98	0.48	0.26	13.97	10.30	54.4	1.78	15.65
	TU-94-02 x LBG-752	5.03	0.76	0.27	17.30	10.28	35.3	1.63	12.58
No. of seeds per pod	LBG-787 x LBG-752	5.75	0.50	0.47	12.32	11.91	93.5	1.36	13.72
	TU-94-02 x KU-1006	5.93	0.47	0.28	11.59	8.84	58.2	1.82	13.90
	TU-94-02 x LBG-752	6.53	0.90	0.20	14.52	6.91	22.6	1.44	6.78
Test weight (g)	LBG-787 x LBG-752	4.69	0.07	0.07	5.69	5.59	76.3	1.53	11.29
	TU-94-02 x KU-1006	4.76	0.07	0.02	5.71	3.10	29.6	1.17	3.48
	TU-94-02 x LBG-752	5.01	0.16	0.08	8.01	5.67	50.1	1.41	8.26
Specific Leaf Area at 30 DAS (cm^2g^{-1})	LBG-787 x LBG-752	215.41	2618.56	2592.25	23.76	23.64	79.1	74.36	48.45
	TU-94-02 x KU-1006	157.05	56.58	43.71	4.79	4.21	77.6	11.97	7.62
	TU-94-02 x LBG-752	245.98	90.81	77.95	3.87	3.59	86.2	16.85	6.85
Specific Leaf Area at 45 DAS (cm^2g^{-1})	LBG-787 x LBG-752	225.13	1541.48	1488.20	17.44	17.14	77.0	78.08	34.68
	TU-94-02 x KU-1006	178.28	110.59	100.39	5.90	5.62	91.0	19.67	11.03
	TU-94-02 x LBG-752	261.28	1485.13	1469.70	14.75	14.67	89.0	78.56	30.07
Specific Leaf Weight at 30 DAS (g^{-1} cm^2)	LBG-787 x LBG-752	4.73	0.34	0.34	12.39	12.34	79.0	1.20	15.33
	TU-94-02 x KU-1006	6.42	0.16	0.15	6.29	6.04	92.1	1.77	11.94
	TU-94-02 x LBG-752	6.70	0.04	0.02	3.03	2.21	53.6	1.22	3.32

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Table 4.5 Contd….

Character	Cross	Mean	PV	GV	PCV	GCV	h^2(bs)	GA	GAM
Specific Leaf Weight at 45 DAS (g^{-1} cm^2)	LBG-787 x LBG-752	5.15	0.65	0.58	15.67	14.81	89.0	1.49	28.85
	TU-94-02 x KU-1006	5.65	0.17	0.15	7.19	6.94	93.0	1.78	13.79
	TU-94-02 x LBG-752	5.63	0.02	0.00	2.65	1.10	17.0	1.05	4.93
SPAD Chlorophyll Meter Reading at 30DAS	LBG-787 x LBG-752	39.53	8.53	6.29	7.39	6.34	54.0	4.44	11.23
	TU-94-02 x KU-1006	54.20	11.07	9.81	6.14	5.78	89.0	6.07	11.20
	TU-94-02 x LBG-752	47.18	42.51	20.62	13.82	9.63	49.0	6.52	13.81
SPAD Chlorophyll Meter Reading at 45DAS	LBG-787 x LBG-752	43.02	4.21	4.01	4.77	4.65	75.0	4.03	9.36
	TU-94-02 x KU-1006	38.46	6.58	5.81	6.67	6.27	88.0	4.67	12.14
	TU-94-02 x LBG-752	35.66	8.46	3.25	8.16	5.06	38.0	2.30	6.46
Biomass per plant (g)	LBG-787 x LBG-752	21.45	18.89	15.72	20.26	18.48	63.0	7.45	34.74
	TU-94-02 x KU-1006	27.62	37.84	32.43	22.27	20.62	86.0	10.86	39.32
	TU-94-02 x LBG-752	28.25	31.49	8.63	19.87	10.40	27.0	3.17	11.21
Harvest Index (%)	LBG-787 x LBG-752	38.19	43.15	28.68	17.20	14.02	47.0	8.99	13.55
	TU-94-02 x KU-1006	41.61	81.77	60.35	21.73	18.67	74.0	13.75	33.04
	TU-94-02 x LBG-752	35.63	52.91	15.01	20.41	10.87	28.0	4.25	11.93
Seed yield per plant (g)	LBG-787 x LBG-752	8.95	12.43	10.41	39.39	36.04	83.7	6.08	67.92
	TU-94-02 x KU-1006	10.42	7.25	6.52	25.84	24.50	89.9	4.99	47.86
	TU-94-02 x LBG-752	12.68	11.71	5.34	26.98	18.22	45.6	3.22	25.35

CV : Coefficient of Variation
PV : Phenotypic Variance
GV : Genotypic Variance
EV : Environmental Variance

PCV : Phenotypic Coefficient of Variation
GCV : Genotypic Coefficient of Variation
ECV : Environmental Coefficient of Variation

h^2 (bs) : Heritability in Broad Sense
GA : Genetic Advance
GAM : Genetic Advance as percent of Mean

broad sense includes both additive and non-additive gene effects. Genetic advance provides information on expected genetic gain resulting from selection of superior individuals. Heritability values along with genetic advance would be more reliable and helpful in predicting the gain under selection than heritability estimate alone.

The estimates of genetic parameters *viz.,* PCV, GCV, heritability in broad sense, genetic advance and genetic advance as per cent of mean were computed for all the characters under study and presented in Table 4.5.

4.3.1 F_3 Progenies of Cross LBG-787 x LBG-752

High estimates of GCV and PCV were observed for characters like plant height (GCV: 37.81 and PCV: 40.13), number of clusters per plant (GCV: 36.29; PCV: 38.62), seed yield per plant (GCV: 36.04; PCV: 39.39), number of pods per cluster (GCV: 36.36; PCV: 38.61), number of pods per plant (GCV: 35.54; PCV: 37.84), number of branches per plant (GCV: 27.07 ; PCV: 30.36) and SLA (30 DAS) (GCV: 23.64; PCV: 23.76). The character biomass per plant (GCV: 18.48; PCV: 20.26) recorded high PCV and moderate GCV.

Characters like SLA (45 DAS) (GCV: 17.14; PCV: 17.44), SLW (45 DAS) (GCV: 14.81 and PCV: 15.67), harvest index (GCV: 14.02; PCV: 17.20), pod length (GCV: 14.03; PCV: 14.53), SLW (30 DAS) (GCV: 12.34; PCV: 12.39) and number of seeds per pod (GCV: 11.91; PCV: 12.32) has recorded moderate GCV and PCV.

Low estimates of GCV and PCV have recorded for SCMR (30 DAS) (GCV: 6.34; PCV: 7.39), test weight (GCV: 5.59; PCV: 5.69), SCMR (45 DAS) (GCV: 4.65; PCV: 4.77), days to 50% flowering (GCV: 4.48; PCV: 4.70) and days to maturity (GCV: 1.59; PCV: 1.93). Among all the characters plant height (GCV: 37.81; PCV: 40.13) recorded highest GCV and PCV.

High estimate of heritability was observed for almost all the characters except for days to maturity, number of branches per plant, SCMR (45 DAS) and harvest index. The highest estimate of heritability was recorded for number of seeds per pod (93.5%) followed by pod length (93.2%), SLW (45 DAS) (89.0%), seed yield per plant (83.7%), SLA (30 DAS) (79.1%), SLW (30 DAS) (79.0%), SLA (45 DAS) (77.0%), test weight (76.3%), SCMR (45 DAS) (75.0%), days to flowering (71.0%), plant height (68.8%), number of pods per cluster (68.7%), number of clusters per plant (68.3%), number of pods per plant (68.2%) and biomass per plant (63.0%). Moderate estimates of variability were recorded for characters such as number of branches per plant (59.5%), SCMR (30 DAS) (54.0%), days to maturity (47.9%) and harvest index (47.0%).

The highest estimate of genetic advance was recorded by SLA (45 DAS) (78.08) followed by SLA (30 DAS) (74.36) and number of pods per plant (26.85). Moderate level of genetic advance was observed in plant height (19.46), number of clusters per plant (13.25) whereas, characters like harvest index(8.99), biomass per plant (7.45), seed yield per plant (6.08), SCMR (30 DAS) (4.44), SCMR (45 DAS) (4.03%), days to 50% flowering (3.29), days to maturity (2.20), SLW (45 DAS) (1.49), number of pods per cluster (1.46), number of branches per plant (1.43), number of seeds per pod (1.36), pod length (1.31), test weight (1.53) and SLW (30 DAS) (1.20).

High genetic advance as per cent of mean was registered for plant height (73.39%) followed by number of pods per cluster (70.54%), number of clusters per plant (70.27%), number of pods per plant (68.75%), seed yield per plant (67.92%), number of branches per plant (49.73%), SLA (30 DAS) (48.45%), biomass per plant (34.74%), SLA (45 DAS) (34.68%) and SLW (45 DAS) (28.85%). Characters such as pod length (17.89%), SLW (30DAS) (15.33%), number of seeds per pod (13.72%), harvest index (13.55%), test weight (11.29%), SCMR (30 DAS) (11.23%) recorded moderate genetic advance as per cent of mean. Low genetic advance as per cent of mean was recorded for SCMR (45 DAS) (9.36%), days to 50% flowering (8.80%) and days to maturity (2.70%).

In cross, LBG-787 x LBG-752 high values of GCV and PCV was observed for plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, SLA (30 DAS) and seed yield per plant which are in accordance with the earlier reports of Sharma *et al.* (2006) and Reddy *et al.* (2011) for plant height and number of pods per plant; Sharma *et al.* (2006) and Neelavati and Govindarasu (2010) for number of branches per plant; Gupta *et al.* (2003), Priyanka *et al.* (2016) and Hemalata *et al.* (2017) for number of clusters per plant; Vijay *et al.* (2015) and Reddy *et al.* (2011) for seed yield per plant.

Pod length, number of seeds per pod, SLA (45 DAS), SLW (30 DAS), SLW (45 DAS) and harvest index recorded moderate GCV and PCV. Similar findings were reported by Ramya *et al.* (2014) for pod length; Deepshika *et al.* (2014), Paramesh *et al.* (2014), Singh *et al.* (2014) for number of seeds per pod; Gupta *et al.* (2003), Anu *et al.* (2017), Rolaniya *et al.* (2017) for harvest index.

Low estimates of GCV and PCV was recorded by days to 50% flowering, days to maturity, SCMR (30 DAS), SCMR (45 DAS) and test weight. Similar findings were reported by Gupta *et al.* (2003), Konda *et al.* (2009), Panigrahi *et al.* (2014), Anu *et al.* (2017) and Patidar *et al.* (2017) for days to 50% flowering, days to maturity and test weight.

Phenotypic co-efficient of variation was of high magnitude than the genotypic co-efficient of variation for all the characters indicating the influence of environment in the expression of these traits. Plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, SLA (30 DAS) and seed yield per plant showed high GCV and PCV values. Therefore, simple selection could be effective for further improvement of these traits.

Number of seeds per pod, pod length, SLW (45 DAS), seed yield per plant, SLA (30 DAS), SLW (30 DAS), test weight, SLA (45 DAS), SCMR (45 DAS), days to 50% flowering, plant height, number of pods per cluster, number of clusters per plant, number of pods per plant, biomass per plant and harvest index recorded high estimates of heritability. So, these characters may serve as effective selection parameters during breeding programme for the improvement of productivity. For improving these characters simple selection based on *per se* performance is more effective. High heritability for seed yield per plant suggested that direct selection for seed yield may be rewarding. Similar results were obtained by Deepshika *et al.* (2014) for number of seeds per pod, pod length, days to flowering, number of clusters per plant, number of pods per plant; Sowmini and Jayamani (2014) and Wani *et al.* (2017) for plant height, number of pods per cluster, number of pods per plant and seed yield per plant; by Rolaniya *et al.* (2017) for plant height, biomass per plant and harvest index.

Moderate estimates of heritability was recorded for characters such as number of branches per plant, SCMR (30 DAS) and days to maturity. This indicated that the selection for these characters is likely to accumulate some additive genes leading to further improvement of their performance. Similar results were stated by Priyanka *et al.* (2016), Rolaniya *et al.* (2017), Anu *et al.* (2017) for days to maturity and number of branches per plant.

High heritability coupled with high genetic advance as per cent of mean was recorded in seed yield per plant, plant height, number of clusters per plant, number of pods per cluster, number of pods per plant, SLA (30 DAS), SLA (45 DAS) and SLW (30 DAS). It indicated the prevalence of additive gene action in the inheritance of these characters and there is less influence of the environment in the expression of these characters. Hence, they are amenable for simple selection resulting in a high genetic gain. Similar results have been reported by Sharma *et al.* (2006) and Rekha and Reddy (2017) for plant height; Gupta *et al.* (2003), Gowsalya *et al.* (2016), Hemalata *et al.* (2017) and Panda *et al.* (2017) for number of clusters per plant, number of pods per plant and seed yield per plant; Sowmini and Jayamani (2013) for number of pods per cluster.

Characters such as pod length, SLW (30 DAS), number of seeds per pod, harvest index, test weight and SCMR (30 DAS) recorded high heritability with moderate genetic advance as per cent of mean. It indicates the presence of non additive gene action and role of environment in the expression of these traits. Therefore, traits which recorded higher estimates of genetic advance as per cent of mean are given priority while deciding the selection strategies. These results are in accordance with the results obtained by Deepshika *et al.* (2014) for pod length and number of seeds per pod; Vijay *et al.* (2015) for harvest index.

Number of branches per plant showed moderate heritability with high genetic advance as per cent of mean. Presence of moderate heritability with high genetic advance as per cent of mean suggested that the individual plant selection can be made for the improvement of this trait.

Moderate heritability with low genetic advance as per cent of mean was recorded for SCMR (45 DAS), days to 50% flowering and days to maturity. It indicates that the character is highly influenced by environmental effects and selection would be ineffective. Similar results were stated by Rolaniya *et al.* (2017), Anu *et al.* (2017) for days to 50% flowering.

4.3.2 F$_3$ Progenies of Cross TU-94-02 x KU-1006

High estimates of GCV and PCV were observed for seed yield per plant (GCV: 24.50 and PCV: 25.84), number of clusters per plant (GCV: 24.03; PCV: 25.54), plant height (GCV: 22.71; PCV: 23.87), number of pods per plant (GCV: 22.32; PCV: 23.06) and biomass per plant (GCV: 20.62; PCV: 22.27). The characters namely harvest index (GCV: 18.67; PCV: 20.26) and number of pods per cluster (GCV: 18.44; PCV: 20.06) recorded moderate GCV with high PCV.

Number of branches per plant (GCV: 18.36; PCV: 19.93) and pod length (GCV: 10.30; PCV: 13.97) registered moderate GCV and PCV whereas, number of seeds per pod (GCV: 8.84; PCV: 11.59) recorded low GCV with moderate PCV. All the other characters, SLW (45 DAS) (GCV:

6.94; PCV: 7.19), SCMR (45 DAS) (GCV: 6.27; PCV: 6.67), SLW (30 DAS) (GCV: 6.04; PCV: 6.29), SCMR (30 DAS) (GCV: 5.78; PCV: 6.14), SLA (45 DAS) (GCV: 5.62; PCV: 5.90), SLA (30 DAS) (GCV: 4.21; PCV: 4.79), test weight (GCV: 3.10; PCV: 5.71), days to 50% flowering (GCV: 2.99; PCV: 3.63) and days to maturity (GCV: 1.73; PCV: 2.43) recorded low estimates of both GCV and PCV. Among all the characters, seed yield per plant (GCV: 24.50; PCV: 25.84) recorded the highest GCV and PCV.

High estimates of heritability were observed for almost all the characters except for number of seeds per pod, pod length, days to maturity and test weight. The highest estimate of heritability was recorded for number of pods per plant (93.7%) followed by SLW (45 DAS) (93.0%), SLW (30

DAS) (92.1%), SLA (45 DAS) (91.0%), plant height (90.5%), seed yield per plant (89.9%), SCMR (30 DAS) (89.0%), number of clusters per plant (88.5%), SCMR (45 DAS) (88.0%), biomass per plant (86.0%), number of branches per plant (84.9%), number of pods per cluster (84.5%), SLA (30 DAS) (77.6%), harvest index (74.0%) and days to 50% flowering (68.2%). Characters *viz.,* number of seeds per pod (58.2%), pod length (54.4%) and days to maturity (50.9%) registered moderate heritability whereas test weight (29.6%) registered low heritability in cross, TU-94-02 xKU-1006.

The highest estimates of genetic advance was recorded for number of pods per plant (20.49). Characters *viz.,* SLA (45 DAS) (19.67), plant height (14.87), harvest index (13.75), SLA (30 DAS) (11.97), number of clusters per plant (10.52), biomass per plant (10.86) recorded moderate genetic advance whereas, other characters like SCMR (30 DAS) (6.07), seed yield per plant (4.99), SCMR (45 DAS) (4.67), days to maturity (2.07), number of pods per cluster (1.88), days to 50% flowering (1.85), number of seeds per pod (1.82), pod length (1.78), SLW (45 DAS) (1.78), SLW (30 DAS) (1.77), number of branches per plant (1.27) and test weight (1.17) registered low genetic advance.

High genetic advance as per cent of mean was registered for seed yield per plant (47.86%), number of clusters per plant (46.57%), number of pods per plant (44.52%), plant height (44.50%), biomass per plant (39.32%), number of pods per cluster (34.92%), number of branches per plant (34.84%) and harvest index (33.04%). Characters such as pod length (15.65%), number of seeds per pod (13.90%), SLW (45 DAS) (13.79%), SCMR (45 DAS) (12.14%), SLW (30 DAS) (11.94%), SCMR (30 DAS) (11.20%) and SLA (45 DAS) (11.03%) recorded moderate genetic advance as per cent of mean. Low genetic advance as per cent of mean was recorded for SLA (30 DAS) (7.62%), days to 50% flowering (5.09%), test weight (3.48%) and days to maturity (2.55%).

In cross, TU-94-02 x KU-1006 high values of GCV and PCV were found for characters like number of pods per plant, seed yield per plant, number of clusters per plant and biomass per plant which are in accordance with the earlier reports of Gupta *et al.* (2003), Patel *et al.* (2014), Priyanka *et al.* (2016) and Hemalata *et al.* (2017) for number of clusters per plant; Sharma *et al.* (2006) and Reddy *et al.* (2011) for number of pods per plant; Vijay *et al.* (2015) and Reddy *et al.* (2011) for seed yield per plant; Rolaniya *et al.* (2017) for biomass per plant.

Number of pods per cluster and harvest index recorded high PCV with moderate GCV. Similar findings were reported by Priyanka *et al.* (2016). Characters like number of branches per plant and pod length registered moderate GCV and PCV. Similar findings were reported by Gupta *et al.* (2003), Anu *et al.* (2017), Rolaniya *et al.* (2017) for harvest index.

Number of seeds per pod recorded moderate PCV and low GCV. Singh *et al.* (2014), Paramesh *et al.* (2014) and Deepshika *et al.* (2014) also observed moderate level of PCV for number of seeds per pod.

Low estimates of GCV and PCV was recorded by SLW (45 DAS), SCMR (45 DAS), SLW (30 DAS), SCMR (30 DAS), SLA (45 DAS), SLA (30 DAS), test weight, days to 50% flowering and days to maturity. Similar findings were reported by Gupta *et al.* (2003), Konda *et al.* (2009), Panigrahi *et al.* (2014), Anu *et al.* (2017) and Patidar *et al.* (2017) for days to 50% flowering, days to maturity and test weight.

Phenotypic co-efficient of variation was of high magnitude than the genotypic co-efficient of variation for all the 19 characters studied indicating the influence of environment in the expression of these traits. Number of pods per plant, seed yield per plant, number of clusters per plant and biomass per plant showed high GCV and PCV values. Therefore, simple selection could be effective for further improvement of these traits in later generations of this cross.

Number of pods per plant, SLW (45 DAS), SLW (30 DAS), SLA (45 DAS), plant height, seed yield per plant, SCMR (30 DAS), number of clusters per plant, SCMR (45 DAS), biomass per plant, number of branches per plant, number of pods per cluster, SLA (30 DAS), harvest index and days to 50% flowering recorded high levels of heritability. Hence, these characters may serve as effective selection parameters during breeding programme for the improvement of productivity. For improvement of these characters, simple selection based on *per se* performance is more effective. High heritability for seed yield per plant suggested that direct selection for seed yield may be rewarding. Similar results were obtained by Deepshika *et al.* (2014) for days to 50% flowering, number of clusters per plant, number of pods per plant; Sowmini and Jayamani (2013) and Wani *et al.* (2017) for plant height, number of pods per cluster, number of pods per plant and seed yield per plant; Rolaniya *et al.* (2017) for plant height, biomass per plant and harvest index.

Moderate estimates of heritability were recorded for number of seeds per pod, pod length and days to maturity whereas, test weight registered low heritability. This indicates that the selection of these leads to further improvement of their performance. Similar results were stated by Rolaniya *et al.* (2017), Anu *et al.* (2017) for days to maturity and pod length.

High heritability coupled with high genetic advance as per cent of mean was recorded for seed yield per plant, number of clusters per plant, number of pods per plant, plant height, biomass per plant, number of pods per cluster, number of branches per plant and harvest index. It indicates the prevalence of additive gene action in the inheritance of these characters and there is less influence of the environment in the expression of these characters. Hence they are amenable for simple selection resulting in a high genetic gain. Similar results have been reported by Panigrahi *et al*. (2014) for number of branches; Sharma *et al.* (2006) and Rekha and Reddy (2017) for plant height; Gupta *et al.* (2003), Gowsalya *et al.* (2016), Hemalata *et al.* (2017) and Panda *et al.* (2017) for number of clusters per plant, number of pods per plant and seed yield per plant; Sowmini and Jayamani (2013) for number of pods per cluster; Rolaniya *et al.* (2017) for biomass per plant.

Characters such as SLW (45 DAS), SCMR (45 DAS), SLW (30 DAS), SCMR (30 DAS) and SLA (45 DAS) recorded high heritability with moderate genetic advance as per cent of mean. It indicates the presence of non additive gene action and role of environment in the expression of these traits. Therefore, traits which recorded high estimates of genetic advance as per cent of mean are given priority while deciding selection strategies.

High heritability with low genetic advance as per cent of mean was recorded by days to 50% flowering and SLA (30 DAS). Vijay *et al* (2015), Priyanka *et al.* (2016) and Panda *et al.* (2016) also recorded high heritability with low genetic advance as per cent of mean.

Pod length and number of seeds per pod recorded moderate heritability with moderate genetic advance as per cent of mean. Moderate heritability with low genetic advance as per cent of mean was recorded by days to maturity. Similar results were stated by Rolaniya *et al.* (2017), Anu *et al.* (2017) for days to maturity and pod length; Panigrahi *et al.* (2014) for number of seeds per pod. Test weight registered low heritability with low genetic advance as per cent of mean. It indicates that the character was highly influenced by environmental effects and selection would be ineffective.

4.3.3 F_3 Progenies of Cross TU-94-02 x LBG-752

Characters such as number of branches per plant (GCV: 18.33 and PCV: 28.19), seed yield per plant (GCV: 18.22; PCV: 26.98), plant height (GCV: 17.04; PCV: 24.48), number of pods per cluster (GCV: 15.17; PCV: 25.13), number of clusters per plant (GCV: 13.58; PCV: 24.89), number of pods per plant (GCV: 11.39; PCV: 21.30) and harvest index(GCV: 10.87; PCV: 20.41) recorded moderate GCV with high PCV. Characters like SLA (45 DAS) (GCV: 14.67; PCV: 14.75), biomass per plant (GCV: 10.40; PCV: 19.87) and pod length (GCV: 10.28; PCV: 17.30) registered moderate GCV and PCV. SCMR (30 DAS) (GCV: 9.63; PCV: 13.82) and number of seeds per pod (GCV: 6.91; PCV: 14.52) recorded low GCV and moderate PCV. All the remaining characters *viz.,* days to 50% flowering (GCV: 6.94; PCV: 7.07), test weight (GCV: 5.67; PCV: 8.01), SCMR (45 DAS) (GCV: 5.06; PCV: 8.16), SLA (30 DAS) (GCV: 3.59; PCV: 3.87), days to maturity (GCV: 2.35; PCV: 2.49), SLW (30 DAS) (GCV: 2.21; PCV: 3.03) and SLW (45 DAS) (GCV: 1.10; PCV: 2.65) recorded low estimates of both GCV and PCV.

High estimates of heritability was recorded by days to 50% flowering (96.3%) followed by days to maturity (89.1%), SLA (45 DAS) (89.0%) and SLA (30 DAS) (86.2%). Characters *viz.,* SLW (30 DAS) (53.6%), test weight (50.1%), SCMR (30 DAS) (49.0%), plant height (48.4%), seed yield per plant (45.6%), number of branches per plant (42.3%), SCMR (45 DAS) (38.0%), number of pods per cluster (36.4%) and pod length (35.3%) registered moderate heritability whereas, number of clusters per plant (29.8%), number of pods per plant (28.6%), harvest index(28.0%), biomass per plant (27.0%), number of seeds per pod (22.6%) and SLW (45 DAS) (17.0%) registered low heritability in cross, TU-94-02 x LBG-752.

Highest estimate of genetic advance was recorded by SLA (45 DAS) (78.56). SLA (30 DAS) (16.85) recorded moderate genetic advance whereas, other characters like plant height (7.72), SCMR (30 DAS) (6.52), number of pods per plant (5.06), days to 50% flowering (4.91), harvest index(4.25), days to maturity (3.79), number of clusters per plant (3.56), seed yield per plant (3.22), biomass per plant (3.17), SCMR (45 DAS) (2.30), number of branches per plant (1.86), pod length (1.63), number of seeds per pod (1.44), number of pods per cluster (1.43), test weight (1.41), SLW (30 DAS) (1.22) and SLW (45 DAS) (1.05) registered low genetic advance.

High genetic advance as per cent of mean was registered for SLA (45 DAS) (30.07%), seed yield per plant (25.35%), number of branches per plant (24.55%) and plant height (24.42%). Characters such as number of pods per cluster (18.86%), number of clusters per plant (15.27%), days to 50% flowering (14.03%), SCMR (30 DAS) (13.81%), number of pods per plant (12.55%), pod length (12.58%), harvest index(11.93%) and biomass per plant (11.21%) recorded moderate genetic advance as per cent of mean. Low genetic advance as per cent of mean was recorded by test weight (8.26%), SLA (30 DAS) (6.85%), number of seeds per pod (6.78%), SCMR (45 DAS) (6.46%), SLW (45 DAS) (4.93%), days to maturity (4.57%) and SLW (30 DAS) (3.32%).

In cross TU-94-02 x LBG-752, characters such as number of branches per plant, seed yield per plant, plant height, number of pods per cluster, number of clusters per plant, number of pods per plant and harvest index recorded high PCV with moderate GCV. These results are in accordance with the earlier reports of Sharma *et al.* (2006) and Reddy *et al.* (2011) for plant height; Sharma *et al*. (2006) and Neelavati and Govindarasu (2010) for number of branches per plant; Gupta *et al.* (2003), Patel *et al.* (2014), Priyanka *et al.* (2016) and Hemalata *et al.* (2017) for number of clusters per plant and number of pods per cluster; Sharma *et al.* (2006) and Reddy *et al.* (2011) for number of pods per plant; Vijay *et al.* (2015) and Reddy *et al.* (2011) for seed yield per plant.

Characters like SLA (45 DAS), biomass per plant and pod length registered moderate GCV and PCV. SCMR (30 DAS) and number of seeds per pod recorded moderate PCV and low GCV. Low GCV was recorded for pod length by Ramya *et al.* (2014); number of seeds per pod by Gupta *et al.* (2003) and Anu *et al.* (2017); biomass per plant by Hemalata *et al.* (2017).

All the remaining characters *viz.,* days to 50% flowering, test weight, SCMR (45 DAS), SLA (30 DAS), days to maturity, SLW (30 DAS) and SLW (45 DAS) recorded low estimates of both GCV and PCV. Similar findings were reported by Gupta *et al.* (2003), Konda *et al.* (2009), Panigrahi *et al.* (2014), Anu *et al.* (2017) and Patidar *et al.* (2017) for days to 50% flowering, days to maturity and test weight.

Phenotypic co-efficient of variation was of high magnitude than the genotypic co-efficient of variation for all the 19 characters studied indicating the influence of environment in the expression of these traits in the cross, TU-94-02 x LBG-752. Characters such as number of branches per plant, seed yield per plant, plant height, number of pods per cluster, number of clusters per plant, number of pods per plant and harvest index recorded high PCV with moderate GCV. Therefore, simple selection could be effective for further improvement of these traits.

Days to 50% flowering, days to maturity, SLA (45 DAS) and SLA (30 DAS) recorded high levels of heritability. These characters may serve as effective selection parameters during breeding program for the improvement of productivity. For improving these characters, simple selection based on *per se* performance is more effective. High heritability for seed yield per plant suggests that direct selection for seed yield may be rewarding. Similar results were obtained by Vijay *et al.* (2015), Priyanka *et al.* (2016) and Panda *et al.* (2016) for days to 50% flowering; Konda *et al.* (2009) and Deepshika *et al.* (2014) for days to maturity.

Moderate estimates of heritability were recorded by characters such as SLW (30 DAS), test weight, SCMR (30 DAS), plant height, seed yield per plant, number of branches per plant, SCMR (45 DAS), number of pods per cluster and pod length. This indicates that the selection of these characters is likely to accumulate more additive genes leading to further improvement of their performance. Similar results were observed by Meshram *et al.* (2013) and Sowmini and Jayamani (2013), Deepshika *et al.* (2014) for plant height; Priyanka *et al.* (2016) for number of branches per plant; Anu *et al.* (2017) and Rolaniya *et al.* (2017) for pod length; Panigrahi *et al.* (2014) for seed yield per plant.

Number of clusters per plant, number of pods per plant, harvest index, biomass per plant, number of seeds per pod and SLW (45 DAS) registered low heritability.

High heritability coupled with high genetic advance as per cent of mean was recorded for SLA (45 DAS). It indicates the prevalence of additive gene action in the inheritance of these characters and there is less influence of the environment in the expression of these characters. Hence they are amenable for simple selection resulting in a high genetic gain.

Characters such as days to 50% flowering, biomass per plant and harvest index recorded high heritability with moderate genetic advance as per cent of mean. It indicates the presence of non additive gene action and role of environment in the expression of these traits. Therefore, traits which recorded higher estimates of genetic advance as per cent of mean are given priority while deciding selection strategies. The results were in accordance with the results reported by Jyothi *et al.* (2017) for harvest index.

Days to maturity, SLA (30 DAS), and SCMR (45 DAS) recorded high heritability with low genetic advance as per cent of mean. Low genetic advance as per cent of mean for days to maturity was observed by Anu *et al.* (2017) and Rolaniya *et al.* (2017).

Plant height, number of branches per plant and seed yield per plant showed moderate heritability with high genetic advance as per cent of mean. Presence of moderate heritability with high genetic advance as per cent of mean suggests that the individual plant selection can be made for the improvement of this trait. Rolaniya *et al.* (2017) observed high genetic advance as per cent of mean for plant height. Sowmini and Jayamani (2013) and Deepshika *et al.* (2014) observed high genetic advance as per cent of mean for number of branches per plant and seed yield per plant.

Moderate heritability with moderate genetic advance as per cent of mean was registered by number of pods per cluster, pod length and SCMR (30 DAS). Moderate heritability with low genetic advance as per cent of mean was recorded by test weight and SLW (45 DAS). It indicates that the character is highly influenced by environmental effects and selection would be ineffective. Moderate heritability with low genetic advance as per cent of mean for test weight was recorded by Veeramani *et al.* (2005) and Vijay *et al.* (2015).

Number of clusters per plant and number of pods per plant recorded low heritability with moderate genetic advance as per cent of mean whereas, number of seeds per pod and SLW (30 DAS) registered low heritability with low genetic advance as per cent of mean.

4.4. CHARACTER ASSOCIATION ANALYSIS

Selection for specific character is known to result in correlated response in certain other characters. Yield is a complex trait determined by several component traits. Hence selection for yield should take into account related traits as well. Correlation coefficient analysis gives the total mutual relationship between the component traits. In this experiment, the correlation coefficients were computed to know the direction and magnitude of association between yield and its components and also with various physiological attributes in F_3 generation of the three crosses, LBG-787 x LBG-752, TU-94-02 x KU-1006 and TU-94-02 x LBG-752.

4.4.1 F_3 Progenies of cross LBG-787 x LBG-752

The results regarding association of seed yield per plant with yield contributing and physiological attributes in cross, LBG-787 x LBG-752 were presented in Table 4.6 and Table 4.7 respectively.

4.4.1.1 Correlation between seed yield and its contributing attributes

The seed yield or economic yield per plant in almost all crops is referred as super character which results from the multiplicative interactions of several other characters that are termed as yield components. Thus, genetic architecture of seed yield in urdbean is based on the balance or overall net effect produced by various yield components directly with one another. Therefore, identification of important yield components and information about their association with yield and also with each other is very useful for selecting efficient genotypes for evolving high yielding varieties.

Seed yield per plant exhibited significant negative correlation with days to maturity (r_p = -0.422**, r_g = -0.472**) indicating that early maturing varieties gives higher yield. Singh *et al.* (2014) also reported negative association between seed yield and days to maturity.

Significant positive correlation was observed between seed yield per plant and number of pods per cluster (r_p = 0.968**, r_g = 0.992**), test weight (r_p = 0.910**, r_g = 0.933**), number of pods per plant (r_p = 0.900**, r_g = 0.935**), plant height (r_p = 0.885**, r_g = 0.911**), number of clusters per plant (r_p = 0.883**, r_g = 0.924**), pod length (r_p = 0.852**, r_g = 0.880**), number of branches per plant (r_p = 0.646**, r_g = 0.679**) and number of seeds per pod (r_p = 0.306*, r_g = 0.318*). Therefore, these characters emerged as most important associates of seed yield per plant. The occurrence of positive association at significant level of seed yield with most of its component traits reveals that the situation is favourable from breeding point of view indicating that the selection for one trait may bring correlated response for improvement of other traits which are positively associated with seed yield per plant.

The existence of positive associations between seed yield and its components for providing rapid improvement of characters due to correlated response during selection is in agreement with the reports of Gupta *et al.* (2003), Singh *et al.* (2007), Mehra *et al.* (2016) and Suguna *et al.* (2017) for plant height; by Santha and Pramasivam (1999), Venkatesan *et al.* (2004),

Table 4.6 Genotypic (r_g) and phenotypic (r_p) correlation coefficients among seed yield and its contributing attributes in F_3 generation of cross LBG-787 x LBG-752 in blackgram

Character		DF	DM	PH	NB	NCP	NPC	NPP	PL	NSP	TW	SY
DF	rg	1.000	0.119	-0.029	0.072	0.196	-0.080	0.036	0.108	0.764**	0.050	-0.163
	rp	1.000	0.161	-0.029	0.083	0.174	-0.075	0.037	0.094	0.713**	0.056	-0.154
DM	rg		1.000	-0.287*	0.003	-0.379**	-0.486**	-0.460**	-0.489**	-0.427**	-0.515**	-0.472**
	rp		1.000	-0.267	0.002	-0.354*	-0.454**	-0.425**	-0.453**	-0.378**	-0.466**	-0.422**
PH	rg			1.000	0.603**	0.932**	0.920**	0.966**	0.858**	0.261	0.825**	0.911**
	rp			1.000	0.577**	0.923**	0.906**	0.962**	0.853**	0.258	0.810**	0.885**
NB	rg				1.000	0.694**	0.713**	0.600**	0.698**	0.224	0.623**	0.679**
	rp				1.000	0.668**	0.696**	0.581**	0.669**	0.210	0.589**	0.646**
NCP	rg					1.000	0.947**	0.959**	0.942**	0.556**	0.931**	0.924**
	rp					1.000	0.930**	0.954**	0.934**	0.544**	0.902**	0.883**
NPC	rg						1.000	0.944**	0.922**	0.382**	0.933**	0.992**
	rp						1.000	0.933**	0.906**	0.374**	0.921**	0.968**
NPP	rg							1.000	0.878**	0.423**	0.918**	0.935**
	rp							1.000	0.871**	0.417**	0.899**	0.900**
PL	rg								1.000	0.493**	0.838**	0.880**
	rp								1.000	0.489**	0.816**	0.852**
NSP	rg									1.000	0.578**	0.318*
	rp									1.000	0.559**	0.306*
TW	rg										1.000	0.933**
	rp										1.000	0.910**
SY	rg											1.000
	rp											1.000

* significant at 5% probability level ** significant at 1% probability level

DF - Days to 50% flowering
NB - No. of branches
NPP - Number of pods per plant
DM - Days to maturity
NCP - No. of clusters per plant
PL - Pod length (cm)
PH - Plant height (cm)
NPC - No. pods per cluster
NSP - No. seeds per pod
TW - Test Weight (g)
SY - Seed Yield per plant (g)

Table 4.7 **Genotypic (r_g) and phenotypic (r_p) correlation coefficients among seed yield and physiological attributes in F_3 generation of cross LBG-787 x LBG-752 in blackgram**

Character		**SLA (30 DAS)**	**SLA (45 DAS)**	**SLW (30 DAS)**	**SLW (45 DAS)**	**SCMR (30DAS)**	**SCMR (45DAS)**	**BMP**	**HI**	**SY**
SLA (30 DAS)	r_g	**1.000**	0.678**	-0.505**	-0.387**	-0.023	-0.357*	-0.754**	0.174	-0.200
	r_p	**1.000**	0.662**	-0.499**	-0.352*	-0.033	-0.345*	-0.684**	0.139	-0.197
SLA (45 DAS)	r_g		**1.000**	-0.338*	-0.676**	0.016	-0.198	-0.503**	0.215	-0.103
	r_p		**1.000**	-0.332*	-0.632**	0.014	-0.179	-0.461**	0.188	-0.096
SLW (30 DAS)	r_g			**1.000**	0.284	0.718**	0.800**	0.950**	0.715**	0.920**
	r_p			**1.000**	0.268	0.621**	0.775**	0.845**	0.608**	0.904**
SLW (45 DAS)	r_g				**1.000**	0.298*	0.421**	0.265	0.242	0.260
	r_p				**1.000**	0.232	0.388**	0.257	0.160	0.237
SCMR (30DAS)	r_g					**1.000**	0.871**	0.563**	0.934**	0.931**
	r_p					**1.000**	0.725**	0.454**	0.645**	0.785**
SCMR (45DAS)	r_g						**1.000**	0.669**	0.806**	0.882**
	r_p						**1.000**	0.588**	0.671**	0.852**
BMP	r_g							**1.000**	0.475**	0.781**
	r_p							**1.000**	0.156	0.644**
HI	r_g								**1.000**	0.897**
	r_p								**1.000**	0.829**
SY	r_g									**1.000**
	r_p									**1.000**

*** significant at 5% probability level** **** significant at 1% probability level**

SLA (30 DAS) - Specific Leaf Area at 30 DAS (cm^2 g^{-1})
SLW (30 DAS) - Specific Leaf Weight at 30 DAS (g cm^{-2})
SCMR (30DAS) - SPAD Chlorophyll Meter Reading at 30 DAS
BMP - Biomass per plant (g)

SLA (45 DAS) - Specific Leaf Area at 45 DAS (cm^2 g^{-1})
SLW (45DAS) - Specific Leaf Weight at 45 DAS (g cm^{-2})
SCMR (45DAS) - SPAD Chlorophyll Meter Reading at 30 DAS
HI - Harvest Index (%)

Chauhan *et al.* (2007) and Sateesh *et al.* (2016) for number of branches per plant; Haritha and Sekhar (2002), Chauhan *et al.* (2007), Konda *et al.* (2008) and Rahim *et al.* (2010) for number of clusters per plant; Wanjari (1988), Babu (1998), Chauhan *et al.* (2007) and Sohel *et al.* (2016) for number of pods per cluster; Patel and Shah (1982), Natarajan and Rathinasamy (1999), Gafoor *et al.* (2000) and Kadam *et al.* (2008) for number of pods per plant; Haritha and Sekhar (2002), Chauhan *et al.* (2007), Singh *et al.* (2007), Konda *et al.* (2008) and Suguna *et al.* (2017) for pod length; Chauhan *et al.* (2007), Singh *et al.* (2007), Konda *et al.* (2008) and Suguna *et al.* (2017) for number of seeds per pod; Gafoor *et al.* (2000), Gupta *et al.* (2003), Mehra *et al.* (2016), Rasel *et al.* (2016) and Suguna *et al.* (2017) for test weight.

Days to 50 % flowering showed significant positive correlation only with number of seeds per pod (r_p = 0.713**, r_g = 0.764**). For all the remaining characters, the correlation is non-significant. Sharma (2015) and Singh *et al.* (2016) observed similar pattern of significant positive association between of days to 50 % flowering and number of seeds per pod.

Days to maturity showed significant negative correlation with all the characters *viz.,* test weight (r_p = -0.466**, r_g = -0.515**), number of pods per cluster (r_p = -0.454**, r_g = -0.486**), pod length (r_p = -0.453**, r_g = -0.489**), number of pods per plant (r_p = -0.425**, r_g = -0.460**), number of seeds per pod (r_p = -0.378**, r_g = -0.427**) and number of clusters per plant (r_p = -0.354*, r_g = -0.354**) except for days to 50% flowering and number of branches per plant. This indicates that selection for early maturing varieties would automatically result in plants with good seed yield contributing characters realizing higher yield. Similar trend of negative association of days to maturity was observed by Gafoor *et al.* (2000) for number of seeds per pod and test weight; Panigrahi *et al.* (2014) and Gowsalya *et al.* (2016) for number of pods per cluster and number of pods per plant.

Plant height exhibited significant positive correlation with number of pods per plant ($r_p = 0.962^{**}$, $r_g = 0.967^{**}$), number of clusters per plant ($r_p = 0.923^{**}$, $r_g = 0.932^{**}$), number of pods per cluster ($r_p = 0.906^{**}$, $r_g = 0.920^{**}$), test weight ($r_p = 0.810^{**}$, $r_g = 0.825^{**}$), pod length ($r_p = 0.853^{**}$, $r_g = 0.858^{**}$) and number of branches per plant ($r_p = 0.577^{**}$, $r_g = 0.603^{**}$). It suggests that selection for tall plants could result in attaining more number of branches with more pod bearing clusters. All these characters could result in higher seed yield since they are also having significant positive association with seed yield. Similar kind of significant and positive association of plant height was reported by Suguna *et al.* (2017) for number of branches per plant and test weight; Kanimoli *et al.* (2015) for number of pods per cluster; Sushmitharaj *et al.* (2018) for number of clusters per plant; Singh *et al.* (2007), Kadam *et al.* (2008), Rahim *et al.* (2010) and Suguna *et al.* (2017) for number of pods per plant; Sunil kumar *et al.* (2003), Singh *et al.* (2007), Isha Parveen *et al.* (2011), Vijay *et al.* (2015) and Suguna *et al.* (2017) for pod length.

Number of branches per plant exhibited significant positive correlation with number of pods per cluster ($r_p = 0.696^{**}$, $r_g = 0.713^{**}$), pod length ($r_p = 0.669^{**}$, $r_g = 0.698^{**}$), number of clusters per plant ($r_p = 0.668^{**}$, $r_g = 0.694^{**}$), test weight ($r_p = 0.589^{**}$, $r_g = 0.623^{**}$), number of pods per plant ($r_p = 0.581^{**}$, $r_g = 0.600^{**}$). The results suggest that plants with more branches have more pods which are longer in size. Similar kind of significant and positive association of number of branches were obtained by Suguna *et al.* (2017) for test weight; Natarajan and Rathinasamy (1999), Kanimoli *et al.*

(2015), Vijay *et al*. (2015) and Suguna *et al.* (2017) for number of clusters per plant; Kanimoli *et al.* (2015) for number of pods per cluster; Natarajan and Rathinasamy (1999), Gafoor *et al.* (2000), Shivade *et al.* (2011), Kanimoli *et al.* (2015) and Suguna *et al.* (2017) for number of pods per plant; Suguna *et al.* (2017) for pod length.

Number of clusters per plant exhibited significant positive correlation with number of pods per plant (r_p = 0.954**, r_g = 0.959**), pod length (r_p = 0.934**, r_g = 0.942**), number of pods per cluster (r_p = 0.930**, r_g = 0.947**), test weight (r_p = 0.902**, r_g = 0.931**) and number of seeds per pod (r_p = 0.544**, r_g = 0.556**). Number of clusters per plant registered significant and positive association with number of pods per plant emphasizing that more the number of pod bearing clusters more will be the number of pods per plant which is an important yield contributing character. This also results in longer pods with more number of seeds. The results were in accordance with results obtained by Kanimoli *et al.* (2015) for number of pods per cluster and test weight; Sunil kumar *et al.* (2003), Venkatesan *et al.* (2004), Isha Parveen *et al*. (2011), Kanimoli *et al.* (2015) and Suguna *et al.* (2017) for number of pods per plant and pod length; Kasundra *et al.* (1995), Chauhan *et al*. (2007), Kishore kumar (2008) and Kanimoli *et al.* (2015) for number of seeds per pod.

Number of pods per cluster exhibited positive correlation with number of pods per plant (r_p = 0.933**, r_g = 0.944**), test weight (r_p = 0.921**, r_g = 0.933**), pod length (r_p = 0.906**, r_g = 0.922**) and number of seeds per pod (r_p = 0.374**, r_g = 0.382**). These results emphasize that more the number of pods per cluster more will be the number of pods per plant. It also indicates that clusters with more number of pods result in longer pods with more number of seeds because with the increase in the number of pods per cluster. This is because, when more number of pods are present within a cluster it will give less space for the girth wise development of the pod. So, the pods will increase length wise to accommodate more pods in a single cluster. The results were in accordance with results obtained by Kanimoli *et al.* (2015) for test weight; Isha Parveen *et al.* (2011) and Kanimoli *et al.* (2015) for number of pods per plant; Singh *et al.* (2009) for pod length in greengram; Kanimoli *et al.* (2015) for number of seeds per pod.

Number of pods per plant exhibited significant positive correlation with test weight ($r_p = 0.899^{**}$, $r_g = 0.918^{**}$), pod length ($r_p = 0.871^{**}$, $r_g = 0.878^{**}$) and number of seeds per pod ($r_p = 0.417^{**}$, $r_g = 0.423^{**}$). These results indicate that selection for plants with more number of pods will result in obtaining longer pods with more number of seeds. The results obtained for number of pods per plant were in accordance with results obtained by Singh *et al.* (2007) for pod length; Gafoor *et al.* (2000), Sunil kumar *et al.* (2003), Konda *et al.* (2008), Suresh *et al.* (2013), Kanimoli *et al.* (2015) and Vijay *et al.* (2015) for number of seeds per pod; Satya *et al.* (2018) for test weight.

Pod length exhibited significant positive correlation with test weight ($r_p = 0.816^{**}$, $r_g = 0.838^{**}$) and number of seeds per pod ($r_p = 0.489^{**}$, $r_g = 0.493^{**}$). These results emphasize that longer pods result in more number of bold seeds per pod which weigh high. Similar kind of positive association of pod length with number of seeds per pod was registered by Umadevi and Meenakshi Ganesan (2005), Singh *et al.* (2007), Vijay *et al.* (2015) and with test weight by and Suguna *et al.* (2017).

Number of seeds per pod exhibited significant positive correlation with test weight ($r_p = 0.559^{**}$, $r_g = 0.578^{**}$). Positive association between seeds per pod and test weight indicates that with increase in the number of seeds, there will be an increase in their weight. Similar findings for significant positive correlation for number of seeds per pod with test weight were reported by Satya *et al.* (2018).

Based on the correlation studies, more emphasis in selection programmes is to be given on number of pods per cluster, test weight, number of pods per plant, plant height, number of clusters per plant, pod length, number of branches per plant and number of seeds per pod. The direct association between seed yield and the above yield contributing characters reveals less complex relationships between them. Therefore selection of one trait result in correlated response for other positively related traits.

4.4.1.2 Correlation between seed yield and physiological attributes

Seed yield per plant has significant positive association with physiological traits like SLW (30 DAS) ($r_p = 0.904^{**}$, $r_g = 0.920^{**}$), SCMR (45 DAS) ($r_p = 0.852^{**}$, $r_g = 0.882^{**}$), harvest index ($r_p = 0.829^{**}$, $r_g = 0.897^{**}$), SCMR (30 DAS) ($r_p = 0.785^{**}$, $r_g = 0.931^{**}$) and biomass per plant ($r_p = 0.644^{**}$, $r_g = 0.781^{**}$). The results suggest that plants with high biomass and harvest index results in high seed yield. Therefore, it can be suggested that direct selection of these three physiological traits will lead to yield improvement. Similar findings were stated by Sudhakar *et al.* (2006) for SCMR; Gupta *et al.* (2003), Shivade *et al.* (2011) and Manish and Hemalata (2017) for biomass per plant; Veeranjaneelu *et al.* (2007), Gul *et al.* (2008), Isha Parveen *et al.* (2011) and Vijay *et al.* (2015) for harvest index. In Groundnut, Kyaw *et al.* (2017) observed significant positive correlation of SCMR with seed yield per plant.

SLA taken at 30 DAS has significant positive correlation with only SLA (45 DAS) ($r_p = 0.662^{**}$, $r_g = 0.678^{**}$) and significant negative association with other physiological traits. Inverse relation between SLA and SLW indicates that with the increase in one character, other character decreases. Plants with low SLA have high chlorophyll content per unit area. Similar type of results was observed by Sudhakar *et al.* (2006).

SLW taken at 30 DAS exhibited significant positive correlation with biomass per plant ($r_p = 0.845^{**}$, $r_g = 0.950^{**}$), SCMR (45 DAS) ($r_p = 0.775^{**}$, $r_g = 0.800^{**}$), SCMR (30 DAS) ($r_p = 621^{**}$, $r_g = 0.718^{**}$) and harvest index ($r_p = 0.608^{**}$, $r_g = 0.715^{**}$). SLW taken at 45 DAS has significant positive correlation with SCMR (45 DAS) ($r_p = 0.388^{**}$, $r_g = 0.421^{**}$). Plants with more SLW have high concentration of chlorophyll per unit area resulting in high biomass and harvest index. Similar finding of SLW with harvest index was observed by Kyaw *et al.* (2017) in groundnut.

SCMR taken at 30 DAS has significant positive correlation with SCMR (45 DAS) ($r_p = 0.725^{**}$, $r_g = 0.871^{**}$), harvest index ($r_p = 0.645^{**}$, $r_g = 0.934^{**}$) and biomass per plant ($r_p = 0.454^{**}$, $r_g = 0.563^{**}$). SCMR taken at 45 DAS has significant positive correlation with harvest index ($r_p = 0.671^{**}$, $r_g = 0.806^{**}$) and biomass per plant ($r_p = 0.588^{**}$, $r_g = 0.669^{**}$). In Groundnut, Kyaw *et al.* (2017) observed significant positive correlation of SCMR with harvest index. From the above results, we can infer that with the increase in SCMR, both biological yield and seed yield increases, thereby increasing harvest index. Sudhakar *et al.* (2006) observed significant positive correlation of SCMR with seed yield per plant.

The above results suggest that the plant types with low leaf area and high SCMR reading recorded high biomass and harvest index which contribute to higher yield. Therefore, selection for these traits results in physiologically robust genotypes with higher seed yield.

4.4.2 F_3 progenies of Cross TU-94-02 x KU-1006

The results regarding association of seed yield per plant with yield contributing and physiological attributes in cross, TU-94-02 x KU-1006 are presented in Table 4.8 and Table 4.9 respectively.

4.4.2.1 Correlation between seed yield and its contributing attributes

Among all the progenies, seed yield per plant has significant positive correlation with number of pods per cluster ($r_p = 0.928^{**}$, $r_g = 0.942^{**}$), number of clusters per plant ($r_p = 0.915^{**}$, $r_g = 0.920^{**}$), number of pods per plant ($r_p = 0.903^{**}$, $r_g = 0.912^{**}$), plant height ($r_p = 0.783^{**}$, $r_g = 0.762^{**}$), pod length ($r_p = 0.0.732^{**}$, $r_g = 0.778^{**}$), number of branches per plant ($r_p = 0.722^{**}$, $r_g = 0.699^{**}$), number of seeds per pod ($r_p = 0.672^{**}$, $r_g =0.676^{**}$),

Table 4.8 Genotypic (r_g) and phenotypic (r_p) correlation coefficients among seed yield and its contributing attributes in F_3 generation of cross TU-94-02 x KU-1006 in blackgram

Character		DF	DM	PH	NB	NCP	NPC	NPP	PL	NSP	TW	SY
DF	r_g	**1.000**	0.575**	0.198	0.423**	0.493**	0.448**	0.500**	0.686**	0.619**	-0.340*	0.381**
	r_p	**1.000**	0.335*	0.183	0.363*	0.416**	0.366*	0.420**	0.505**	0.473**	-0.102	0.328*
DM	r_g		**1.000**	0.041	0.194	0.386**	0.203	0.349*	-0.080	0.061	-0.235	0.332*
	r_p		**1.000**	0.097	0.213	0.355*	0.224	0.300*	0.123	0.188	0.179	0.293*
PH	r_g			**1.000**	0.675**	0.486**	0.646**	0.481**	0.555**	0.805**	-0.507**	0.762**
	r_p			**1.000**	0.703**	0.530**	0.674**	0.516**	0.583**	0.771**	-0.240	0.783**
NB	r_g				**1.000**	0.712**	0.501**	0.706**	0.656**	0.777**	-0.180	0.699**
	r_p				**1.000**	0.732**	0.561**	0.717**	0.688**	0.782**	-0.056	0.722**
NCP	r_g					**1.000**	0.884**	0.901**	0.811**	0.566**	-0.027	0.920**
	r_p					**1.000**	0.873**	0.989**	0.776**	0.611**	0.014	0.915**
NPC	r_g						**1.000**	0.890**	0.855**	0.635**	-0.206	0.942**
	r_p						**1.000**	0.880**	0.820**	0.677**	-0.074	0.928**
NPP	r_g							**1.000**	0.854**	0.587**	0.006	0.912**
	r_p							**1.000**	0.764**	0.585**	0.022	0.903**
PL	r_g								**1.000**	0.794**	-0.191	0.778**
	r_p								**1.000**	0.879**	-0.036	0.732**
NSP	r_g									**1.000**	-0.361*	0.676**
	r_p									**1.000**	-0.114	0.672**
TW	r_g										**1.000**	-0.277
	r_p										**1.000**	-0.125
SY	r_g											**1.000**
	r_p											**1.000**

*** significant at 5% probability level** **** significant at 1% probability level**

DF - Days to 50% flowering
DM - Days to maturity
PH - Plant height (cm)
TW - Test Weight (g)
NB - No. of branches
NCP - No. of clusters per plant
NPC - No. pods per cluster
SY - Seed Yield per plant (g)
NPP - Number of pods per plant
PL - Pod length (cm)
NSP - No. seeds per pod

Table 4.9 Genotypic (r_g) and phenotypic (r_p) correlation coefficients among seed yield and physiological attributes in F_3 generation of cross TU-94-02 x KU-1006 in blackgram

Character		**SLA (30 DAS)**	**SLA (45 DAS)**	**SLW (30 DAS)**	**SLW (45 DAS)**	**SCMR (30DAS)**	**SCMR (45DAS)**	**BMP**	**HI**	**SY**
SLA (30 DAS)	r_g	**1.000**	0.980**	-0.981**	-0.954**	-0.975**	-0.817**	-0.657**	-0.638**	-0.625**
	r_p	**1.000**	0.878**	-0.893**	-0.834**	-0.886**	-0.750**	-0.652**	-0.609**	-0.607**
SLA (45 DAS)	r_g		**1.000**	-0.968**	-0.992**	-0.911**	-0.690**	-0.473**	-0.456**	-0.446**
	r_p		**1.000**	-0.943**	-0.985**	-0.953**	-0.706**	-0.507**	-0.505**	-0.487**
SLW (30 DAS)	r_g			**1.000**	0.979**	0.940**	0.588**	0.399**	0.366*	0.353*
	r_p			**1.000**	0.952**	0.931**	0.603**	0.428**	0.418**	0.388**
SLW (45 DAS)	r_g				**1.000**	0.990**	0.584**	0.354*	0.332*	0.322*
	r_p				**1.000**	0.935**	0.605**	0.388**	0.384**	0.366**
SCMR (30DAS)	r_g					**1.000**	0.745**	0.534**	0.508**	0.514**
	r_p					**1.000**	0.749**	0.556**	0.545**	0.536**
SCMR (45DAS)	r_g						**1.000**	0.959**	0.924**	0.956**
	r_p						**1.000**	0.950**	0.912**	0.957**
BMP	r_g							**1.000**	0.972**	0.997**
	r_p							**1.000**	0.935**	0.989**
HI	r_g								**1.000**	0.963**
	r_p								**1.000**	0.940**
SY	r_g									**1.000**
	r_p									**1.000**

*** significant at 5% probability level** **** significant at 1% probability level**

SLA (30 DAS) - Specific Leaf Area at 30 DAS ($cm^2 g^{-1}$)
SLW (30 DAS) - Specific Leaf Weight at 30 DAS ($g cm^{-2}$)
SCMR (30DAS) - SPAD Chlorophyll Meter Reading at 30 DAS
BMP - Biomass per plant (g)
SLA (45 DAS) - Specific Leaf Area at 45 DAS ($cm^2 g^{-1}$)
SLW (45DAS) - Specific Leaf Weight at 45 DAS ($g cm^{-2}$)
SCMR (45DAS) - SPAD Chlorophyll Meter Reading at 30 DAS
HI - Harvest Index (%)

days to 50% flowering (r_p = 0.328*, r_g = 0.381**) and days to maturity (r_p = 0.293*, r_g = 0.332*). The results infer that tall plants produce more number of branches along with increased number of pods per plant. This ultimately enhances the seed yield of the plant. The existence of positive associations between seed yield and its components for providing rapid improvement of characters due to correlated response during selection is in agreement with the reports of by Sharma (2015) and Singh *et al.* (2016) for days to 50% flowering; Singh *et al.* (2014) for days to maturity Parameshwarappa and Kumar (2005), Gupta *et al.* (2003), Singh *et al.* (2007), Mehra *et al.* (2016) and Suguna *et al.* (2017) for plant height; by Santha and Pramasivam (1999), Venkatesan *et al.* (2004), Chauhan *et al.* (2007), Sateesh *et al.* (2016) for number of branches per plant; Haritha and Sekhar (2002), Chauhan *et al*. (2007), Konda *et al.* (2008) and Rahim *et al.* (2010) for number of clusters per plant; Wanjari (1988), Babu (1998), Chauhan *et al.* (2007) and Sohel *et al.* (2016) for number of pods per cluster; Patel and Shah (1982), Natarajan and Rathinasamy (1999), Gafoor *et al.* (2000) and Kadam *et al.* (2008) for number of pods per plant; Haritha and Sekhar (2002), Chauhan *et al.* (2007), Singh *et al.* (2007), Konda *et al.* (2008) and Suguna *et al.* (2017) for pod length; Chauhan *et al.* (2007), Singh *et al.* (2007), Konda *et al.* (2008) and Suguna *et al.* (2017) for number of seeds per pod.

Days to 50 % flowering exhibited significant positive correlation with all the characters *viz.,* pod length (r_p = 0.505**, r_g = 0.686**), number of seeds per pod (r_p = 0.473**, r_g = 0.619**), number of pods per plant (r_p = 0.420*, r_g = 0.500**), number of clusters per plant (r_p = 0.416**, r_g = 0.493**), number of pods per cluster (r_p = 0.366*, r_g = 0.448**), number of branches per plant (r_p = 0.363*, r_g = 0.423**) and days to maturity (r_p = 0.335*, r_g = 0.575**) except for plant height and test weight. On contrary, negative relation of days to 50% flowering was observed by Bandi *et al.* (2018) for number of clusters per plant, number of pods per plant whereas, Gafoor *et al.* (2000) and Mehra *et al.* (2016) observed positive association with days to maturity; Sharma *et al.* (2015) and Singh *et al.* (2016) for number of seeds per pod.

Significant positive correlation was observed between days to maturity, number of clusters per plant ($r_p = 0.355^*$, $r_g = 0.386^{**}$) and number of pods per plant ($r_p = 0.300^*$, $r_g = 0.349^{**}$) whereas, plant height registered significant positive association with number of seeds per pod ($r_p = 0.771^{**}$, $r_g = 0.805^{**}$), number of branches per plant ($r_p = 0.703^{**}$, $r_g = 0.675^{**}$), number of pods per cluster ($r_p = 0.674^{**}$, $r_g = 0.646^{**}$), pod length ($r_p = 0.583^{**}$, $r_g = 0.555^{**}$), number of clusters per plant ($r_p = 0.530^{**}$, $r_g = 0.486^{**}$) and number of pods per plant ($r_p = 0.516^{**}$, $r_g = 0.481^{**}$). Selection of tall plants result in obtaining plants with more number of pods bearing clusters as they are directly associated. Direct selection for these characters helps us in enhancing seed yield. Similar kind of significant and positive association of plant height was reported by Suguna *et al.* (2017) for number of branches and number of seeds per pod; Kanimoli *et al.* (2015) for number of pods per cluster; Singh *et al.* (2007), Kadam *et al.* (2008), Rahim *et al.* (2010) and Suguna *et al.* (2017) for number of pods per plant; Sunil kumar *et al.* (2003), Singh *et al.* (2007), Isha Parveen *et al.* (2011), Vijay *et al.* (2015) and Suguna *et al.* (2017) for pod length.

Number of branches per plant recorded significant positive correlation with number of seeds per pod ($r_p = 0.782^{**}$, $r_g = 0.777^{**}$), number of clusters per plant ($r_p = 0.732^{**}$, $r_g = 0.712^{**}$), number of pods per plant ($r_p = 0.717^{**}$, $r_g = 0.706^{**}$), pod length ($r_p = 0.688^{**}$, $r_g = 0.656^{**}$) and number of pods per cluster ($r_p = 0.561^{**}$, $r_g = 0.501^{**}$). Selection for plants with more number of branches results in plants with more number of pods as they are positively associated. Such kind of plants are desirable as they are high yielders.Similar kind of significant and positive association of number of branches was obtained by Natarajan and Rathinasamy (1999), Kanimoli *et al.* (2015), Vijay *et al.* (2015) and Suguna *et al.* (2017) for number of clusters per plant; Kanimoli *et al.* (2015) for number of pods per cluster; Natarajan and Rathinasamy (1999), Gafoor *et al.* (2000), Shivade *et al.* (2011), Kanimoli *et al.* (2015) and Suguna *et al.* (2017) for number of pods per plant; Suguna *et al.* (2017) for pod length and number of seeds per pod.

Number of clusters per plant has significant positive association with number of pods per plant ($r_p = 0.989^{**}$, $r_g = 0.901^{**}$), number of pods per cluster ($r_p = 0.873^{**}$, $r_g = 0.884$), pod length ($r_p = 0.776^{**}$, $r_g = 0.811^{**}$) and number of seeds per pod ($r_p = 0.611^{**}$, $r_g = 0.566^{**}$). The results were in accordance with results obtained by Kanimoli *et al.* (2015) for number of pods per cluster; Sunil kumar *et al.* (2003), Venkatesan *et al.* (2004), Isha Parveen *et al.* (2011), Kanimoli *et al.* (2015) and Suguna *et al.* (2017) for number of pods per plant and pod length; Kasundra *et al.* (1995), Chauhan *et al.* (2007), Kishore kumar *et al.* (2008) and Kanimoli *et al.* (2015) for number of seeds per pod. The results indicate that if the number of clusters are more then there will be increase in number of pods per plant due to positive association present between them.

Number of pods per cluster has registered significant positive correlation with number of pods per plant ($r_p = 0.880^{**}$, $r_g = 0.890^{**}$), pod length ($r_p = 0.820^{**}$, $r_g = 0.855^{**}$) and number of seeds per pod ($r_p = 0.677^{**}$, $r_g = 0.635^{**}$). As the number of clusters per plant increases, number of pods automatically increases the seed yield. In addition, with the increase in number of pods per plant, the pod length also increases accommodating more number of seeds. Similar results were obtained by Singh *et al.* (2009) for pod length in greengram; Isha Parveen *et al.* (2011) and Kanimoli *et al.* (2015) for number of pods per plant; Kanimoli *et al.* (2015) for number of seeds per pod.

Number of pods per plant has shown significant positive correlation with pod length ($r_p = 0.764^{**}$, $r_g = 0.854^{**}$) and number of seeds per pod ($r_p = 0.585^{**}$, $r_g = 0.587^{**}$). The results suggest that plants bearing large number of pods have longer pods with more number of seeds. Similar results were noticed by Singh *et al.* (2007) for pod length; Gafoor *et al.* (2000), Sunil kumar *et al.* (2003), Konda *et al.* (2008) and Suresh *et al.* (2013) for number of seeds per pod.

Pod length has significant positive correlation with number of seeds per pod ($r_p = 0.879^{**}$, $r_g = 0.794^{**}$). From the results it can be concluded that long pods have more number of seeds.Direct association between pod length and number of seeds per pod was also observed by Gafoor *et al.* (2000), Umadevi and Meenakshi Ganesan (2005), Singh *et al.* (2007), Vijay *et al.* (2015) and Suguna *et al.* (2017)

In brief, on the basis of association studies in cross TU-94-02 x KU-1006 more emphasis is to be given on number of clusters per plant, number of pods per cluster, number of pods per plant, plant height, pod length, number of branches per plant and number of seeds per pod during selection of genotypes as selection of one trait results in correlated response for other positively related traits. The results indicate that there is less complex relationships between them as they are positively associated.

4.4.2.2 Correlation between seed yield and physiological attributes

Seed yield per plant has significant positive correlation with biomass per plant (r_p = 0.989**, r_g = 0.997**), SCMR (45 DAS) (r_p = 0.957**, r_g = 0.956**), harvest index (r_p = 0.940**, r_g = 0.963**), SCMR (30 DAS) (r_p = 0.536**, r_g = 0.514**), SLW (30 DAS) (r_p = 0.388**, r_g = 0.353*) and SLW (45 DAS) (r_p = 0.366**, r_g = 0.322*). From the results, it can be concluded that direct selection for the above physiological traits will lead to yield enhancement as they result in plants with high biomass and harvest index.

SLA taken at 30 DAS has significant positive correlation with SLA (45 DAS) (r_p = 0.878**, r_g = 0.980**) and significant negative correlation with SLW (30 DAS) (r_p = -0.893**, r_g = -0.981**), SCMR (30 DAS) (r_p = -0.886**, r_g = -0.975**), SLW (45 DAS) (r_p = -0.834**, r_g = -0.954**), SCMR (45 DAS) (r_p = -0.750**, r_g = -0.817**), biomass per plant (r_p = -0.652**, r_g = -0.657**) and harvest index (r_p = -0.609**, r_g = -0.638**). SLA taken at 45 DAS has significant negative correlation with SLW (45 DAS) (r_p = -0.985**, r_g = -0.992**), SCMR (30 DAS) (r_p = -0.953**, r_g = -0.911**), SLW (30 DAS) (r_p = -0.943**, r_g = -0.968**), SCMR (45 DAS) (r_p = -0.706**, r_g = -0.690**), biomass per plant (r_p = -0.507**, r_g = -0.473**) and harvest index (r_p = -0.505**, r_g = -0.456**). The results infer that with the decrease in leaf area, the amount of transpiration decreases, thereby more water is available for photosynthesis. This increases biomass ultimately enhancing yield. Similar finding of negative correlation of SLA with SCMR was observed by Sudhakar *et al.* (2006).

SLW taken at 30 DAS recorded significant positive correlation with SLW (45 DAS) (r_p = 0.952**, r_g = 0.979**), SCMR (30 DAS) (r_p = 931**, r_g = 0.940**), SCMR (45 DAS) (r_p = 0.603**, r_g = 0.588**), biomass per plant (r_p = 0.428**, r_g = 0.399**) and harvest index (r_p = 0.418**, r_g = 0.366*). SLW taken at 45 DAS registered significant positive correlation with SCMR (30 DAS) (r_p = 935**, r_g = 0.990**), SCMR (45 DAS) (r_p = 0.605**, r_g = 0.584**), biomass per plant (r_p = 0.388**, r_g = 0.354*) and harvest index (r_p = 0.384**, r_g = 0.332*). Hence, positive association between SLW and SCMR indicate that with the increase in chlorophyll content in leaves, leaf weight increases resulting in increased biomass per plant.

SCMR taken at 30 DAS shown significant positive correlation with SCMR (45 DAS) (r_p = 0.749**, r_g = 0.745**), biomass per plant (r_p = 0.556**, r_g = 0.534**) and harvest index (r_p = 0.545**, r_g = 0.508**). SCMR taken at 45 DAS has significant positive correlation with biomass per plant (r_p = 0.950**, r_g = 0.959**) and harvest index (r_p = 0.912**, r_g = 0.924**). From the above results, we can infer that with the increase in SCMR, both biological yield and seed yield increases, thereby increasing harvest index. In groundnut, Kyaw *et al.* (2017) observed significant positive correlation of SCMR with harvest index.

Biomass per plant has significant positive correlation with harvest index (r_p = 0.935**, r_g = 0.972**). It indicates that plants with high economic yield has high biomass per plant therefore, biomass per plant and harvest index has positive association. Similar result of significant positive correlation of biomass per plant with harvest index was observed by Gupta *et al.* (2003), Shivade *et al.* (2011) and Manish and Hemalata (2017).

4.4.3 F$_3$ progenies of Cross TU-94-02 x LBG-752

The results regarding association of seed yield per plant with yield contributing and physiological attributes in cross TU-94-02 x LBG-752 are presented in Table 4.10 and Table 4.11 respectively.

4.4.3.1 Correlation between seed yield and its contributing attributes

Seed yield per plant has significant negative correlation with days to 50% flowering (r_p = -0.322**, r_g = -0.017) and significant positive correlation with number of clusters per plant (r_p = 0.937**, r_g = 0.964**), number of pods per cluster (r_p = 0.916**, r_g = 0.971**), pod length (r_p = 0.901**, r_g = 0.988**), number of pods per plant (r_p = 0.777**, r_g = 0.996**), plant height (r_p = 0.773**, r_g = 0.960**), number of branches per plant (r_p = 0.661**, r_g = 0.921**) and number of seeds per plant (r_p = 0.626**, r_g = 0.993**). The results indicate that the above mentioned characters are considered as the most important associates for increasing seed yield per plant. Therefore selection for one trait helps in the improvement of other positively related traits which help in yield enhancement.

The presence of positive association between seed yield and its components is in agreement with the earlier reports of by Sharma *et al.* (2015) and Singh *et al.* (2016) for days to 50% flowering; Parameshwarappa and Kumar (2005), Gupta *et al.* (2003), Singh *et al.* (2007), Mehra *et al.* (2016), Suguna *et al.* (2017) for plant height; by Santha and Pramasivam (1999), Venkatesan *et al.* (2004), Chauhan *et al.* (2007), Sateesh *et al.* (2016) for number of branches per plant; Haritha and Sekhar (2002), Chauhan *et al.* (2007), Konda *et al.* (2008) and Rahim *et al.* (2010) for number of clusters per plant; Wanjari (1988), Babu (1998), Chauhan *et al.* (2007) and Sohel *et al.* (2016) for number of pods per cluster; Patel and Shah (1982), Natarajan and Rathinasamy (1999), Gafoor *et al.* (2000) and Kadam *et al.* (2008) for number

Table 4.10 Genotypic (r_g) and phenotypic (r_p) correlation coefficients among seed yield and its contributing attributes in F_3 generation of cross TU-94-02 x LBG-752 in blackgram

Character		DF	DM	PH	NB	NCP	NPC	NPP	PL	NSP	TW	SY
DF	r_g	**1.000**	1.012	0.084	0.111	0.300*	0.076	0.023	0.088	-0.072	0.411**	-0.017
	r_p	**1.000**	0.025	-0.139	-0.380**	-0.146	-0.380**	0.221	-0.400**	0.443**	0.138	-0.322*
DM	r_g		**1.000**	-0.298*	-0.298*	-0.166	-0.354*	-0.340*	-0.272	-0.379**	0.727**	-0.347*
	r_p		**1.000**	-0.277	-0.265	-0.098	-0.202	-0.366*	-0.129	-0.424**	0.185	-0.184
PH	r_g			**1.000**	0.992**	0.956**	0.974**	0.972**	0.977**	0.969**	-0.773**	0.960**
	r_p			**1.000**	0.921**	0.813**	0.671**	0.812**	0.679**	0.694**	-0.082	0.773**
NB	r_g				**1.000**	0.928**	0.952**	0.935**	0.940**	0.931**	-0.648**	0.921**
	r_p				**1.000**	0.668**	0.575**	0.589**	0.580**	0.434**	-0.104	0.661**
NCP	r_g					**1.000**	0.974**	0.962**	0.958**	0.939**	-0.595**	0.964**
	r_p					**1.000**	0.915**	0.827**	0.863**	0.698**	-0.251	0.937**
NPC	r_g						**1.000**	0.983**	0.970**	0.966**	-0.809**	0.971**
	r_p						**1.000**	0.687**	0.924**	0.537**	-0.378**	0.916**
NPP	r_g							**1.000**	0.995**	0.994**	-0.877**	0.996**
	r_p							**1.000**	0.676**	0.952**	-0.193	0.777**
PL	r_g								**1.000**	0.993**	-0.912**	0.988**
	r_p								**1.000**	0.511**	-0.349*	0.901**
NSP	r_g									**1.000**	-0.992**	0.993**
	r_p									**1.000**	-0.192	0.626**
TW	r_g										**1.000**	-0.884**
	r_p										**1.000**	-0.280
SY	r_g											**1.000**
	r_p											**1.000**

*** significant at 5% probability level** **** significant at 1% probability level**

DF - Days to 50% flowering
DM - Days to maturity
PH - Plant height (cm)
TW - Test Weight (g)
NB - No. of branches
NCP - No. of clusters per plant
NPC - No. pods per cluster
SY - Seed Yield per plant (g)
NPP - Number of pods per plant
PL - Pod length (cm)
NSP - No. seeds per pod

Table 4.11 Genotypic (r_g) and phenotypic (r_p) correlation coefficients among seed yield and physiological attributes in F_3 generation of cross TU-94-02 x LBG-752 in blackgram

Character		SLA (30 DAS)	SLA (45 DAS)	SLW (30 DAS)	SLW (45 DAS)	SCMR (30DAS)	SCMR (45DAS)	BMP	HI	SY
SLA (30 DAS)	r_g	**1.000**	0.892**	-0.557**	-0.347*	-0.820**	-0.815**	-0.329*	-0.169	-0.275
	r_p	**1.000**	0.830**	-0.346*	-0.213	-0.679**	-0.663**	-0.241	-0.106	-0.301*
SLA (45 DAS)	r_g		**1.000**	-0.133	-0.179	-0.796**	-0.780**	-0.240	0.002	-0.441**
	r_p		**1.000**	-0.091	-0.154	-0.753**	-0.728**	-0.219	0.006	-0.433**
SLW (30 DAS)	r_g			**1.000**	0.421**	0.355*	0.426**	0.381**	0.453**	0.265
	r_p			**1.000**	0.344*	0.286*	0.352*	0.313*	0.341*	0.218
SLW (45 DAS)	r_g				**1.000**	0.624**	0.730**	0.973**	0.965**	0.781**
	r_p				**1.000**	0.644**	0.735**	0.944**	0.935**	0.770**
SCMR (30DAS)	r_g					**1.000**	0.939**	0.696**	0.487**	0.118
	r_p					**1.000**	0.930**	0.701**	0.506**	0.163
SCMR (45DAS)	r_g						**1.000**	0.773**	0.599**	0.200
	r_p						**1.000**	0.777**	0.613**	0.251
BMP	r_g							**1.000**	0.959**	0.767**
	r_p							**1.000**	0.944**	0.782**
HI	r_g								**1.000**	0.883**
	r_p								**1.000**	0.880**
SY	r_g									**1.000**
	r_p									**1.000**

*** significant at 5% probability level** **** significant at 1% probability level**

SLA (30 DAS) - Specific Leaf Area at 30 DAS (cm^2 g^{-1})
SLW (30 DAS) - Specific Leaf Weight at 30 DAS (g cm^{-2})
SCMR (30DAS) - SPAD Chlorophyll Meter Reading at 30 DAS
BMP - Biomass per plant (g)
SLA (45 DAS) - Specific Leaf Area at 45 DAS (cm^2 g^{-1})
SLW (45DAS) - Specific Leaf Weight at 45 DAS (g cm^{-2})
SCMR (45DAS) - SPAD Chlorophyll Meter Reading at 30 DAS
HI - Harvest Index (%)

of pods per plant; Haritha and Sekhar (2002), Chauhan *et al.* (2007), Singh *et al.* (2007), Konda *et al.* (2008), Suguna *et al.* (2017) forpod length; Chauhan *et al.* (2007), Singh *et al.* (2007), Konda *et al.* (2008) and Suguna *et al.* (2017) for number of seeds per pod.

Days to 50 % flowering exhibited significant negative correlation with pod length (r_p = -0.400**, r_g = 0.088), number of branches per plant (r_p = -0.380**, r_g = 0.111), number of pods per cluster (r_p = -0.380**, r_g = 0.076) and significant positive correlation with number of seeds per pod (r_p = 0.443**, r_g = -0.072). The results infer that genotypes with short vegetative period have more number of branches with longer pods. Similar trend of negative association was observed by Gowsalya *et al.* (2016) for pod length; Sharma *et al.* (2015) for number of branches per plant; Singh *et al.* (2016) for number of seeds per pod.

Days to maturity exhibited significant negative association with number of pods per plant (r_p = -0.366*, r_g = -0.340*) and number of seeds per pod (r_p = -0.424**, r_g = -0.379**). From the results, it can be concluded that early maturing genotypes bear more number of pods. In addition, number of seeds per pod also increases with decrease in maturity period. Gafoor *et al.* (2000) observed significant negative correlation of days to maturity with number of seeds per pod whereas, Panigrahi *et al*. (2014) and Gowsalya *et al.* (2016) observed negative correlation with number of pods per plant.

Plant height has recorded significant positive correlation with number of branches per plant (r_p = 0.921**, r_g = 0.992**), number of seeds per pod (r_p = 0.694**, r_g = 0.969**), number of pods per cluster (r_p = 0.671**, r_g = 0.974**), pod length (r_p = 0.679**, r_g = 0.977**), number of clusters per plant (r_p = 0.813**, r_g = 0.956**) and number of pods per plant (r_p = 0.812**, r_g = 0.972**). The results indicate that plants with more number of branches have more number of pods which ultimately increases yield. Similar kind of significant and positive association of plant height was reported by Suguna *et al.* (2017) for number of branches; Gowsalya *et al.* (2016) for number of clusters per plant; Kanimoli *et al.* (2015) for number of pods per cluster; Singh *et al.* (2007), Kadam *et al.* (2008), Rahim *et al.* (2010) and Suguna *et al.* (2017) for number of pods per plant; Sunil kumar *et al.* (2003), Singh *et al.* (2007), Isha Parveen *et al.* (2011), Vijay *et al.* (2015) and Suguna *et al.* (2017) for pod length and number of seeds per pod.

Number of branches per plant registered significant positive correlation with number of clusters per plant ($r_p = 0.668^{**}$, $r_g = 0.928^{**}$), number of pods per plant ($r_p = 0.589^{**}$, $r_g = 0.935^{**}$), pod length ($r_p = 0.580^{**}$, $r_g = 0.940^{**}$), number of pods per cluster ($r_p = 0.575^{**}$, $r_g = 0.952^{**}$) and number of seeds per pod ($r_p = 0.434^{**}$, $r_g = 0.931^{**}$). Plants with more number of branches also have more pods with more number of seeds per pod. Similar kind of significant and positive association of number of branches were obtained by Natarajan and Rathinasamy (1999), Kanimoli *et al.* (2015), Vijay *et al.* (2015) and Suguna *et al.* (2017) for number of clusters per plant; Kanimoli *et al.* (2015) for number of pods per cluster; Natarajan and Rathinasamy (1999), Gafoor *et al.* (2000), Shivade *et al.* (2011), Kanimoli *et al.* (2015), Suguna *et al.* (2017) for number of pods per plant; Suguna *et al.* (2017) for pod length and number of seeds per pod.

Number of clusters per plant has significant positive correlation with number of pods per cluster ($r_p = 0.915^{**}$, $r_g = 0.974^{**}$), pod length ($r_p = 0.863^{**}$, $r_g = 0.958^{**}$), number of pods per plant ($r_p = 0.827^{**}$, $r_g = 0.962^{**}$) and number of seeds per pod ($r_p = 0.698^{**}$, $r_g = 0.939^{**}$). If there is more number of clusters per plant, then it will automatically have more number of pods per plant realizing higher yields. The results obtained for number of clusters per plant were in accordance with results obtained by Kanimoli *et al.* (2015) for number of pods per cluster; Sunil kumar *et al.* (2003), Venkatesan *et al.* (2004) and Isha Parveen *et al.* (2011) for number of pods per plant and pod length; Kasundra *et al.* (1995), Chauhan *et al.* (2007), Kishore kumar *et al.* (2008) and Kanimoli *et al.* (2015) for number of seeds per pod.

Number of pods per cluster has registered significant positive correlation with number of pods per plant (r_p = 0.687**, r_g = 0.983**), pod length (r_p = 0.924**, r_g = 0.970**) and number of seeds per pod (r_p = 0.537**, r_g = 0.966**). If the number of pods per cluster is high then number of pods per pant will also be high which is positive for seed yield. The results obtained were in accordance with results by Singh *et al.* (2009) for pod length; Singh *et al.* (2009) and Isha Parveen *et al.* (2011) for number of pods per plant; Kanimoli *et al.* (2015) and Singh *et al.* (2009) for number of seeds per pod. It recorded significant negative correlation with test weight (r_p = -0.378**, r_g = -0.808**). On contrary, Kanimoli *et al.* (2015) observed positive association between number of pods per plant and test weight.

Number of pods per plant recorded significant positive association with number of seeds per pod (r_p = 0.952**, r_g = 0.994**) and pod length (r_p = 0.676**, r_g = 0.995**) Plants with more number of pods have higher pod length with more number of seeds per pod. Similar findings were reported by Singh *et al.* (2007) for pod length; Gafoor *et al.* (2000), Sunil kumar *et al.* (2003), Konda *et al.* (2008) and Suresh *et al.* (2013), Kanimoli *et al.* (2015) and Vijay *et al.* (2015) for number of seeds per pod.

Pod length has registered significant positive association with number of seeds per pod (r_p = 0.511**, r_g = 0.993**). As the length of the pod increases the number of seeds per pod also increases, increasing seed yield. Similar trend of association was also reported by Gafoor *et al.* (2000), Umadevi and Meenakshi Ganesan (2005), Singh *et al.* (2007), Vijay *et al.* (2015) and Suguna *et al.* (2017) for number of seeds per pod. Pod length recorded significant negative association with test weight (r_p = -0.349*, r_g = -0.912**).On contrary positive association of pod length with test weight was observed by Sohel *et al.* (2016).

Based on the correlation studies, more importance is to be given to number of pods per cluster, number of pods per plant, plant height, number of clusters per plant, pod length, number of branches per plant and number of seeds per pod while selecting better genotypes in latter generations of the cross, TU-94-02 x LBG-752. The direct association between seed yield and the above yield contributing characters reveals less complex relationships between them. Therefore selection of one trait result in correlated response for other positively related traits. Negative association between yield components is mainly due to undesirable linkage which can be broken through recombination breeding.

4.4.3.2 Correlation between seed yield and physiological attributes

Seed yield per plant has significant negative correlation with SLA (45 DAS) ($r_p = -0.433^{**}$, $r_g = -0.441^{*}$), SLA (30 DAS) ($r_p = -0.301^{*}$, $r_g = -0.275$) and significant positive correlation with harvest index ($r_p = 0.880^{**}$, $r_g = 0.883^{**}$), biomass per plant ($r_p = 0.782^{**}$, $r_g = 0.767^{**}$) and SLW (45 DAS) ($r_p = 0.770^{**}$, $r_g = 0.781^{**}$). The results indicate that plants with less leaf are have higher biomass and harvest index realizing more seed yield. Similar findings of associations with seed yield were stated by Sudhakar *et al.* (2006) for SCMR; Gupta *et al.* (2003), Shivade *et al.* (2011) and Manish and Hemalata (2017) for biomass per plant; Veeranjaneelu *et al.* (2007), Gul *et al.* (2008), Isha Parveen *et al.* (2011) and Vijay *et al.* (2015) for harvest index. In Groundnut, Kyaw *et al.* (2017) observed significant positive correlation SCMR with seed yield per plant.

SLA taken at 30 DAS has significant positive association with SLA (45 DAS) ($r_p = 0.830^{**}$, $r_g = 0.892^{**}$) and significant negative correlation with SCMR (30 DAS) ($r_p = -0.679^{**}$, $r_g = -0.820^{**}$), SCMR (45 DAS) ($r_p = -0.663^{**}$, $r_g = -0.815^{**}$) and SLW (30 DAS) ($r_p = -0.346^{*}$, $r_g = -0.557^{**}$). SLA taken at 45 DAS exhibited significant negative correlation with SCMR (30 DAS) ($r_p = -0.753^{**}$, $r_g = -0.796^{**}$) and SCMR (45 DAS) ($r_p = -0.728^{**}$, $r_g = -0.780^{**}$). Inverse relation between SLA and SCMR indicates that the plants with less leaf area have more chlorophyll content per unit area. Similar finding of negative correlation of SLA with SCMR was observed by Sudhakar *et al.* (2006).

SLW taken at 30 DAS has significant positive correlation with SCMR (45 DAS) ($r_p = 0.352^*$, $r_g = 0.426^{**}$), SLW (45 DAS) ($r_p = 0.344^*$, $r_g = 0.421^*$), harvest index ($r_p = 0.341^*$, $r_g = 0.453^{**}$), biomass per plant ($r_p = 0.313^*$, $r_g = 0.381^{**}$) and SCMR (30 DAS) ($r_p = 286^*$, $r_g = 0.355^*$). SLW taken at 45 DAS has shown significant positive correlation with biomass per plant ($r_p = 0.944^{**}$, $r_g = 0.973^{**}$), harvest index ($r_p = 0.935^{**}$, $r_g = 0.965^{**}$), SCMR (45 DAS) ($r_p = 0.735^{**}$, $r_g = 0.730^{**}$) and SCMR (30 DAS) ($r_p = 644^{**}$, $r_g = 0.624^{**}$).The results infer that plants with low SLW have more chlorophyll content per unit area thereby having increased biomass per plant. Similar finding of SLW with harvest index was observed by Kyaw *et al.* (2017) in Groundnut.

SCMR taken at 30 DAS has significant positive correlation with SCMR (45 DAS) ($r_p = 0.930^{**}$, $r_g = 0.939^{**}$), biomass per plant ($r_p = 0.701^{**}$, $r_g = 0.696^{**}$) and harvest index ($r_p = 0.506^{**}$, $r_g = 0.487^{**}$). SCMR taken at 45 DAS has significant positive correlation with biomass per plant ($r_p = 0.777^{**}$, $r_g = 0.773^{**}$) and harvest index ($r_p = 0.613^{**}$, $r_g = 0.599^{**}$). Selection for plants with high SCMR results in more accumulation of biomass increasing seed yield per pant. In Groundnut, Kyaw *et al.* (2017) observed significant positive correlation of SCMR with harvest index.

Significant positive association was noticed between biomass per plant and harvest index ($r_p = 0.944^{**}$, $r_g = 0.959^{**}$). Positive association between biomass and harvest index indicates that with the increase in economic yield, both biomass and harvest index increases. Similar results of significant positive correlation of biomass per plant with harvest index was observed by Gupta *et al.* (2003), by Shivade *et al.* (2011) and by Manish and Hemalata (2017).

From the above results, it can be concluded that genotypes with low leaf area and high SCMR reading had high biomass and harvest index. This results in higher economic yield. Therefore, selection for these traits results in physiologically superior genotypes along with higher seed yield.

4.5 PATH COEFFICIENT ANALYSIS

The path analysis reveals whether the association of characters with yield is due to their direct effect on yield or is a consequence of their indirect effects through other component characters. It acts as an effective measure in finding out direct and indirect causes of association and presents a critical examination of the specific forces acting to produce a given correlation.

Based on the data recorded in the present investigation, the phenotypic correlations were estimated to determine direct effect and indirect effect of yield, yield contributing characters and physiological attributes in blackgram. As discussed in character association, based on the importance of phenotypic effects, the present results of phenotypic and genotypic path coefficients are discussed here under.

4.5.1 F_3 Progenies of the Cross LBG-787 x LBG-752

Path coefficient analysis was done for yield contributing attributes and physiological attributes separately and the results are presented in Table 4.12 and Table 4.13 respectively. The phenotypic and genotypic path diagrams regarding direct and indirect effects of yield contributing attributes on seed yield are provided in Fig.4.1 and Fig. 4.2 whereas, effects of physiological attributes were provided in Fig. 4.3 and Fig. 4.4.

4.5.1.1 Direct and indirect effects of yield contributing attributes and seed yield

The trait number of pods per cluster has high positive direct effect (0.638) and significant positive correlation (0.968^{**}) on seed yield per plant. Moderate indirect negative effects through number of pods per plant (-0.366) and number of clusters per plant (-0.205) are balanced by high positive indirect effects through plant height (0.446) and test weight (0.389) resulting in significant positive correlation with seed yield per plant. Positive direct effect of number of pods per cluster on seed yield per plant along with significant positive association was also observed by Umadevi and Meenakshi Ganesan (2005) and Konda *et al.* (2008).

Plant height has high positive direct effect (0.492) on seed yield per plant with significant positive correlation (0.885^{**}). It is mainly due to high positive direct (0.492) and indirect effects of plant height through number of pods per cluster (0.578) and test weight (0.341). Similar results regarding plant height were observed by Shivade *et al.* (2011), Isha Parveen *et al.* (2011), Shridevi *et al.* (2012) and Jyothsna *et al.* (2016).

The trait test weight has high positive direct effect (0.421) and significant positive correlation (0.910^{**}) on seed yield per plant. The significant positive indirect effects through number of pods per cluster (0.588) and plant height (0.398) along with significant positive direct effect of test weight mainly contributed to significant positive correlation of test weight with seed yield per plant. Similar kind of association was also reported by Singh and Singh (1994), Arya *et al.* (2017) and Gill *et al.* (2017).

Pod length has negligible positive direct effect (0.034) on seed yield per plant where as its correlation with seed yield per plant is positive and significant (0.852^{**}). The significant positive correlation is mainly due to high positive indirect effects through number of pods per cluster (0.579), plant height (0.420) and test weight (0.344). The low level of positive direct effect of pod length on seed yield per plant was also observed by Singh *et al.* (2018).

The significant positive correlation between number of branches per plant and seed yield (0.646^{**}) is mainly due to indirect positive effects through number of pods per cluster (0.444), plant height (0.284) and test weight (0.249) though the direct effect is negligible (0.025). Positive direct effect of number of branches per plant on seed yield per plant along with significant positive association was observed by Umadevi and Meenakshi Ganesan (2005)

Table 4.12 Genotypic (G) and phenotypic (P) path coefficients for seed yield and its attributes in F₃ generation of cross LBG-787 x LBG-752 in blackgram

Character		DF	DM	PH	NB	NCP	NPC	NPP	PL	NSP	TW	SY
DF	**G**	**-0.721**	0.093	-0.030	0.005	-0.740	-0.106	0.043	0.105	0.190	-0.002	-0.163
	P	**-0.072**	-0.003	-0.014	0.002	-0.038	-0.048	-0.014	0.003	0.007	0.024	-0.154
DM	**G**	-0.086	**0.786**	-0.297	0.000	0.430	-0.645	-0.541	-0.476	-0.664	0.022	-0.472**
	P	-0.012	**-0.019**	-0.131	0.000	0.078	-0.289	0.167	-0.015	-0.004	-0.196	-0.422**
PH	**G**	0.021	-0.227	**0.029**	0.043	-0.520	0.221	0.137	0.836	0.406	-0.035	0.911**
	P	0.002	0.005	**0.492**	0.015	-0.203	0.578	-0.377	0.029	0.003	0.341	0.885**
NB	**G**	-0.052	0.002	0.621	**0.071**	-0.618	0.946	0.706	0.681	0.349	-0.026	0.679**
	P	-0.006	0.000	0.284	**0.025**	-0.147	0.444	-0.228	0.023	0.002	0.249	0.646**
NCP	**G**	-0.141	-0.298	0.960	0.049	**-0.775**	0.657	0.128	0.918	0.866	-0.040	0.924**
	P	-0.013	0.007	0.454	0.017	**-0.220**	0.593	-0.374	0.032	0.005	0.380	0.883**
NPC	**G**	0.058	-0.382	0.947	0.051	-0.574	**0.327**	0.110	0.899	0.595	-0.040	0.992**
	P	0.005	0.009	0.446	0.018	-0.205	**0.638**	-0.366	0.031	0.004	0.389	0.968**
NPP	**G**	-0.026	-0.361	0.995	0.043	-0.620	0.253	**0.176**	0.856	0.658	-0.039	0.935**
	P	-0.003	0.008	0.473	0.015	-0.210	0.595	**-0.392**	0.030	0.004	0.379	0.899**
PL	**G**	-0.078	-0.384	0.883	0.050	-0.554	0.224	0.033	**0.975**	0.768	-0.036	0.880**
	P	-0.007	0.009	0.420	0.017	-0.205	0.579	-0.342	**0.034**	0.005	0.344	0.852**
NSP	**G**	-0.551	-0.335	0.268	0.016	-0.098	0.507	0.497	0.481	**0.557**	-0.025	0.318*
	P	-0.051	0.007	0.127	0.005	-0.120	0.238	-0.164	0.017	**0.010**	0.235	0.306*
TW	**G**	-0.036	-0.404	0.850	0.044	-0.513	0.238	0.080	0.817	0.900	**-0.042**	0.933**
	P	-0.004	0.009	0.398	0.015	-0.198	0.588	-0.353	0.028	0.006	**0.422**	0.910**

*** significant at 5% probability level** **** significant at 1% probability level**

Residual effect at genotypic level=0.157 Residual effect at phenotypic level =0.208

DF - Days to 50% flowering
NB - No. of branches
NPP - No. of pods per plant
DM - Days to maturity
NCP - No. of clusters per plant
PL - Pod length (cm)
PH - Plant height (cm)
NPC - No. pods per cluster
NSP - No. seeds per pod
TW - Test Weight (g)
SY - Seed Yield per plant (g)

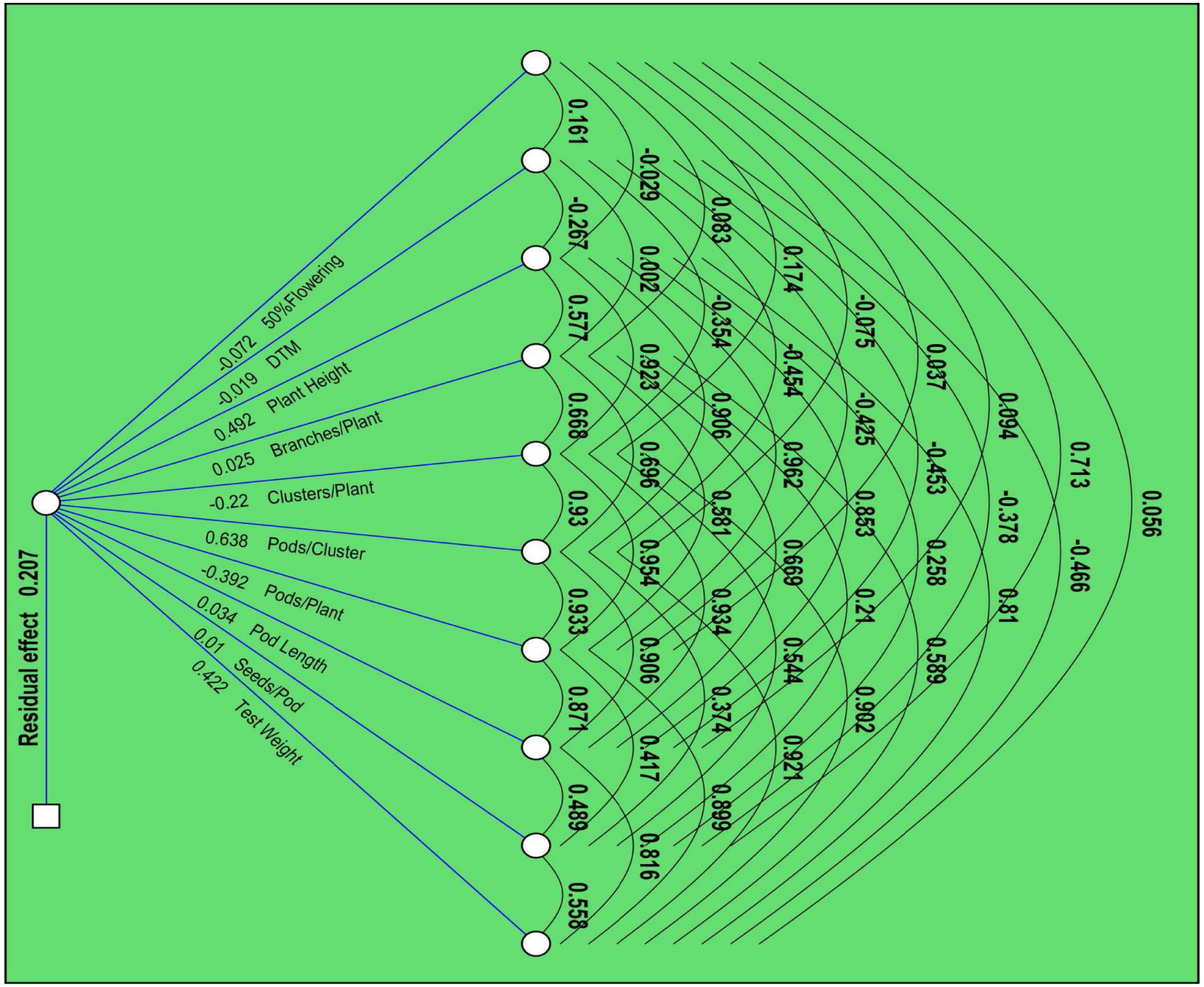


Fig. 4.1 Phenotypic path diagram for seed yield and its contributing attributes in F_3 generation of cross LBG-787 x LBG-752 in blackgram

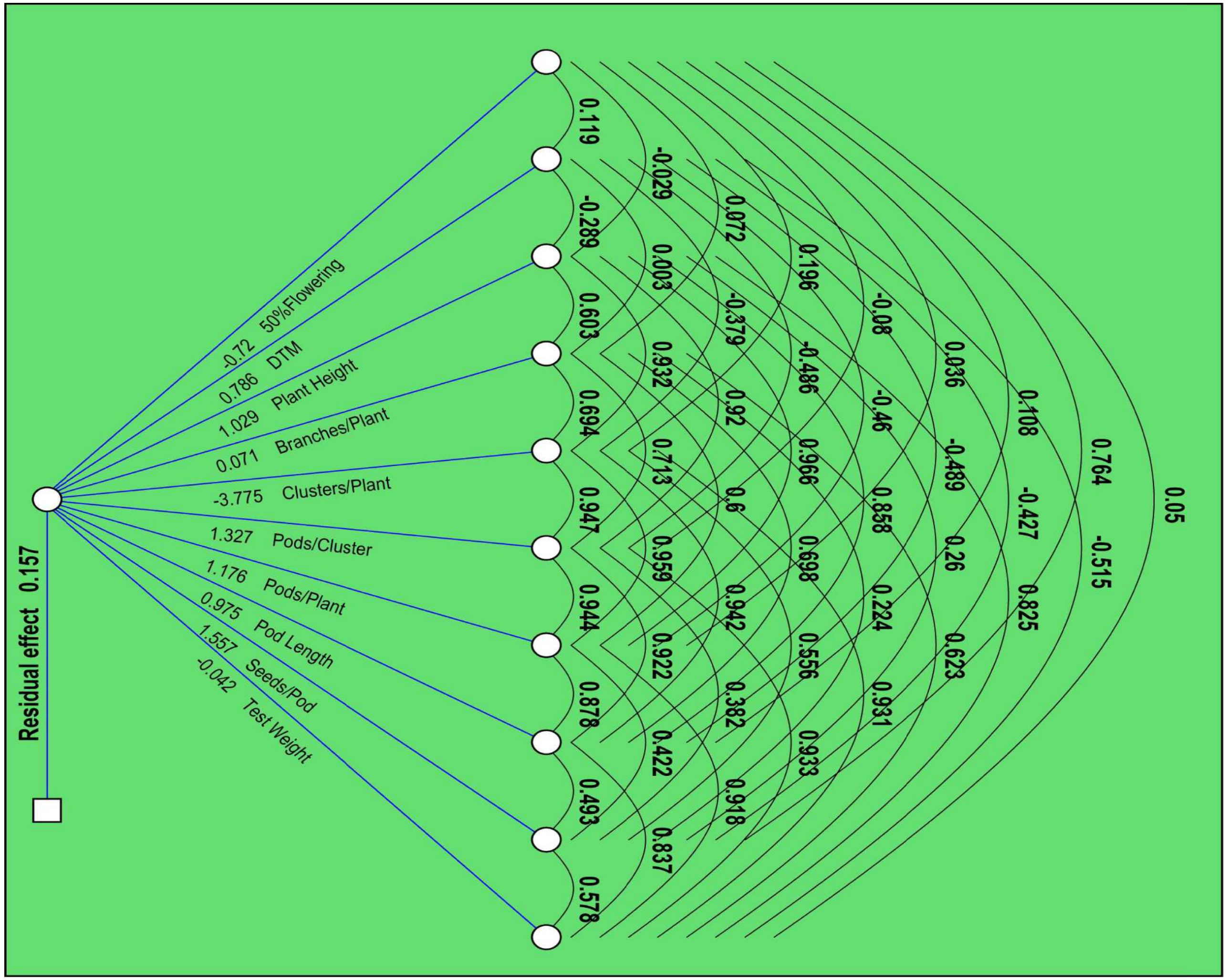


Fig. 4.2 Genotypic path diagram for seed yield and its contributing attributes in F_3 generation of cross LBG-787 x LBG-752 in blackgram

The correlation of number of seeds per pod is positive and significant (0.306^{*}) with seed yield per plant. Number of pods per cluster (0.238), test weight (0.235) and plant height (0.127) has remarkable positive indirect effects on seed yield per plant which led to significant positive correlation even though the direct effect is negligible (0.010). Similar findings were also reported by Singh *et al.* (2018).

Number of pods per plant has significant positive correlation with seed yield per plant (0.899^{**}), even though it has high negative direct effect (-0.392) on seed yield per plant. The positive direct effects shown by characters like number of pods per cluster (0.595), plant height (0.473) and test weight (0.379) resulted in significant positive correlation. Similar results regarding number of pods per plant were observed by Shivade *et al.* (2011), Isha Parveen *et al.* (2011), Shridevi *et al.* (2011) and Jyothsna *et al.* (2016).

The trait number of clusters per plant exhibited significant positive correlation with seed yield per plant (0.883^{**}) even though its direct effect is negative and moderate (-0.220). The negative direct and indirect effects are supressed mainly by positive indirect effects through number of pods per cluster (0.593), plant height (0.454) and test weight (0.380). Natarajan and Rathinasamy (1999), Kumar *et al.* (1999) and observed similar kind of association between number of clusters per plant and seed yield per plant.

Days to maturity has significant negative phenotypic correlation (-0.422^{**}) even though it has negligible negative direct effect (-0.019) on seed yield per plant. The significant negative association is mainly due to the negative indirect effects of days to maturity through number of pods per cluster (-0.289), test weight (-0.196) and plant height (-0.131). Similar result was recorded by Parameshwarappa (1993) in blackgram.

In the cross LBG-787 x LBG-752, among the yield contributing characters, number of pods per cluster exerted the high positive direct effect

Table 4.13 Genotypic (G) and phenotypic (P) path coefficients for seed yield and physiological attributes in F_3 generation of cross LBG-787 x LBG-752 in blackgram

Character		SLA (30 DAS)	SLA (45 DAS)	SLW (30 DAS)	SLW (45 DAS)	SCMR (30DAS)	SCMR (45DAS)	BMP	HI	SY
SLA (30 DAS)	**G**	**0.056**	-0.161	0.090	0.078	-0.003	-0.041	-0.340	0.120	-0.200
	P	**0.176**	-0.054	-0.094	0.022	-0.003	-0.059	-0.253	0.068	-0.197
SLA (45 DAS)	**G**	0.038	**-0.238**	0.060	0.136	0.002	-0.023	-0.227	0.148	-0.103
	P	0.117	**-0.081**	-0.062	0.039	0.001	-0.031	-0.171	0.092	-0.096
SLW (30 DAS)	**G**	-0.028	0.080	**-0.179**	-0.057	0.091	0.091	0.428	0.494	0.920**
	P	0.027	-0.088	**0.187**	-0.017	0.051	0.132	0.313	0.298	0.904**
SLW (45 DAS)	**G**	-0.022	0.161	-0.051	**-0.201**	0.038	0.048	0.119	0.167	0.260
	P	0.051	-0.062	0.050	**-0.062**	0.019	0.066	0.095	0.078	0.237
SCMR (30DAS)	**G**	-0.001	-0.004	-0.128	-0.060	**0.126**	0.099	0.254	0.645	0.931**
	P	-0.001	-0.006	0.116	-0.014	**0.083**	0.124	0.168	0.316	0.785**
SCMR (45DAS)	**G**	-0.020	0.047	-0.143	-0.085	0.110	**0.114**	0.301	0.557	0.882**
	P	0.015	-0.061	0.145	-0.024	0.060	**0.171**	0.218	0.329	0.852**
BMP	**G**	-0.042	0.120	-0.170	-0.053	0.071	0.076	**0.451**	0.328	0.781**
	P	0.036	-0.120	0.158	-0.016	0.038	0.100	**0.370**	0.076	0.644**
HI	**G**	0.010	-0.051	-0.128	-0.049	0.118	0.092	0.214	**0.691**	0.897**
	P	-0.015	0.024	0.114	-0.010	0.053	0.115	0.058	**0.490**	0.829**

*** significant at 5% probability level** **** significant at 1% probability level**

Residual effect at genotypic level=0.117 Residual effect at phenotypic level =0.133

SLA (30 DAS) - Specific Leaf Area at 30 DAS ($cm^2 g^{-1}$)
SLW (30 DAS) - Specific Leaf Weight at 30 DAS ($g cm^{-2}$)
SCMR (30DAS) - SPAD Chlorophyll Meter Reading at 30 DAS
BMP - Biomass per plant (g)

SLA (45 DAS) - Specific Leaf Area at 45 DAS ($cm^2 g^{-1}$)
SLW (45DAS) - Specific Leaf Weight at 45 DAS ($g cm^{-2}$)
SCMR (45DAS) - SPAD Chlorophyll Meter Reading at 30 DAS
HI - Harvest Index (%)

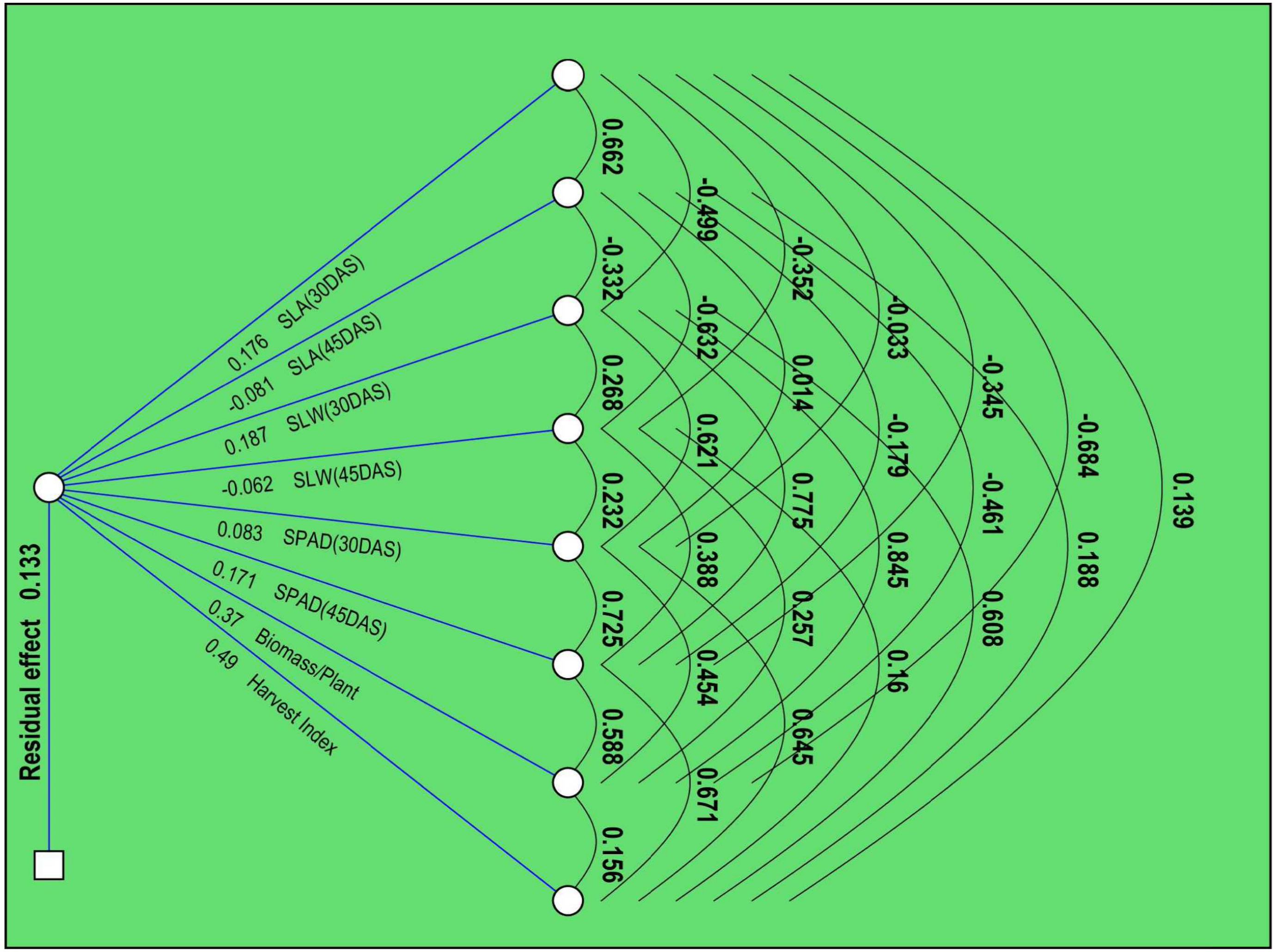


Fig. 4.3 Phenotypic path diagram for seed yield and physiological attributes in F_3 generation of cross LBG-787 x LBG-752 in blackgram

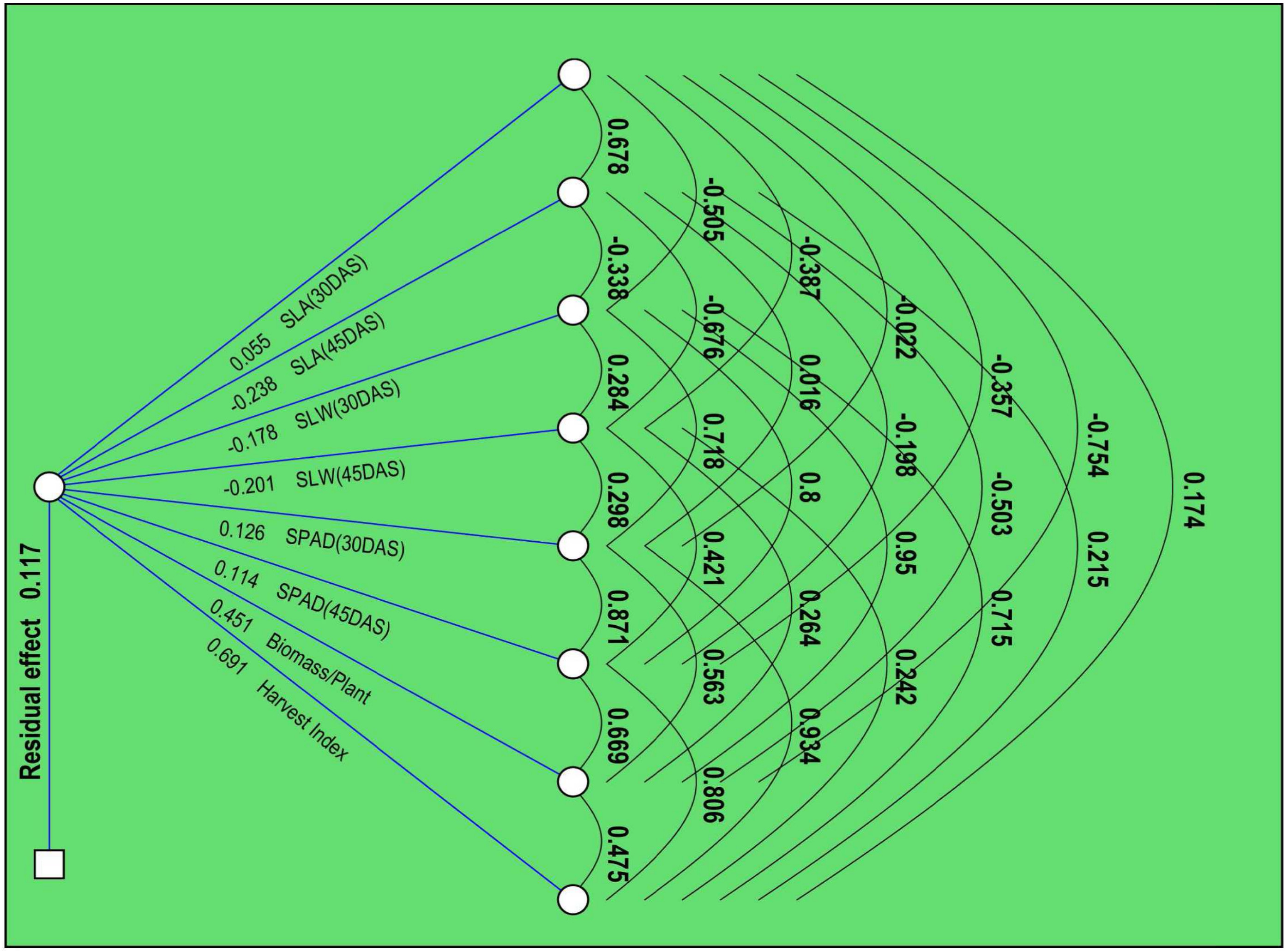


Fig. 4.4 Genotypic path diagram for seed yield and physiological attributes in F_3 generation of cross LBG-787 x LBG-752 in blackgram

on seed yield per plant followed by plant height, test weight, pod length, number of branches per plant, number of seeds per pod, number of pods per plant and number of clusters per plant. Days to maturity and days to 50% flowering exerted negative direct effect on seed yield per plant.

Considering the nature and magnitude of character association and their direct and indirect effects, it can be concluded that manifestation of number of pods per cluster, plant height and test weight resulted in simultaneous improvement of seed yield per plant. Hence, these characters should be considered at the time of formulating selection strategy in further segregating generations for developing high yielding blackgram genotypes.

The phenotypic and genotypic residual effects, 0.207 and 0.157 respectively are indicating that the characters included in the study contribute about 79.20 per cent of variability pertaining to the dependent variable. Hence besides the characters included in the study, there are some other attributes contributing to yield which are to be included in further studies.

4.5.1.2 Direct and indirect effects of physiological attributes on seed yield

The trait harvest index has significant positive correlation (0.829^{**}) with seed yield per plant. The significant positive correlation is mainly due to high positive direct effect (0.490) of harvest index and indirect effects through SCMR (45 DAS) (0.115) and SLW (30 DAS) (0.114), biomass per plant (0.058), SCMR (30 DAS) (0.053) and SLA (45 DAS) (0.024) on seed yield per plant. Similar findings were reported by Patil and Deshmukh (1989), Govindaraj and Subramanian (2001), Umadevi and Meenakshi Ganesan (2005), Chauhan *et al.* (2007) and Isha Parveen *et al.* (2011) and Arya *et al.* (2017).

The trait biomass per plant has significant positive correlation (0.644^{**}) with seed yield per plant. The significant positive correlation is mainly due to high positive direct effect (0.370) of biomass per plant on seed yield per plant and also due to positive indirect effects through SLW (30 DAS) (0.158) and

SCMR (45 DAS) (0.100). Similar results were observed by Usha rani and Rao (1981), Venkateswarlu (2001), Kanimoli *et al.* (2015) and Rajasekhar *et al.* (2017).

SLW taken at 30 DAS has significant positive correlation (0.904**) with seed yield per plant, even though the direct effect shown is low (0.187). Positive indirect effects of biomass per plant (0.313), harvest index (0.298) and SCMR (45 DAS) (0.132) majorly contributed to significant positive correlation with seed yield per plant. A significant relationship was observed between SLW and seed yield per plant was earlier reported by Rao *et al.* (2001) in groundnut and by Sudhakar *et al.* (2006) in blackgram.

The trait SCMR taken at 45 DAS has significant positive correlation (0.852**) and low positive direct effect (0.171) with seed yield per plant. The significant positive correlation is mainly due to positive indirect effects of harvest index (0.329), biomass per plant (0.218) and SLW (30 DAS) (0.145). Similar positive correlation between SCMR and seed yield per plant has earlier been reported by Rao *et al.* (2001) in groundnut and by Sudhakar *et al.* (2006) in blackgram.

The trait SCMR taken at 30 DAS has significant positive phenotypic correlation (0.785**) with seed yield per plant. But its direct effect on seed yield per plant is negligible (0.083). The significant positive correlation is due to positive indirect effects through harvest index (0.316), biomass per plant (0.168), SCMR (45 DAS) (0.124) and SLW (30 DAS) (0.116). Similar positive correlation between SCMR and seed yield per plant has earlier been reported by Rao *et al.* (2001) in groundnut and by Sudhakar *et al.* (2006) in blackgram.

Among all the physiological characters studied in this cross harvest index exerted high positive direct effect on seed yield per plant followed by biomass per plant, SLA (30 DAS), SCMR (45 DAS) and SCMR (30 DAS).

Characters like SLA (45 DAS) and SLW (45 DAS) exerted negative direct effect on seed yield per plant.

As per the nature and magnitude of character association and their direct and indirect effects, it was observed that characters like harvest index and biomass per plant can be manipulated in order to improve yield.

The phenotypic and genotypic residual effects recorded are 0.133 and 0.117 respectively, indicating that the characters included in the study contribute about 86.70 per cent of variability pertaining to the dependent variable.

4.5.2 F_3 Progenies of Cross TU-94-02 x KU-1006

Path coefficient analysis was done for all the yield contributing traits and physiological traits separately and the results were presented in Table 4.14 and Table 4.15 respectively. The phenotypic and genotypic path diagrams regarding direct and indirect effects of yield contributing attributes on seed yield are provided in Fig.4.5 and Fig. 4.6 whereas, effects of physiological attributes were provided in Fig. 4.7 and Fig. 4.8.

4.5.2.1 Direct and indirect effects of yield contributing attributes on seed yield

High positive direct effect (0.470) on seed yield per plant was exhibited by number of clusters per plant which resulted in significant positive correlation with seed yield per plant (0.915^{**}). Along with the direct effect, indirect positive effects through plant height (0.248), number of pods per cluster (0.184) and number of pods per plant (0.169) also contributed for significant positive association with seed yield. Kumar *et al.* (1999), Natarajan and Rathinasamy (1999) and Umadevi and Meenakshi Ganesan (2005) also observed significant positive direct effect and significant positive correlation of number of clusters per plant with seed yield per plant.

Table 4.14 Genotypic (G) and phenotypic (P) path coefficients for seed yield and its attributes in F_3 generation of cross TU-94-02 x KU-1006 in blackgram

Character		DF	DM	PH	NB	NCP	NPC	NPP	PL	NSP	TW	SY
DF	**G**	**0.272**	-0.086	-0.069	0.521	0.809	0.031	-0.429	-0.395	-0.233	-0.040	0.381**
	P	**-0.005**	0.011	0.086	-0.020	0.196	0.077	0.072	-0.026	-0.066	0.004	0.328*
DM	**G**	0.156	**-0.150**	-0.014	0.239	0.635	0.468	-0.997	0.046	-0.023	-0.028	0.332*
	P	-0.002	**0.034**	0.046	-0.012	0.167	0.047	0.051	-0.006	-0.026	-0.006	0.293*
PH	**G**	0.054	-0.006	**-0.346**	0.831	0.799	0.487	-0.374	-0.320	-0.303	-0.060	0.762**
	P	-0.001	0.003	**0.469**	-0.039	0.249	0.142	0.088	-0.030	-0.108	0.008	0.783**
NB	**G**	0.115	-0.029	-0.234	**0.231**	0.470	0.155	-0.217	-0.378	-0.293	-0.021	0.699**
	P	-0.002	0.007	0.330	**-0.055**	0.344	0.118	0.122	-0.035	-0.109	0.002	0.722**
NCP	**G**	0.134	-0.058	-0.168	0.877	**0.643**	0.036	-0.860	-0.467	-0.213	-0.003	0.920**
	P	-0.002	0.012	0.248	-0.041	**0.470**	0.184	0.169	-0.040	-0.085	-0.001	0.915**
NPC	**G**	0.122	-0.030	-0.224	0.617	0.452	**0.303**	-0.543	-0.493	-0.239	-0.024	0.942**
	P	-0.002	0.008	0.316	-0.031	0.411	**0.211**	0.150	-0.042	-0.095	0.003	0.928**
NPP	**G**	0.136	-0.052	-0.167	0.869	0.645	0.250	**-0.857**	-0.492	-0.221	0.001	0.912**
	P	-0.002	0.010	0.242	-0.040	0.465	0.185	**0.170**	-0.039	-0.082	-0.001	0.910**
PL	**G**	0.187	0.012	-0.192	0.807	0.432	0.969	-0.439	**-0.576**	-0.299	-0.023	0.778**
	P	-0.003	0.004	0.274	-0.038	0.365	0.173	0.130	**-0.051**	-0.123	0.001	0.732**
NSP	**G**	0.169	-0.009	-0.279	0.956	0.930	0.463	-0.677	-0.458	**-0.377**	-0.042	0.676**
	P	-0.002	0.006	0.362	-0.043	0.288	0.143	0.100	-0.045	**-0.140**	0.004	0.672**
TW	**G**	-0.092	0.035	0.176	-0.221	-0.044	-0.475	-0.018	0.110	0.136	**0.117**	-0.277
	P	0.001	0.006	-0.113	0.003	0.007	-0.016	0.004	0.002	0.016	**-0.034**	-0.125

*** significant at 5% probability level** **** significant at 1% probability level**

Residual effect at genotypic level=0.085 Residual effect at phenotypic level =0.103

DF - Days to 50% flowering
DM - Days to maturity
PH - Plant height (cm)
TW - Test Weight (g)
NB - No. of branches
NCP - No. of clusters per plant
NPC - No. pods per cluster
SY - Seed Yield per plant (g)
NPP - No. of pods per plant
PL - Pod length (cm)
NSP - No. seeds per pod

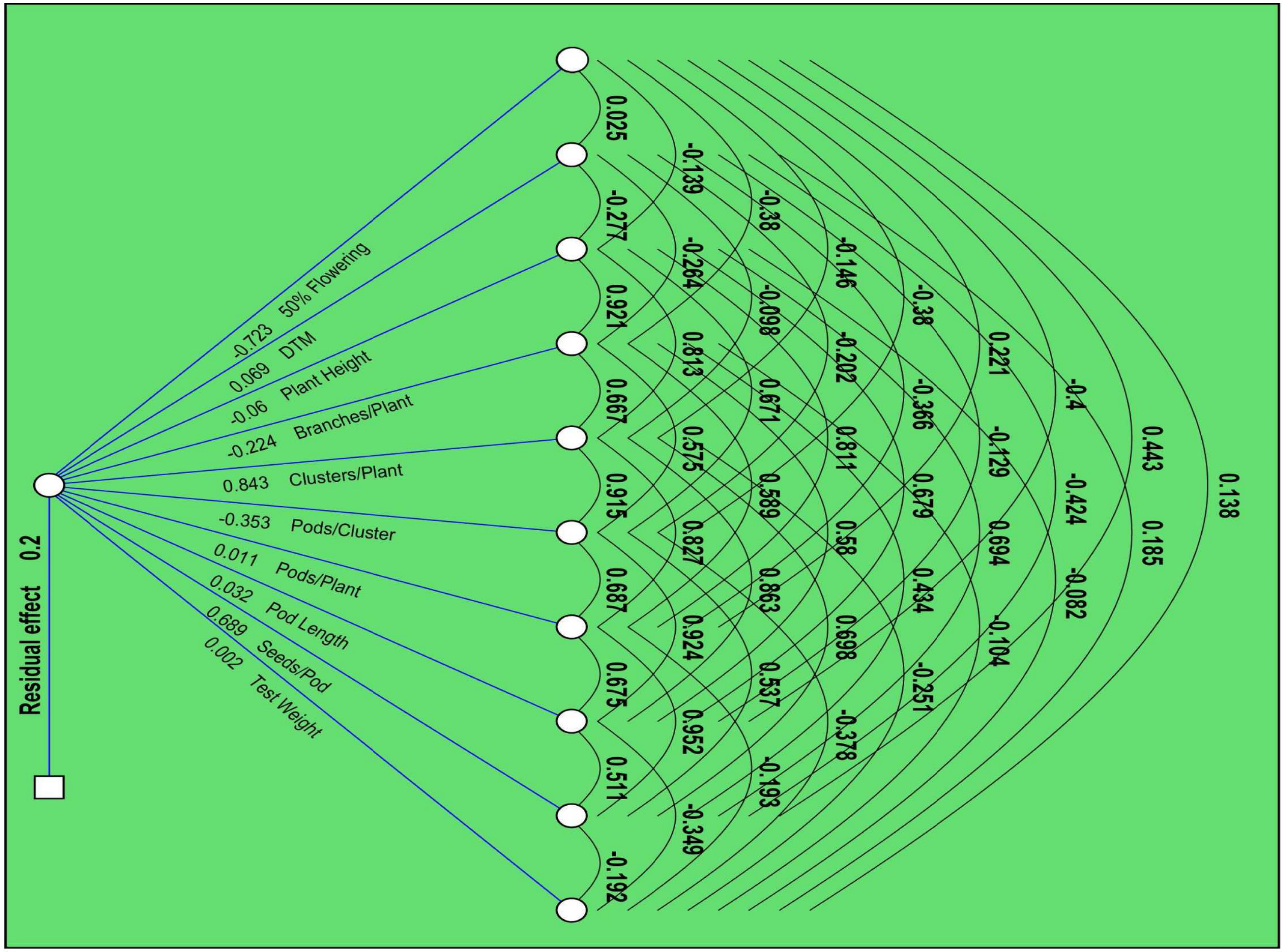


Fig. 4.5 Phenotypic path diagram for seed yield and its contributing attributes in F_3 generation of cross TU-94-02 x KU-1006 in blackgram

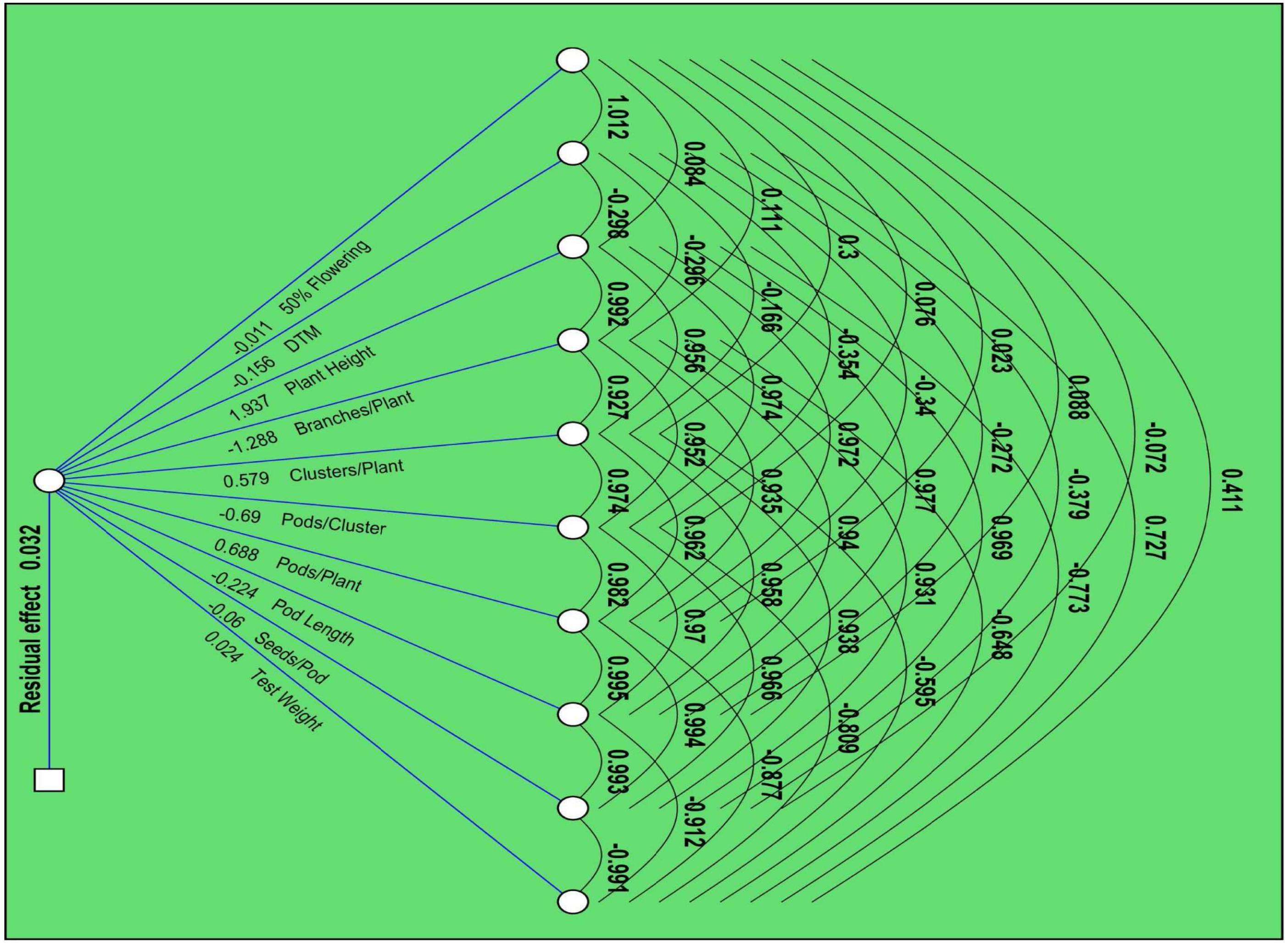


Fig. 4.6 Genotypic path diagram for seed yield and its contributing attributes in F_3 generation of cross TU-94-02 x KU-1006 in blackgram

Direct effect of plant height on seed yield per plant is significant and positive (0.469). It has shown significant positive correlation with seed yield per plant (0.783**) which is the result of direct positive effect of plant height and positive indirect effects through number of clusters per plant (0.249) and number of pods per cluster (0.142). Similar kind of association regarding plant height with seed yield per plant was observed by Shivade *et al.* (2011), Isha Parveen *et al.* (2011), Shridevi *et al.* (2011) and Jyothsna *et al.* (2016).

The trait number of pods per cluster has moderate positive direct effect (0.211) and significant positive correlation (0.928**) with seed yield per plant. Number of clusters per plant (0.411), plant height (0.316) and number of pods per plant (0.150) contributed indirect effects on seed yield per plant through this trait and resulted in significant positive association of number of pods per cluster with seed yield per plant.

Number of pods per plant has significant positive correlation with seed yield per plant (0.910**) even though its direct effect is low (0.170). It is due to the positive indirect effects of number of clusters per plant (0.465), plant height (0.242) and number of pods per cluster (0.185). Positive direct effect of number of pods per cluster on seed yield per plant along with significant positive association was observed by Umadevi and Meenakshi Ganesan (2005) and Konda *et al.* (2008).

Days to maturity has positive correlation (0.293*) even though it has negligible positive direct effect (0.034) on seed yield per plant. The significant positive correlation is due to positive indirect effects through number of clusters per plant (0.167), number of pods per cluster (0.047), plant height (0.046) and number of pods per plant (0.051). Positive and negligible direct effect of days to maturity on seed yield per plant was also reported by Singh *et al.* (2016).

Low negative direct effect (-0.140) was registered by number of seeds per pod on seed yield per plant, but its correlation is positive and significant

(0.672^{**}) with seed yield per plant. The positive indirect effects plant height (0.362), number of clusters per plant (0.288), number of pods per cluster (0.143) and number of pods per plant (0.100) majorly contributed to significant positive correlation even though the direct effect is negligible. Gill *et al.* (2017) also observed negative direct effect of number of seeds per pod on seed yield per plant.

Even though number of branches per plant showed negligible negative direct effect (-0.055) on seed yield per plant, it has significant positive association (0.722^{**}) with seed yield per plant. It is mainly due to indirect positive effects through plant height (0.330), number of clusters per plant (0.344), number of pods per cluster (0.118) and number of pods per plant (0.122). Umadevi and Meenakshi Ganesan (2005), Veeranjaneyulu *et al.* (2007) and Isha Parveen *et al.* (2011) reported similar results in blackgram.

Pod length has negligible negative direct effect (-0.051) on seed yield per plant where as its correlation with seed yield per plant is positive and significant (0.732^{**}). The significant positive correlation is due to positive indirect effects through number of clusters per plant (0.365), plant height (0.274), number of pods per cluster (0.173) and number of pods per plant (0.130). Similar findings were reported by Gopi Krishnan *et al.* (2002), Yashoda *et al.* (2013) and Arya *et al.* (2017).

Days to 50% flowering has negligible negative direct effect (-0.005) and significant positive correlation (0.328^{*}) with seed yield per plant. The significant positive correlation is due to positive indirect effects of this trait through number of clusters per plant (0.196), plant height (0.086), number of pods per cluster (0.077), number of pods per plant (0.072), days to maturity (0.011) and test weight (0.004). Negative direct effect of days to 50% flowering on seed yield per plant was reported by Punia *et al.* (2014) and Arya *et al.* (2017).

In the cross TU-94-02 x KU-1006, among the yield contributing characters number of clusters per plant exerted the high positive direct effect on seed yield per plant followed by plant height, number of pods per cluster, number of pods per plant and days to maturity.

When the nature and magnitude of character association and their direct and indirect effects are considered, it can be concluded that manifestation of number of clusters per plant, plant height and number of pods per cluster result in simultaneous improvement of seed yield per plant. These characters should be considered at the time of formulating selection strategy in further segregating generations for developing high yielding blackgram genotypes.

The phenotypic and genotypic residual effects recorded are 0.1026 and 0.0848 respectively, indicating that the characters included in the study contribute about 89.74 per cent of variability pertaining to the dependent variable. Hence, besides the characters included in the study there are some other attributes contributing to yield which are to be included in further studies.

4.5.2.2 Direct and indirect effects of physiological characters on seed yield

The trait SCMR (45 DAS) has significant positive correlation (0.957^{**}) with seed yield per plant. The very high positive correlation is due to high positive direct effect of SCMR (45 DAS) (0.986) and positive indirect effects through biomass per plant (0.193) on seed yield per plant. Similar positive correlation between SCMR and seed yield per plant has earlier been reported by Rao *et al.* (2001) in groundnut and by Sudhakar *et al.* (2006) in blackgram.

The trait SLA taken at 45 DAS has significant negative correlation (-0.487^{**}) and low positive direct effect (0.144) on seed yield per plant. Significant negative correlation is mainly due to negative indirect effects through SCMR (45 DAS) (-0.696) and biomass per plant (-0.103). Sudhakar *et al.* (2006) reported that there is significant inverse relationship of SLA with seed yield per plant.

Table 4.15 Genotypic (G) and phenotypic (P) path coefficients for seed yield and physiological attributes in F_3 generation of cross TU-94-02 x KU-1006 in blackgram

Character		SLA (30 DAS)	SLA (45 DAS)	SLW (30 DAS)	SLW (45 DAS)	SCMR (30DAS)	SCMR (45DAS)	BMP	HI	SY
SLA (30 DAS)	**G**	**0.253**	0.388	0.443	-0.982	-0.203	0.257	-0.020	0.229	-0.625**
	P	**-0.057**	0.126	-0.067	0.038	0.237	-0.739	-0.133	-0.012	-0.607**
SLA (45 DAS)	**G**	0.228	**0.416**	0.423	-0.100	-0.286	0.602	-0.894	0.164	-0.446**
	P	-0.050	**0.144**	-0.071	0.044	0.255	-0.696	-0.103	-0.010	-0.487**
SLW (30 DAS)	**G**	-0.229	-0.370	**-0.471**	0.059	0.125	-0.070	0.439	-0.131	0.353*
	P	0.051	-0.135	**0.075**	-0.043	-0.249	0.594	0.087	0.008	0.388**
SLW (45 DAS)	**G**	-0.195	-0.404	-0.440	**0.126**	0.238	-0.051	0.168	-0.119	0.322*
	P	0.048	-0.141	0.072	**-0.045**	-0.250	0.596	0.079	0.008	0.365*
SCMR (30DAS)	**G**	-0.221	-0.432	-0.383	0.095	**0.260**	-0.891	0.268	-0.183	0.514**
	P	0.051	-0.137	0.070	-0.042	**-0.267**	0.738	0.113	0.011	0.536**
SCMR (45DAS)	**G**	-0.024	-0.976	-0.864	0.826	0.684	**-0.224**	0.866	-0.332	0.956**
	P	0.043	-0.101	0.045	-0.027	-0.200	**0.986**	0.193	0.018	0.957**
BMP	**G**	-0.823	-0.670	-0.586	0.107	0.207	-0.009	**0.119**	-0.349	0.997**
	P	0.037	-0.073	0.032	-0.017	-0.149	0.936	**0.204**	0.019	0.989**
HI	**G**	-0.799	-0.646	-0.538	0.036	0.149	-0.827	0.946	**-0.359**	0.963**
	P	0.035	-0.073	0.031	-0.017	-0.146	0.899	0.191	**0.020**	0.940**

*** significant at 5% probability level** **** significant at 1% probability level**

Residual effect at genotypic level=0.089 Residual effect at phenotypic level =0.056

SLA (30 DAS) - Specific Leaf Area at 30 DAS (cm^2 g^{-1})
SLA (45 DAS) - Specific Leaf Area at 45 DAS (cm^2 g^{-1})
SLW (30 DAS) - Specific Leaf Weight at 30 DAS (g cm^{-2})
SLW (45DAS) - Specific Leaf Weight at 45 DAS (g cm^{-2})
SCMR (30DAS) - SPAD Chlorophyll Meter Reading at 30 DAS
SCMR (45DAS) - SPAD Chlorophyll Meter Reading at 30 DAS
BMP - Biomass per plant (g)
HI - Harvest Index (%)

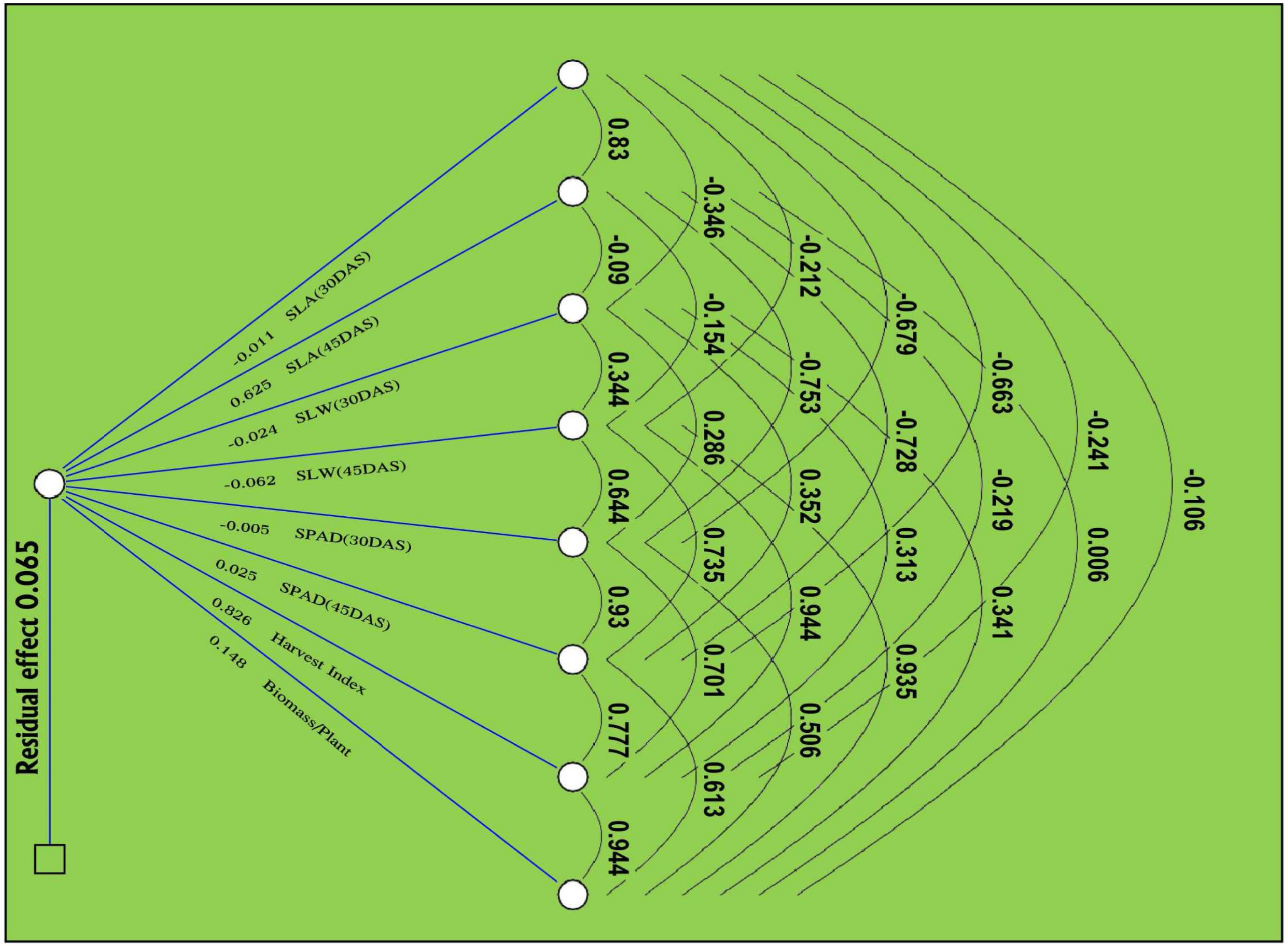


Fig. 4.7 Phenotypic path diagram for seed yield and physiological attributes in F_3 generation of TU-94-02 x KU-1006 in blackgram

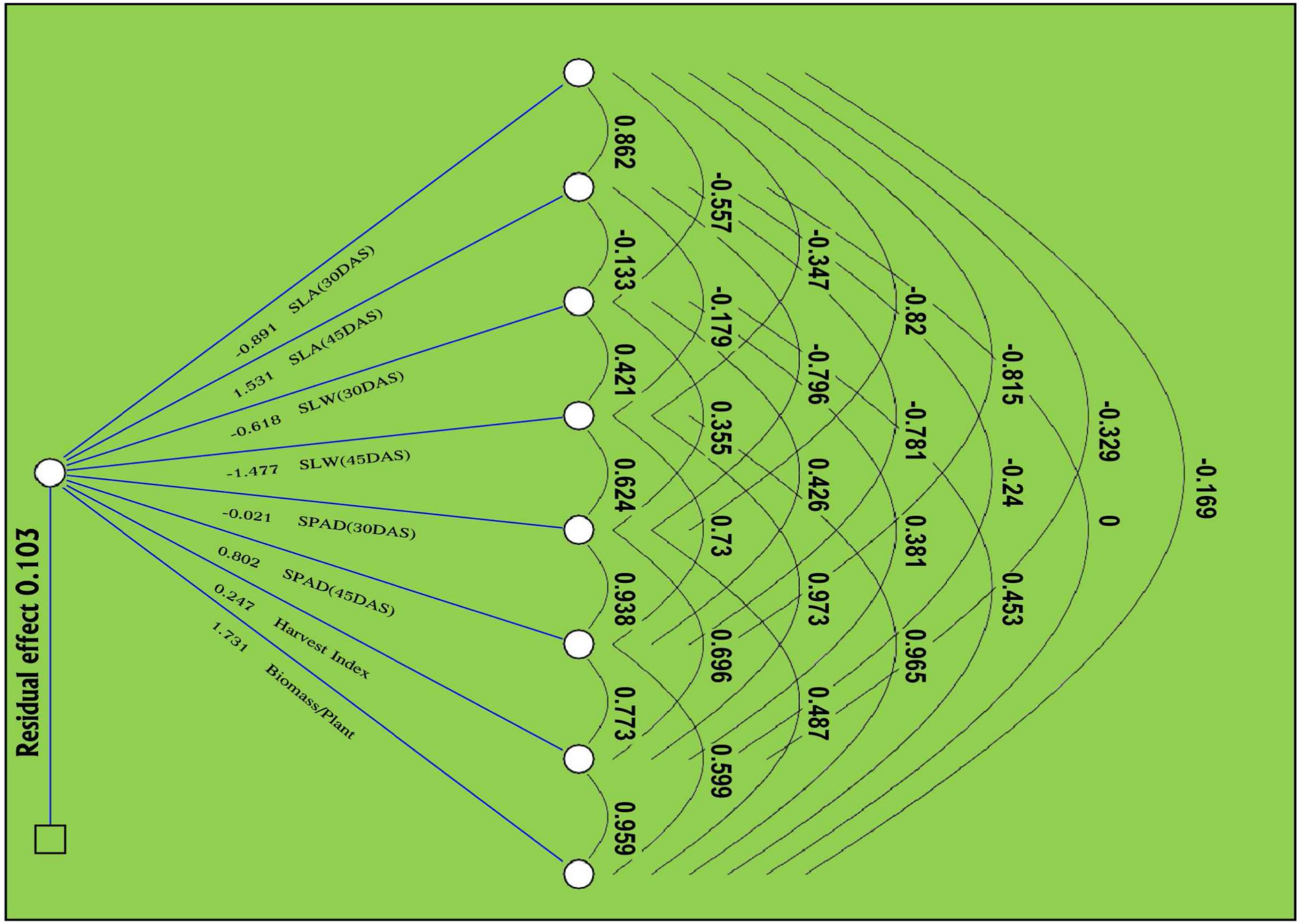


Fig. 4.8 Genotypic path diagram for seed yield and physiological attributes in F_3 generation of TU-94-02 x KU-1006 in blackgram

The trait biomass per plant has significant positive correlation (0.989**) with seed yield per plant. The significant positive correlation is due to moderate positive direct effect of biomass per plant (0.204) and positive indirect effects of the trait through SCMR (45 DAS) (0.936), SLA (30 DAS) (0.037), SLW (30 DAS) (0.032) and harvest index (0.019) on seed yield per plant. Similar results were observed by Usha rani *et al.* (1981), Venkateswarlu (2001), Kanimoli *et al.* (2015) and Rajasekhar *et al.* (2017).

SLW taken at 30 DAS has significant positive correlation (0.388**) with seed yield per plant, even though the direct effect shown is negligible (0.075). The significant positive correlation of SLW (30 DAS) with seed yield per plant is mainly due to positive indirect effects of SCMR (45 DAS) (0.594). A significant relationship between SLW with seed yield per plant was earlier reported by Rao *et al.* (2001) in groundnut and by Sudhakar *et al.* (2006) in blackgram.

The trait harvest index has significant positive correlation (0.940**) with seed yield per plant. Even though the direct effect of harvest index on seed yield per plant is negligible (0.020) the correlation is positive and significant due to high positive indirect effects through SCMR (45 DAS) (0.899) and biomass per plant (0.191) on seed yield per plant. Similar findings were earlier reported by Patil and Deshmukh (1989), Govindaraj and Subramanian (2001), Umadevi and Meenakshi Ganesan (2005), Chauhan *et al.* (2007) and Isha Parveen *et al.* (2011) and Arya *et al.* (2017).

The trait SCMR taken at 30 DAS has significant positive correlation (0.536**) with seed yield per plant. But its direct effect on seed yield per plant is negative (-0.267). The significant positive correlation is mainly due to positive indirect effects of SCMR (45 DAS) (0.738) and biomass per plant (0.113). Similar positive correlation between SCMR and seed yield per plant has earlier been reported by Rao *et al.* (2001) in groundnut and by Sudhakar *et al.* (2006) in blackgram.

The trait SLA taken at 30 DAS has significant negative correlation (-0.607**) with seed yield per plant and negligible negative direct effect (-0.057) on seed yield per plant. Significant correlation is mainly due to negative indirect effects through SCMR (45 DAS) (-0.739) and biomass per plant (-0.133). Sudhakar *et al.* (2006) reported that there is significant inverse relationship of SLA with seed yield per plant.

SLW taken at 45 DAS has significant positive correlation (0.365**) with seed yield per plant, even though the direct effect is negative and negligible (-0.045). The significant positive correlation of SLW (45 DAS) with seed yield per plant is mainly due to positive indirect effect via SCMR (45 DAS) (0.596). A significant relationship was observed between SLW with seed yield per plant by Rao *et al.* (2001) in groundnut and by Sudhakar *et al.* (2006) in blackgram.

In the cross TU-94-02 x KU-1006, among physiological characters, SCMR (45 DAS) exerted high positive direct effect on seed yield per plant followed by biomass per plant, SLA (45 DAS), SLW (30 DAS) and harvest index. Characters such as SCMR (30 DAS), SLW (45 DAS), SLA (30 DAS) exerted negative direct effect on seed yield per plant.

Considering the nature and magnitude of character association and their direct and indirect effects, it can be concluded that manifestation of character, SCMR (45 DAS) improves yield.

The phenotypic residual and genotypic residual effects recorded are 0.056 and 0.089 respectively, indicating that the characters included in the study contribute about 91.10 per cent of variability pertaining to the dependent variable.

4.5.3 F$_3$ Progenies of the Cross TU-94-02 x LBG-752

Path coefficient analysis was done for all the yield contributing attributes and physiological attributes separately and the results were presented in Table 4.16 and Table 4.17 respectively. The phenotypic and

Table 4.16 Genotypic (G) and phenotypic (P) path coefficients for seed yield and its attributes in F_3 generation of cross TU-94-02 x LBG-752 In blackgram

Character		DF	DM	PH	NB	NCP	NPC	NPP	PL	NSP	TW	SY
DF	**G**	**-0.011**	-0.158	0.162	-0.143	0.174	-0.053	0.016	-0.020	0.004	0.010	-0.017
	P	**-0.723**	0.002	0.008	0.085	-0.123	0.134	0.003	-0.013	-0.013	0.305	-0.322*
DM	**G**	-0.280	**-0.156**	-0.577	0.382	-0.096	0.244	-0.234	0.061	0.023	0.017	-0.347*
	P	-0.018	**0.069**	0.017	0.059	-0.082	0.072	-0.004	-0.004	-0.292	0.000	-0.184
PH	**G**	-0.001	0.046	**0.937**	-0.278	0.554	-0.672	0.669	-0.218	-0.058	-0.018	0.960**
	P	0.101	-0.019	**-0.060**	-0.206	0.685	-0.237	0.009	0.022	0.478	0.000	0.773**
NB	**G**	-0.001	0.046	0.922	**-0.288**	0.537	-0.657	0.644	-0.210	-0.056	-0.015	0.921**
	P	0.275	-0.018	-0.055	**-0.224**	0.562	-0.203	0.007	0.018	0.299	0.000	0.661**
NCP	**G**	-0.003	0.026	0.851	-0.194	**0.579**	-0.672	0.662	-0.214	-0.056	-0.014	0.964**
	P	0.106	-0.007	-0.049	-0.149	**0.843**	-0.323	0.010	0.027	0.480	-0.001	0.937**
NPC	**G**	-0.001	0.055	0.886	-0.226	0.564	**-0.690**	0.676	-0.217	-0.058	-0.019	0.971**
	P	0.275	-0.014	-0.040	-0.129	0.771	**-0.353**	0.008	0.029	0.370	-0.001	0.916**
NPP	**G**	0.000	0.053	0.883	-0.204	0.557	-0.678	**0.688**	-0.223	-0.060	-0.021	0.996**
	P	-0.160	-0.025	-0.049	-0.132	0.697	-0.243	**0.012**	0.021	0.656	0.000	0.777**
PL	**G**	-0.001	0.042	0.892	-0.211	0.555	-0.669	0.685	**-0.224**	-0.060	-0.022	0.988**
	P	0.289	-0.009	-0.041	-0.130	0.727	-0.326	0.008	**0.032**	0.352	-0.001	0.901**
NSP	**G**	0.001	0.059	0.877	-0.199	0.544	-0.666	0.684	-0.222	**-0.060**	-0.024	0.993**
	P	-0.320	-0.029	-0.042	-0.097	0.588	-0.190	0.011	0.016	**0.689**	0.000	0.626**
TW	**G**	-0.004	-0.113	-0.498	0.834	-0.345	0.558	-0.603	0.204	0.060	**0.024**	-0.884**
	P	-0.100	0.013	0.005	0.023	-0.212	0.133	-0.002	-0.011	-0.132	**0.002**	-0.280*

*** significant at 5% probability level** **** significant at 1% probability level**

Residual effect at genotypic level=0.032 Residual effect at phenotypic level =0.200

DF - Days to 50% flowering
DM - Days to maturity
PH - Plant height (cm)
TW - Test Weight (g)
NB - No. of branches
NCP - No. of clusters per plant
NPC - No. pods per cluster
SY - Seed Yield per plant (g)
NPP - Number of pods per plant
PL - Pod length (cm)
NSP - No. seeds per pod

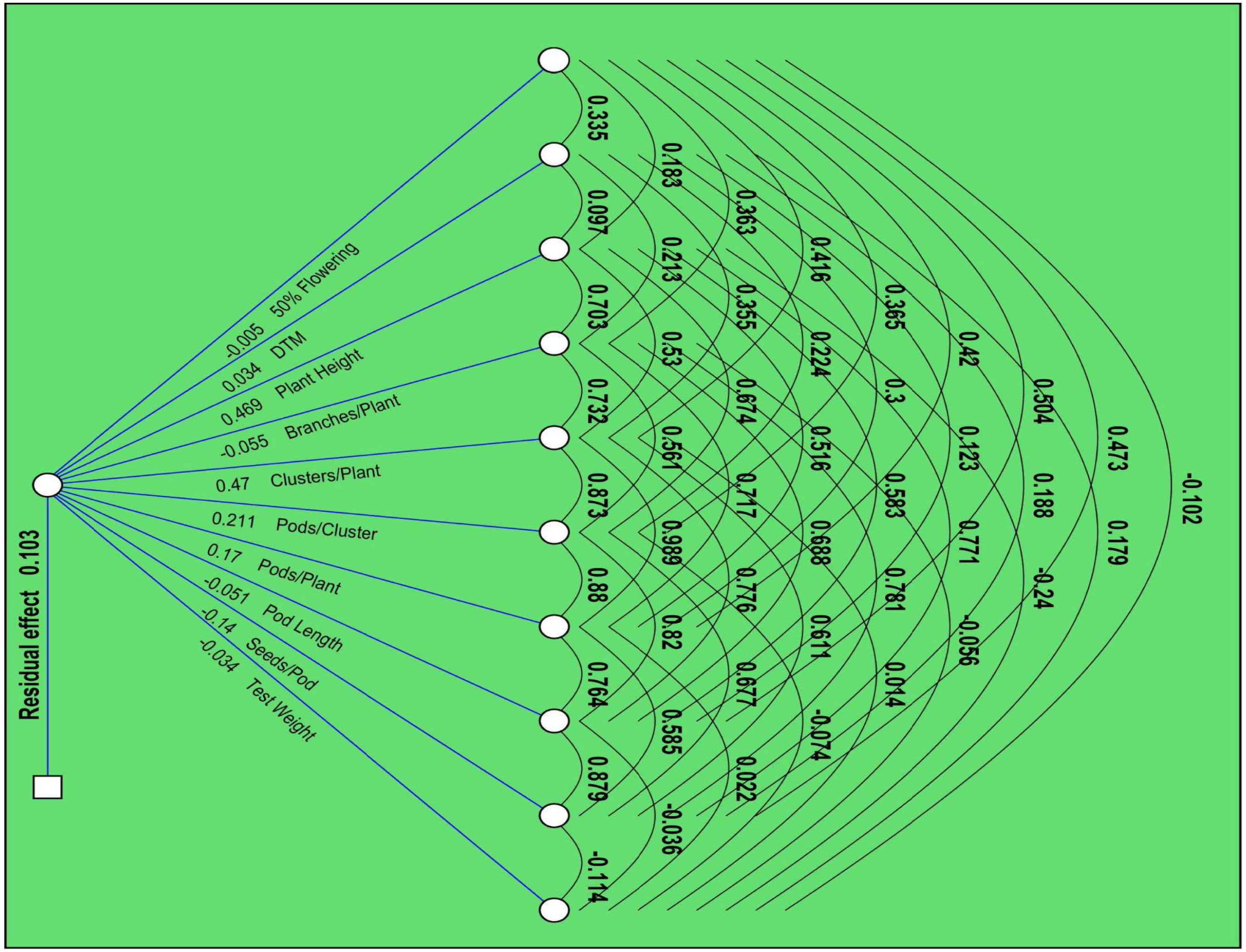


Fig. 4.9 Phenotypic path diagram for seed yield and its contributing attributes in F_3 generation of cross TU-94-02 x LBG-752 in blackgram

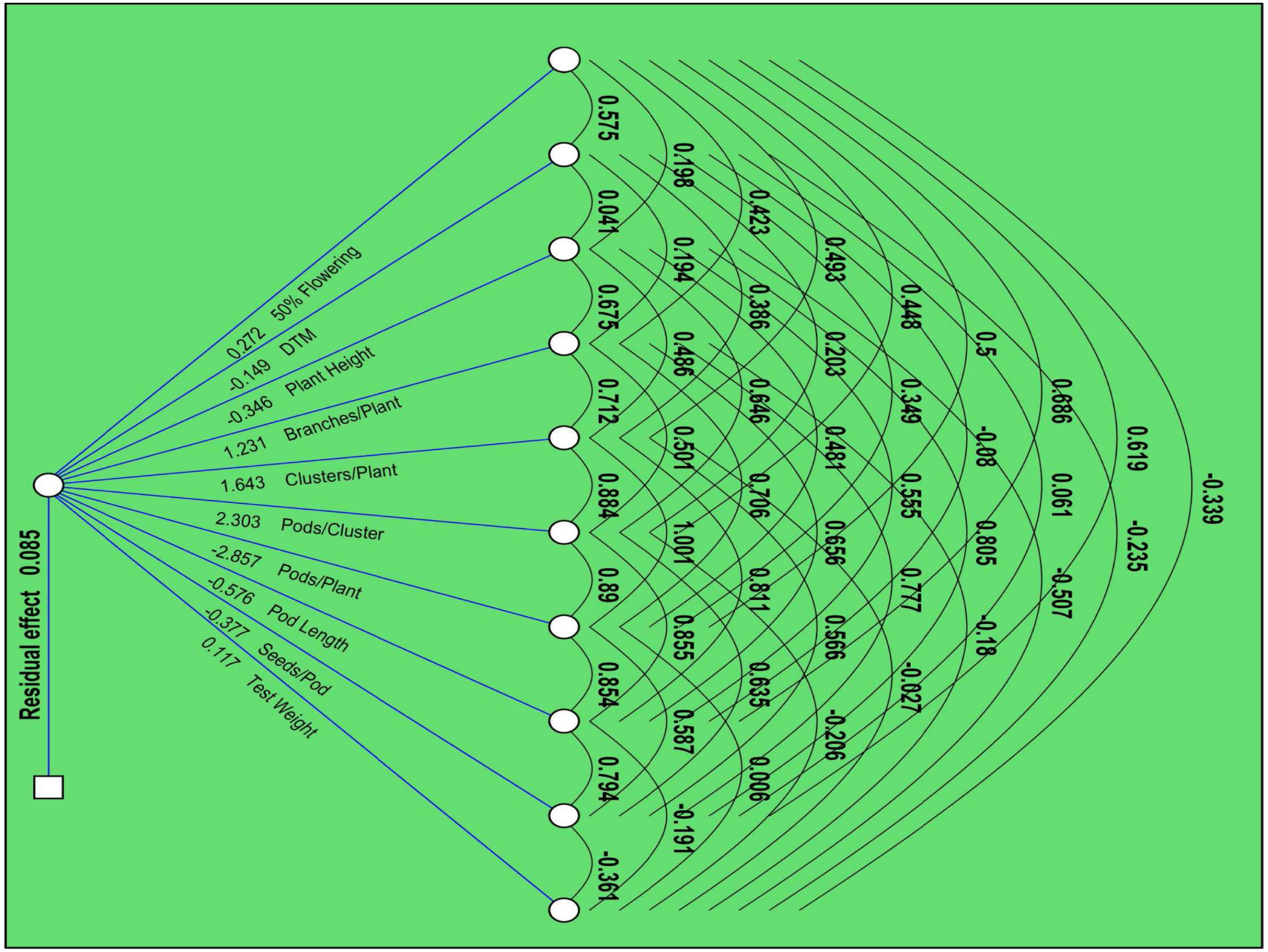


Fig. 4.10 Phenotypic path diagram for seed yield and its contributing attributes in F_3 generation of cross TU-94-02 x LBG-752 in blackgram

genotypic path diagrams regarding direct and indirect effects of yield contributing attributes on seed yield are provided in Fig. 4.9 and Fig. 4.10 whereas, effects of physiological attributes were provided in Fig. 4.11 and Fig. 4.12.

4.5.3.1 Direct and indirect effects of yield contributing characters on seed yield

The trait number of clusters per plant has high positive direct effect (0.843) and significant positive correlation with seed yield per plant (0.937^{**}). The negative indirect effects of this trait through number of pods per cluster (-0.323) and number of branches per plant (-0.149) were balanced by positive indirect effects through number of seeds per pod (0.480), days to 50% flowering (0.106). Kumar *et al.* (1999), Natarajan and Rathinasamy (1999) and Umadevi and Meenakshi Ganesan (2005) also observed significant positive direct effect and significant positive correlation between number of clusters per plant and seed yield per plant.

Number of seeds per pod has very high positive direct effect (0.689) and significant positive correlation (0.626^{**}) with seed yield per plant. The significant positive correlation is mainly due to very high positive direct effect (0.689) and positive indirect effects of the trait through number of clusters per plant (0.588). The negligible negative indirect effects of other characters are also suppressed by the positive indirect effects of the above characters. The results were in accordance with Patil and Deshmukh (1989), Govindaraj and Subramanian (2001), Umadevi and Meenakshi Ganesan (2005), Chauhan *et al.* (2007) and Isha Parveen *et al.* (2011).

Pod length has expressed negligible positive direct effect (0.032) on seed yield per plant but its correlation with seed yield per plant is significant and positive (0.902^{**}). The significant positive correlation is mainly due to positive indirect effects of the trait through number of clusters per plant (0.727), number of seeds per pod (0.352) and days to 50% flowering (0.289).

The negligible negative indirect effects of remaining characters are also suppressed by the positive indirect effects of the above characters. Similar results were observed by Shivade *et al.* (2011), Isha Parveen *et al.* (2011), Shridevi *et al.* (2011) and Jyothsna *et al.* (2016).

Number of pods per plant has negligible positive direct effect (0.012) on seed yield per plant but its correlation with seed yield per plant is significant and positive (0.777^{**}). The significant positive correlation is mainly due to very high positive indirect effects of the trait through number of clusters per plant (0.697) and number of seeds per pod (0.656). Similar results of negligible positive direct effect of number of pods per plant on seed yield was observed by Abbas (1999)in lentil and Hassan *et al.* (2003) in blackgram.

The trait test weight has negligible positive direct effect (0.002) but its correlation with seed yield per plant is significant and negative (-0.280^{*}). The significant negative correlation is mainly due to negative indirect effects via number of clusters per plant (-0.212) and number of seeds per pod (-0.132). Similar findings were reported by Abbas (1999) in lentil and Hassan *et al.* (2003) in blackgram.

Days to 50% flowering has very high negative direct effect (-0.723) and significant negative correlation (-0.322^{*}) with seed yield per plant. Though characters like test weight (0.305) and number of pods per cluster (0.134) showed positive indirect effects, it is suppressed by negative direct effect of days to 50% flowering resulting in significant negative correlation with seed yield per plant. Punia *et al.* (2014) and Kanimoli *et al.* (2015) also observed negative direct effect and significant negative phenotypic correlation of days to 50% flowering with seed yield per plant.

The trait number of pods per cluster has moderate negative direct effect (-0.353) and significant positive correlation (0.916^{**}) with seed yield per plant. The negative direct effect of number of pods per cluster was supressed by positive indirect effects through number of clusters per plant (0.771),

Table 4.17 Genotypic (G) and phenotypic (P) path coefficients for seed yield and physiological attributes in F_3 generation of cross TU-94-02 x LBG-752 in blackgram

Character		SLA (30 DAS)	SLA (45 DAS)	SLW (30 DAS)	SLW (45 DAS)	SCMR (30DAS)	SCMR (45DAS)	BMP	HI	SY
SLA (30 DAS)	**G**	**-0.891**	0.320	0.345	0.512	0.017	-0.654	-0.292	-0.081	0.275
	P	**-0.011**	0.518	0.008	0.013	0.004	-0.017	-0.016	-0.199	0.301*
SLA (45 DAS)	**G**	-0.769	**0.531**	0.082	0.265	0.017	-0.626	0.000	-0.059	0.441**
	P	-0.009	**0.625**	0.002	0.010	0.004	-0.019	0.001	-0.181	0.433**
SLW (30 DAS)	**G**	0.497	-0.204	**-0.618**	-0.623	-0.007	0.342	0.784	0.094	0.265
	P	0.004	-0.057	**-0.024**	-0.022	-0.002	0.009	0.051	0.258	0.218
SLW (45 DAS)	**G**	0.309	-0.275	-0.260	**-0.477**	-0.013	0.586	0.671	0.240	0.781**
	P	0.002	-0.096	-0.008	**-0.062**	-0.003	0.019	0.139	0.780	0.769**
SCMR (30DAS)	**G**	0.731	-0.519	-0.219	-0.922	**-0.021**	0.753	0.844	0.172	0.118
	P	0.007	-0.470	-0.007	-0.040	**-0.005**	0.024	0.075	0.579	0.163
SCMR (45DAS)	**G**	0.726	-0.495	-0.263	-0.078	-0.020	**0.802**	0.137	0.191	0.200
	P	0.007	-0.455	-0.009	-0.046	-0.005	**0.025**	0.091	0.642	0.251
BMP	**G**	0.150	0.000	-0.280	-0.426	-0.010	0.481	**0.731**	0.237	0.883**
	P	0.001	0.004	-0.008	-0.058	-0.003	0.016	**0.148**	0.780	0.880**
HI	**G**	0.294	-0.367	-0.236	-0.437	-0.015	0.620	0.660	**0.247**	0.767**
	P	0.003	-0.137	-0.008	-0.059	-0.004	0.020	0.140	**0.826**	0.782**

*** significant at 5% probability level** **** significant at 1% probability level**

Residual effect at genotypic level=0.103 Residual effect at phenotypic level =0.065

SLA (30 DAS) - Specific Leaf Area at 30 DAS (cm^2 g^{-1})
SLW (30 DAS) - Specific Leaf Weight at 30 DAS (g cm^{-2})
SCMR (30DAS) - SPAD Chlorophyll Meter Reading at 30 DAS
BMP - Biomass per plant (g)
SLA (45 DAS) - Specific Leaf Area at 45 DAS (cm^2 g^{-1})
SLW (45DAS) - Specific Leaf Weight at 45 DAS (g cm^{-2})
SCMR (45DAS) - SPAD Chlorophyll Meter Reading at 30 DAS
HI - Harvest Index (%)

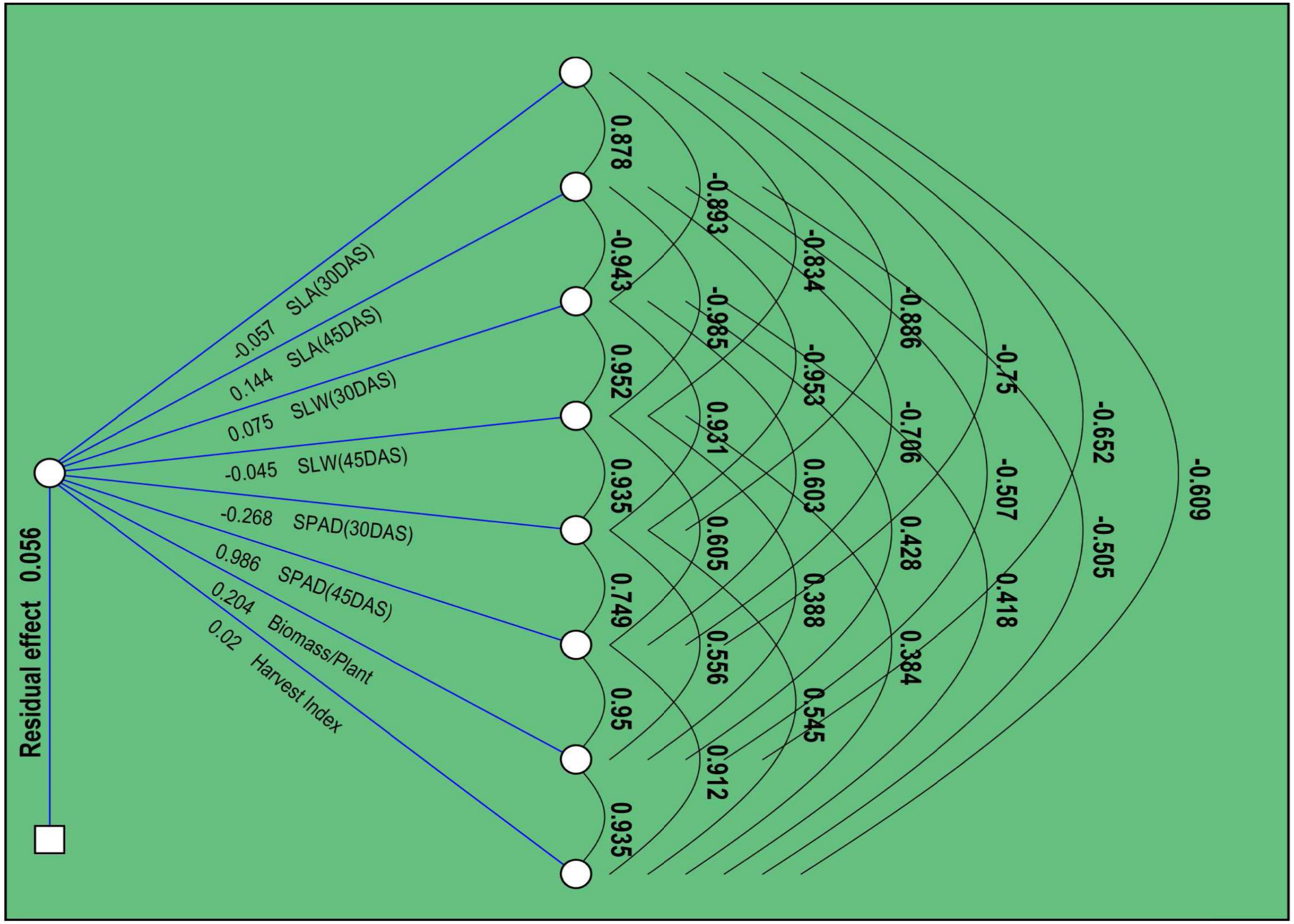


Fig. 4.11 Phenotypic path diagram for seed yield and physiological attributes in F_3 generation of TU-94-02 x LBG-752 in blackgram

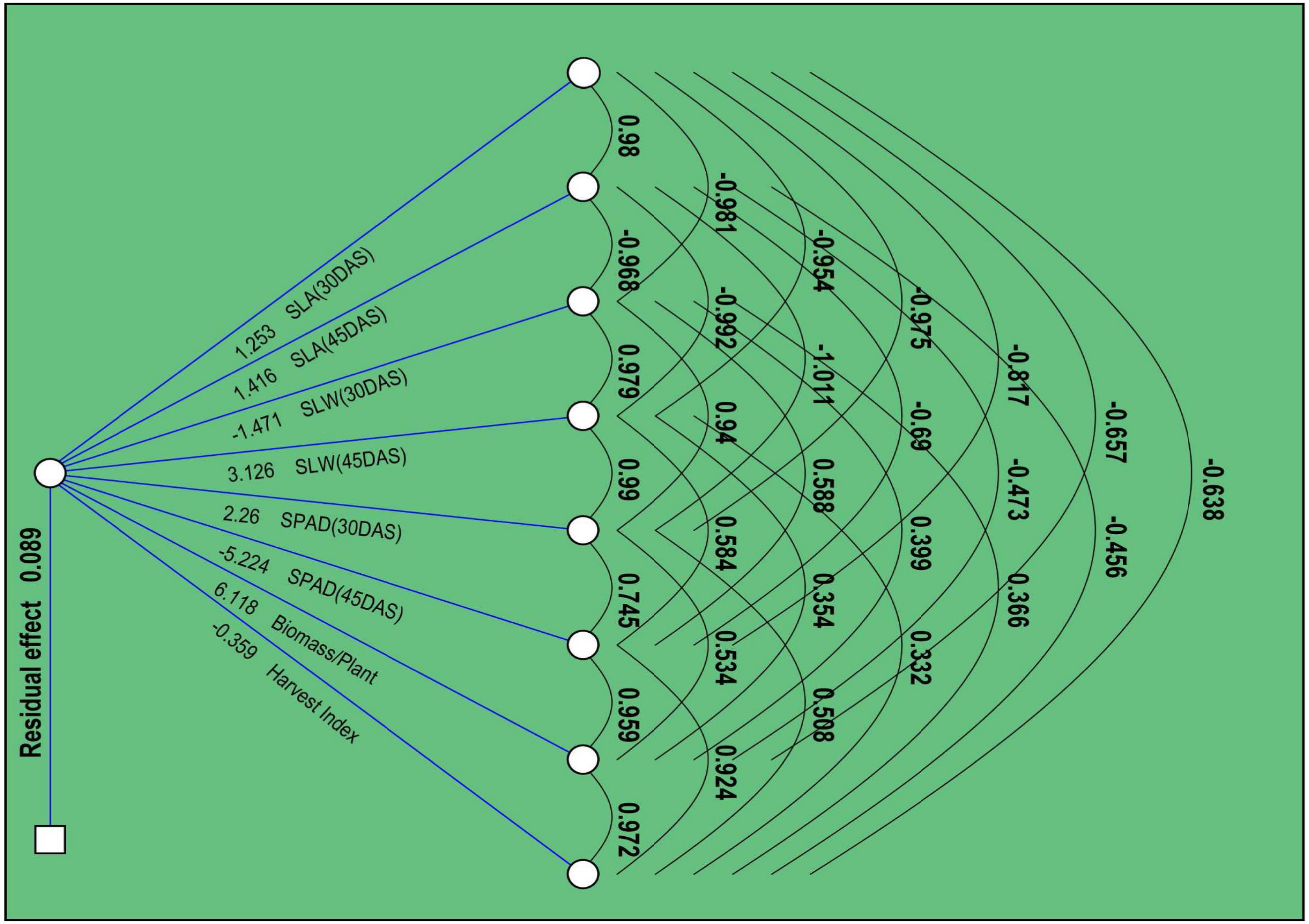


Fig. 4.12 Genotypic path diagram for seed yield and physiological attributes in F_3 generation of TU-94-02 x LBG-752 in blackgram

number of seeds per pod (0.370) and days to 50% flowering (0.275) resulting in significant positive correlation with seed yield per plant. Gopi Krishna *et al.* (2002), Reddy *et al.* (2011) and Sinha *et al.* (2018) also observed moderate negative direct effect and significant positive correlation of number of pods per cluster with seed yield per plant.

Number of branches per plant has moderate negative direct effect (-0.224) on seed yield per plant but the correlation is positive and significant (0.661**). The negative indirect effects of this trait through number of pods per cluster (-0.203) and negative direct effect of number of branches per plant were supressed by positive indirect effects through number of clusters per plant (0.562), number of seeds per pod (0.299) and days to 50% flowering (0.275) resulting in significant positive correlation (0.661**) on seed yield per plant. Similar findings were reported by Umadevi and Meenakshi Ganesan (2005), Veeranjaneyulu *et al.* (2007) and Isha Parveen *et al.* (2011).

Plant height has recorded significant positive correlation (0.960**) with seed yield per plant but the direct effect is negligible (-0.060). The significant positive correlation is due to positive indirect effects of number of clusters per plant (0.685), number of seeds per pod (0.478) and days to 50% flowering (0.101). Negative direct effect of plant height on seed yield per plant with significant positive correlation was reported by Umadevi and Meenakshi Ganesan (2005), Veeranjaneyulu *et al.* (2007) and Isha Parveen *et al.* (2011).

Among the yield contributing characters in this cross, number of clusters per plant exerted positive direct effect on seed yield per plant followed by number of seeds per pod, days to maturity, pod length, number of pods per plant and test weight. Days to 50% flowering, number of pods per cluster and plant height exerted negative direct effects on seed yield per plant.

Based on the nature and magnitude of character association and their direct and indirect effects, it can be suggested that manifestation of number of clusters per plant and number of seeds per pod result in simultaneous improvement of seed yield per plant. These characters should be considered at the time of formulating selection strategy in further segregating generations of the cross TU-94-02 x LBG-752 for developing high yielding blackgram genotypes.

The phenotypic residual effect and genotypic residual effect are 0.200 and 0.032 respectively, indicating that the characters included in the study contribute about 80.00 per cent of variability pertaining to the dependent variable. Hence, besides the characters included in the study some other attributes contributing to yield should also be included in further studies.

4.5.3.2 Direct and indirect effects of physiological attributes on seed yield

The trait harvest index has significant positive correlation (0.782**) with seed yield per plant. The significant positive correlation is due to high positive direct effect (0.826) of harvest index. Similar findings were recorded by Patil and Deshmukh (1989), Govindaraj and Subramanian (2001), Umadevi and Meenakshi Ganesan (2005), Chauhan *et al.* (2007) and Isha Parveen *et al.* (2011) and Arya *et al.* (2017).

SLA taken at 45 DAS has significant positive correlation (0.433**) with seed yield per plant which is the result of its very high direct effect (0.625). Sudhakar *et al.* (2006) reported that there is significant inverse relationship of SLA with seed yield per plant.

The trait biomass per plant has significant positive correlation (0.880**) with seed yield per plant but its direct effect is low (0.148). The significant positive correlation is mainly due to positive indirect effect of biomass per plant through harvest index (0.780). Similar results were observed by Usha rani *et al.* (1981), Venkateswarlu (2001), Kanimoli *et al.* (2015) and Rajasekhar *et al.* (2017).

The trait SLW taken at 45 DAS has significant correlation (0.769**) with seed yield per plant. It has negligible negative direct effect (-0.062) on seed yield per plant. The significant positive correlation is mainly due to positive indirect effects of the trait through harvest index (0.780) and biomass per plant (0.139). A significant relationship was observed between SLW and seed yield per plant was earlier reported by Sudhakar *et al.* (2006) in blackgram and by Rao *et al.* (2001) in groundnut.

The trait SLA taken at 30 DAS has significant correlation (0.301^*) with seed yield per plant. It has negligible negative direct effect (-0.011) on seed yield per plant. Significant correlation is due to positive indirect effect through SLA (45 DAS) (0.518), SLW (45 DAS) (0.013) and SLW (30 DAS) (0.008).

In the cross TU-94-02 x LBG-752, among physiological characters, harvest index exerted high positive direct effect on seed yield per plant followed by SLA (45 DAS), biomass per plant while SCMR (45 DAS). SLW (45 DAS), SLW (30 DAS). On contrary, SCMR (30 DAS) has exerted negative direct effect on seed yield per plant.

Considering the nature and magnitude of character association and their direct and indirect effects, it can be concluded that among all the physiological traits studied, manifestation of harvest index and SLA (45 DAS) improves seed yield per plant.

The phenotypic residual and genotypic residual effects recorded are 0.103 and 0.065 respectively, indicating that the characters included in the study contribute about 89.70 per cent of variability pertaining to the dependent variable.

4.6 TRANSGRESSIVE SEGREGATION

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

Table 4.18 Transgressive segregants for nineteen characters in F_3 population of three blackgram crosses

Trait/Cross	F_3 generation		Parents		No. of transgressive segregants	
	Highest plant value	Lowest Plant value	Higher parent value	Lower parent value	Higher than highest parent	Lower than lowest parent
Days to 50% flowering						
LBG-787 x LBG-752	38.00	35.00	42.00 (LBG-752)	38.00 (LBG-787)	50 (6.24%)	20 (2.50%)
TU-94-02 x KU-1006	38.00	34.00	36.00 (TU-94-02)	35.00 (KU-1006)	64 (8.00%)	50 (6.25%)
TU-94-02 x LBG-752	36.00	32.00	42.00 (LBG-752)	36.00 (TU-94-02)	80 (10.00%)	34 (4.25%)
Days to maturity						
LBG-787 x LBG-752	85.00	80.00	82.00 (LBG-752)	78.00 (LBG-787)	60 (7.50%)	22 (2.75%)
TU-94-02 x KU-1006	83.00	75.00	81.00 (TU-94-02)	79.00 (KU-1006)	78 (9.75%)	64 (8.00%)
TU-94-02 x LBG-752	87.00	79.00	82.00 (LBG-752)	81.00 (TU-94-02)	102 (12.75%)	46 (5.75%)
Plant height						
LBG-787 x LBG-752	46.00	12.00	25.93 (LBG-752)	17.83 (LBG-787)	212 (26.50%)	130 (16.25%)
TU-94-02 x KU-1006	50.00	11.00	41.80 (TU-94-02)	38.24 (KU-1006)	420 (52.50%)	112 (14.00%)
TU-94-02 x LBG-752	59.00	17.00	41.80 (TU-94-02)	25.91 (LBG-752)	236 (29.50%)	86 (10.75%)
Number of branches per plant						
LBG-787 x LBG-752	7.00	2.00	2.82 (LBG-752)	2.69 (LBG-787)	84 (10.50%)	112 (14.00%)
TU-94-02 x KU-1006	7.00	1.00	4.95 (TU-94-02)	2.58 (KU-1006)	192 (24.00%)	146 (18.25%)
TU-94-02 x LBG-752	6.00	1.00	4.93 (TU-94-02)	2.83 (LBG-752)	170 (21.25%)	154 (19.25%)
Number of clusters per plant						
LBG-787 x LBG-752	48.00	4.00	20.00 (LBG-752)	16.45 (LBG-787)	206 (25.75%)	182 (22.75 %)
TU-94-02 x KU-1006	47.00	5.00	20.53 (TU-94-02)	11.68 (KU-1006)	238 (29.75%)	148 (18.50%)
TU-94-02 x LBG-752	47.00	5.00	21.13 (TU-94-02)	20.39 (LBG-752)	162 (20.25%)	118 (14.75%)

Cont….

Table 4.18 contd….

Trait/Cross	F_3 generation		Parents		No. of transgressive segregants	
	Highest plant value	Lowest Plant value	Higher parent value	Lower parent value	Higher than highest parent	Lower than lowest parent
Number of pods per cluster						
LBG-787 x LBG-752	6.00	1.00	1.91 (LBG-787)	1.87 (LBG-752)	84 (10.48%)	206 (25.84%)
TU-94-02 x KU-1006	7.00	1.00	2.22 (KU-1006)	2.03 (TU-94-02)	184 (23.12%)	150 (18.87%)
TU-94-02 x LBG-752	7.00	1.00	1.93 (LBG-752)	1.84 (TU-94-02)	106 (13.21%)	188 (23.53%)
Number of pods per plant						
LBG-787 x LBG-752	150.00	6.00	37.63 (LBG-752)	30.73 (LBG-787)	96 (12.11%)	100 (12.60%)
TU-94-02 x KU-1006	104.00	4.00	41.52 (TU-94-02)	25.94 (KU-1006)	122 (15.39%)	238 (29.76%)
TU-94-02 x LBG-752	94.00	4.00	39.20 (LBG-752)	38.40 (TU-94-02)	114 (14.24%)	190 (23.80%)
Pod length						
LBG-787 x LBG-752	5.52	3.72	4.98 (LBG-752)	4.75 (LBG-787)	84 (10.60%)	72 (8.89%)
TU-94-02 x KU-1006	5.40	3.60	4.83 (TU-94-02)	4.51 (KU-1006)	214 (26.80%)	52 (6.40%)
TU-94-02 x LBG-752	5.48	3.60	4.99 (TU-94-02)	4.81 (LBG-752)	64 (8.11%)	62 (7.83%)
Number of seeds per pod						
LBG-787 x LBG-752	8.41	3.20	7.15 (LBG-752)	7.02 (LBG-787)	144 (18.12%)	122 (15.26%)
TU-94-02 x KU-1006	7.80	3.80	6.25 (TU-94-02)	5.89 (KU-1006)	174 (21.87%)	146 (18.26%)
TU-94-02 x LBG-752	8.20	3.20	7.06 (LBG-752)	6.54 (TU-94-02)	122 (15.26%)	124 (15.44%)
Test weight						
LBG-787 x LBG-752	6.58	2.51	4.80 (LBG-787)	4.75 (LBG-752)	162 (20.16%)	88 (11.04%)
TU-94-02 x KU-1006	6.84	2.69	4.68 (TU-94-02)	4.63 (KU-1006)	258 (32.36%)	138 (17.26%)
TU-94-02 x LBG-752	6.20	2.56	5.55 (TU-94-02)	4.94 (LBG-752)	222 (27.72%)	118 (14.69%)

Cont….

Table 4.18 contd….

Trait/Cross	F_3 generation		Parents		No. of transgressive segregants	
	Highest plant value	Lowest Plant value	Higher parent value	Lower parent value	Higher than highest parent	Lower than lowest parent
Specific Leaf Area at 30 DAS						
LBG-787 x LBG-752	517.75	133.29	239.11 (LBG-752)	123.35 (LBG-787)	188 (23.39%)	110 (13.72%)
TU-94-02 x KU-1006	566.60	111.50	145.14 (KU-1006)	161.30 (TU-94-02)	316 (39.40%)	86 (10.73%)
TU-94-02 x LBG-752	656.60	164.27	239.18 (LBG-752)	169.72 (TU-94-02)	370 (46.33%)	148 (18.42%)
Specific Leaf Area at 45 DAS						
LBG-787 x LBG-752	577.14	172.95	183.40 (LBG-752)	165.49 (LBG-787)	222 (27.69%)	226 (28.19%)
TU-94-02 x KU-1006	556.72	109.78	156.30 (KU-1006)	176.47 (TU-94-02)	236 (29.40%)	324 (40.46%)
TU-94-02 x LBG-752	456.50	107.86	187.73 (LBG-752)	180.88 (TU-94-02)	302 (37.85%)	312 (38.96%)
Specific Leaf Weight at 30 DAS						
LBG-787 x LBG-752	7.50	1.93	5.15 (LBG-787)	4.88 (LBG-752)	224 (27.91%)	232 (28.96%)
TU-94-02 x KU-1006	8.96	1.76	7.38 (KU-1006)	6.18 (TU-94-02)	318 (39.64%)	240 (30.04%)
TU-94-02 x LBG-752	6.08	1.52	7.23 (TU-94-02)	4.90 (LBG-752)	302 (37.69%)	308 (38.58%)
Specific Leaf Weight at 45 DAS						
LBG-787 x LBG-752	5.78	1.73	5.50 (LBG-787)	4.66 (LBG-752)	126 (15.72%)	186 (23.30%)
TU-94-02 x KU-1006	9.10	1.79	6.63 (KU-1006)	5.70 (TU-94-02)	102 (12.73%)	326 (40.90%)
TU-94-02 x LBG-752	9.27	2.19	5.53 (TU-94-02)	4.70 (LBG-752)	220 (27.42%)	360 (45.01%)
SPAD Chlorophyll Meter Reading at 30 DAS						
LBG-787 x LBG-752	55.30	26.60	38.81 (LBG-752)	35.83 (LBG-787)	332 (41.48%)	94 (11.78%)
TU-94-02 x KU-1006	53.10	25.50	60.45 (KU-1006)	55.24 (TU-94-02)	116 (14.61%)	162 (20.28%)
TU-94-02 x LBG-752	54.30	27.60	54.80 (TU-94-02)	38.30 (LBG-752)	126 (15.90%)	300 (37.48%)

Cont….

Table 4.18 contd….

Trait/Cross	F_3 generation		Parents		No. of transgressive segregants	
	Highest plant value	Lowest Plant value	Higher parent value	Lower parent value	Higher than highest parent	Lower than lowest parent
SPAD Chlorophyll Meter Reading at 45 DAS						
LBG-787 x LBG-752	55.80	23.80	43.40 (LBG-787)	41.80 (LBG-752)	166 (20.78%)	264 (32.96%)
TU-94-02 x KU-1006	58.70	27.80	38.63 (TU-94-02)	38.14 (KU-1006)	112 (14.02%)	176 (22.03%)
TU-94-02 x LBG-752	57.80	28.20	41.63 (LBG-752)	38.14 (TU-94-02)	188 (23.60%)	206 (25.81%)
Biomass per plant						
LBG-787 x LBG-752	42.52	7.88	27.16 (LBG-752)	24.89 (LBG-787)	74 (9.35%)	152 (19.05%)
TU-94-02 x KU-1006	57.78	13.15	25.35 (TU-94-02)	22.67 (KU-1006)	52 (6.55%)	230 (28.76%)
TU-94-02 x LBG-752	60.37	8.69	26.16 (LBG-752)	30.82 (TU-94-02)	154 (19.17%)	98 (12.24%)
Harvest Index						
LBG-787 x LBG-752	59.27	4.16	34.26 (LBG-787)	29.19 (LBG-752)	78 (9.65%)	248 (31.05%)
TU-94-02 x KU-1006	65.04	6.50	39.37 (TU-94-02)	34.75 (KU-1006)	44 (5.53%)	398 (49.76%)
TU-94-02 x LBG-752	62.15	6.68	37.33 (TU-94-02)	28.25 (LBG-752)	122 (15.17%)	338 (42.24%)
Seed yield per plant						
LBG-787 x LBG-752	31.18	1.89	8.07 (LBG-787)	7.87 (LBG-752)	226 (28.22%)	92 (11.60%)
TU-94-02 x KU-1006	38.30	1.26	9.95 (TU-94-02)	7.84 (KU-1006)	268 (33.60%)	74 (9.26%)
TU-94-02 x LBG-752	27.88	1.29	9.88 (TU-94-02)	7.90 (LBG-752)	254 (31.69%)	136 (17.02%)

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. Success in obtaining desired transgressive segregants depends on obtaining genetic recombination between both linked and unlinked alleles (Briggs and Allard, 1953). Keeping the importance of transgressive segregants in view, an analysis of transgressive segregation for both yield contributing attributes and physiological attributes was carried out in the present investigation.

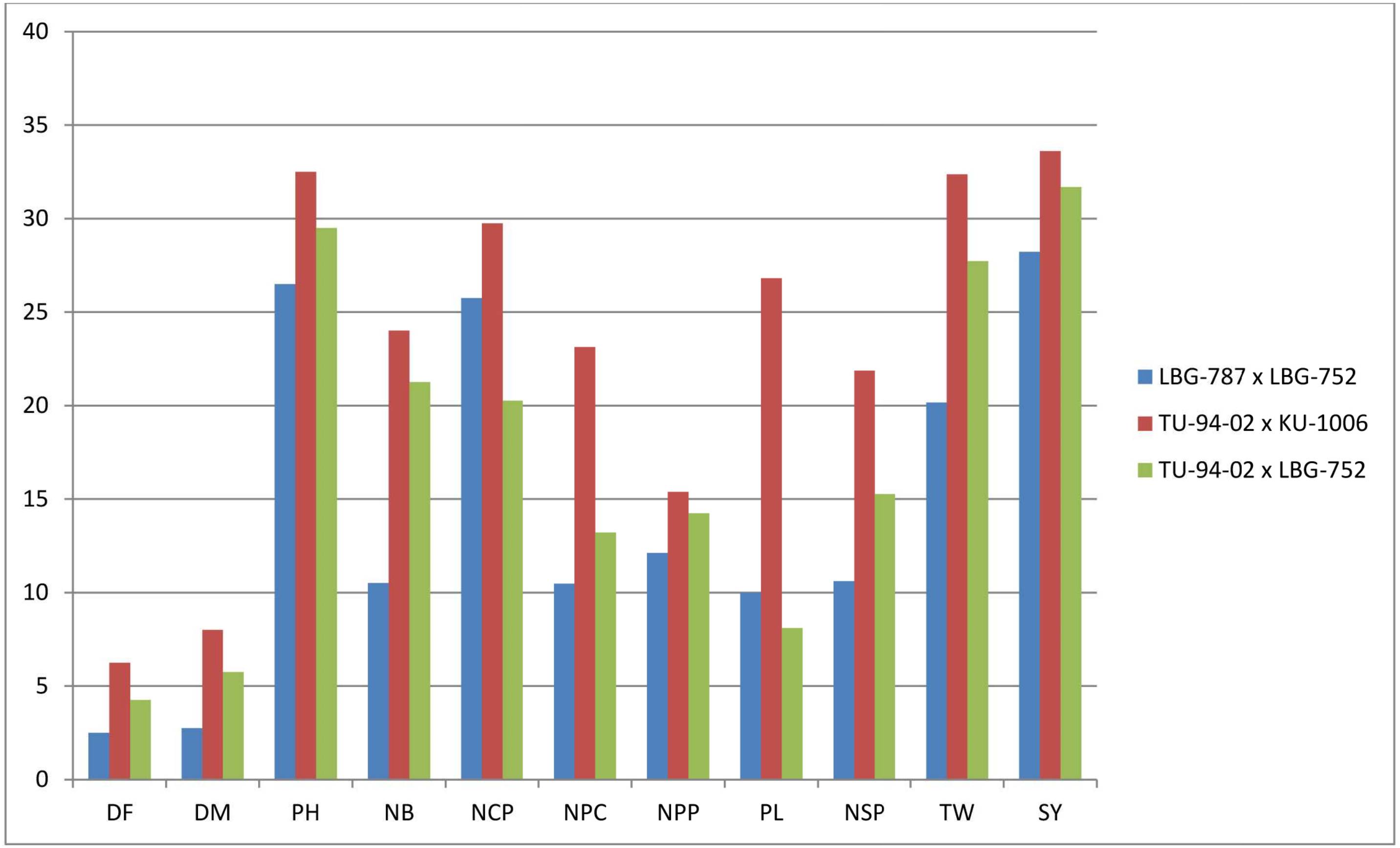
The present study was conducted with 800 plants in each cross. The plants which had values exceeding the mean value of the higher parent or lagging behind the mean value of the lower parent were identified as transgressive segregants. The number of such plants that fitted this definition among all the three crosses is presented in Table 4.18 and the percentage of the transgressive segregants in each cross for yield contributing and physiological attributes were presented in Fig. 4.13 and Fig. 4.14.

4.6.1 Days to 50% Flowering

The number of desirable transgressive segregants for days to 50% flowering were high in cross TU-94-02 x LBG-752 (80 plants; 10.00%) followed by TU-94-02 x KU-1006 (64 plants; 8.00%) and LBG-787 x LBG-752 (50 plants; 6.24%), whereas the number of undesirable transgressive segregants were high in TU-94-02 x KU-1006 (50 plants; 6.25%) followed by TU-94-02 x LBG-752 (34 plants; 4.25%) and LBG-787 x LBG-752 (20 plants; 2.50%).

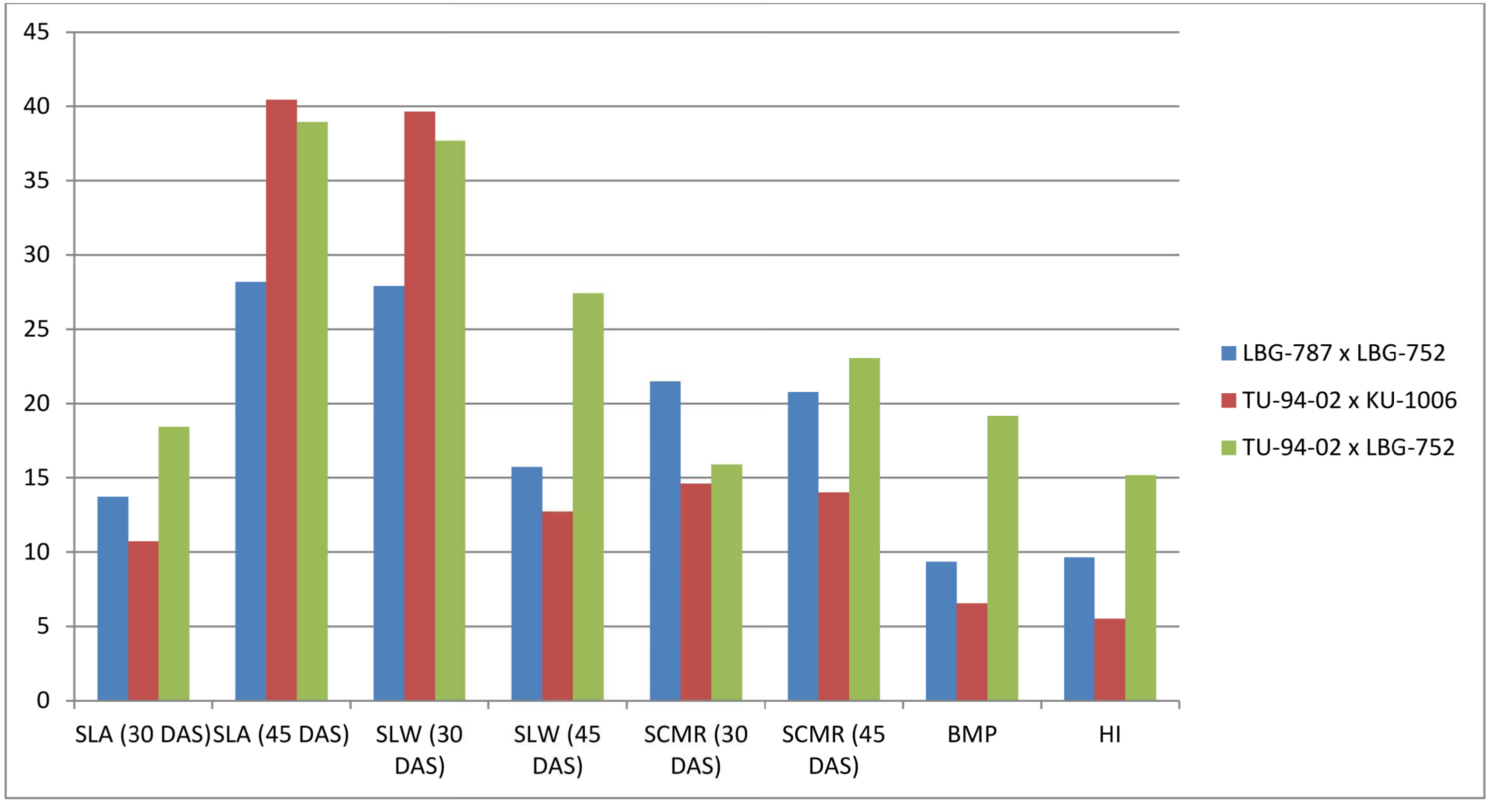
4.6.2 Days to Maturity

Transgressive segregants for days to maturity which are superior than the better parent were more in cross TU-94-02 x LBG-752 (102 plants; 12.75%) followed by TU-94-02 x KU-1006 (78 plants; 9.75%) and LBG-787 x LBG-752 (60 plants; 7.50%) and which are weaker than the inferior parent



DF - Days to 50% flowering
DM - Days to maturity
PH - Plant height (cm)
TW - Test Weight (g)
NB - No. of branches
NCP - No. of clusters per plant
NPC - No. pods per cluster
SY - Seed Yield per plant (g)
NPP - No. of pods per plant
PL - Pod length (cm)
NSP - No. seeds per pod

Fig. 4.13 Bar chart representing percentage of positive transgressive segregants for eleven yield and yield contributing attributes in three crosses of blackgram



SLA (30 DAS)	-	Specific Leaf Area at 30 DAS (cm^2 g^{-1})	SLA (45 DAS)	-	Specific Leaf Area at 45 DAS (cm^2 g^{-1})
SLW (30 DAS)	-	Specific Leaf Weight at 30 DAS (g cm^{-2})	SLW (45DAS)	-	Specific Leaf Weight at 45 DAS (g cm^{-2})
SCMR (30DAS)	-	SPAD Chlorophyll Meter Reading at 30 DAS	SCMR (45DAS)	-	SPAD Chlorophyll Meter Reading at 30 DAS
BMP	-	Biomass per plant (g)	HI	-	Harvest Index (%)

Fig. 4.14 Bar chart representing percentage of positive transgressive segregants eight physiological attributes in three crosses of blackgram

were high in TU-94-02 x KU-1006 (64 plants; 8.00%) followed by TU-94-02 x LBG-752 (46 plants; 5.75%) and LBG-787 x LBG-752 (22 plants; 2.75%).

4.6.3 Plant Height

TU-94-02 x KU-1006 has shown large proportion of transgressive segregants for plant height (420 plants; 52.50%) followed by TU-94-02 x LBG-752 (236 plants; 29.50%) and LBG-787 x LBG-752 (212 plants; 26.50%) whereas, large proportion of undesirable transgressive segregants were recorded in LBG-787 x LBG-752 (130 plants; 16.25%) followed by TU-94-02 x KU-1006 (112 plants; 14.00%) and TU-94-02 x LBG-752 (86 plants; 10.75%).

4.6.4 Number of Branches per Plant

A total of 192 plants (24.00%) have shown higher performance than the better parent in cross TU-94-02 x KU-1006 whereas, in other crosses, TU-94-02 x LBG-752 and LBG-787 x LBG-752 registered 21.25% (170 plants) and 10.50% (84 plants) transgressive segregants respectively. Negative transgressive segregants were high in TU-94-02 x LBG-752 (154 plants; 19.25%) followed by LBG-787 x LBG-752 (146 plants; 18.25%) and TU-94-02 x KU-1006 (112 plants; 14.00%).

4.6.5 Number of Clusters per Plant

The cross, TU-94-02 x KU-1006 recorded high percentage of positive transgressive segregants (238 plants; 29.75%) for number of clusters followed by LBG-787 x LBG-752 (206 plants; 25.75%) and TU-94-02 x LBG-752 (162 plants; 20.25%). In contrary high percentage of negative transgressive segregants was recorded in LBG-787 x LBG-752 (182 plants; 22.75%) followed by TU-94-02 x KU-1006 (148 plants; 18.50%) and TU-94-02 x LBG-752 (118 plants; 14.75%).

4.6.6 Number of Pods per Cluster

More number of positive transgressive segregants were observed in cross TU-94-02 x KU-1006 (184 plants; 23.12%) followed by TU-94-02 x LBG-752 (106 plants; 13.21%) and LBG-787 x LBG-752 (84 plants; 10.48%) for number of pods per plant whereas, negative transgressive segregants were high in LBG-787 x LBG-752 (206 plants; 25.84%) followed by TU-94-02 x LBG-752 (188 plants; 23.53%) and TU-94-02 x KU-1006 (150 plants; 18.87%).

4.6.7 Number of Pods per Plant

Among the three crosses, more number of superior transgressive segregants were registered in cross TU-94-02 x KU-1006 (122 plants; 15.39%) followed by TU-94-02 x LBG-752 (114 plants; 14.24%) and LBG-787 x LBG-752 (96 plants; 12.11%) while more number of inferior transgressive segregants were registered in TU-94-02 x KU-1006 (238 plants; 29.76%) followed by TU-94-02 x LBG-752 (190 plants; 23.80%) and LBG-787 x LBG-752 (100 plants; 12.60%).

4.6.8 Pod Length

Proportion of desirable transgressive segregants for pod length was high in cross TU-94-02 x KU-1006 (214 plants; 26.80%) followed by TU-94-02 x LBG-752 (84 plants; 10.60%) and LBG-787 x LBG-752 (64 plants; 8.11%) whereas, LBG-787 x LBG-752 (72 plants; 8.89%) showed high proportion of negative transgressive segregants followed by TU-94-02 x LBG-752 (62 plants; 7.83%) and TU-94-02 x KU-1006 (52 plants; 6.40%).

4.6.9 Number of Seeds per Pod

More number of positive transgressive segregants for number of seeds per pod higher were registered by TU-94-02 x KU-1006 (174 plants; 21.87%) followed by LBG-787 x LBG-752 (144 plants; 18.12%) and

TU-94-02 x LBG-752 (122 plants; 15.26%) while, TU-94-02 x KU-1006 (146 plants; 18.26%) recorded more number of negative transgressive segregants followed by TU-94-02 x LBG-752 (124 plants; 15.44%) and LBG-787 x LBG-752 (122 plants; 15.26%).

4.6.10 Test Weight

TU-94-02 x KU-1006 contributed high percentage of desirable transgressive segregants (258 plants; 32.36%) for test weight followed by TU-94-02 x LBG-752 (222 plants; 27.72%) and LBG-787 x LBG-752 (162 plants; 20.16%). TU-94-02 x KU-1006 has shown high percentage of inferior transgressive segregants (138 plants; 17.26%) followed by TU-94-02 x LBG-752 (118 plants; 14.69%) and LBG-787 x LBG-752 (88 plants; 11.04%).

4.6.11 Specific Leaf Area (SLA) (30 DAS)

TU-94-02 x LBG-752, TU-94-02 x KU-1006 and LBG-787 x LBG-752 has shown 46.33% (370 plants), 39.40% (316 plants) and 23.39% (188 plants) of desirable transgressive segregants for SLA taken at 30 DAS respectively. In contrary 18.42% (148 plants), 13.72% (110 plants) and 10.73% (86 plants) of undesirable transgressive segregants were reorded in TU-94-02 x LBG-752 followed by LBG-787 x LBG-752 and TU-94-02 x KU- 1006 respectively.

4.6.12 Specific Leaf Area (SLA) (45 DAS)

Transgressive segregants superior than the better parent for SLA taken at 45 DAS were high in cross TU-94-02 x LBG-752 (302 plants; 37.85%) followed by TU-94-02 x KU-1006 (236 plants; 29.40%) and LBG-787 x LBG-752 (222 plants; 27.69%) and transgressive segregants inferior than the lower parent value were high in TU-94-02 x KU-1006 (324 plants; 40.46%) followed by TU-94-02 x LBG-752 (312 plants; 38.96%) and LBG-787 x LBG-752 (226 plants; 28.19%).

4.6.13 Specific Leaf Weight (SLW) (30 DAS)

TU-94-02 x KU-1006 showed high number of positive transgressive segregants (318 plants; 39.64%) for SLW taken at 30 DAS followed by TU-94-02 x LBG-752 (302 plants; 37.69%) and LBG-787 x LBG-752 (224 plants; 27.91%). In contrary high number of negative transgressive segregants were observed in TU-94-02 x LBG-752 (308 plants; 38.58%) followed by TU-94-02 x KU-1006 (240 plants; 30.04%) and LBG-787 x LBG-752 (232 plants; 28.96%).

4.6.14 Specific Leaf Weight (SLW) (45 DAS)

The number of desirable transgressive segregants for SLW taken at 45 DAS were high in cross TU-94-02 x LBG-752 (220 plants; 27.42%), LBG-787 x LBG-752 (126 plants; 15.72%) followed by TU-94-02 x KU-1006 (102 plants; 12.73%). The number of undesirable transgressive segregants were high in TU-94-02 x LBG-752 (360 plants; 45.01%) followed by TU-94-02 x KU-1006 (326 plants; 40.9%) and LBG-787 x LBG-752 (186 plants; 23.30%).

4.6.15 SPAD Chlorophyll Meter Reading (30 DAS)

Transgressive segregants for SCMR taken at 30 DAS which are better than the superior parent were high in cross LBG-787 x LBG-752 (332 plants; 41.48%) followed by TU-94-02 x LBG-752 (126 plants; 15.90%) and TU-94-02 x KU-1006 (116 plants; 14.61%). TU-94-02 x LBG-752 registered high number of inferior transgressive segregants (300 plants; 37.48%) followed by TU-94-02 x KU-1006 (162 plants; 20.28%) and LBG-787 x LBG-752 (94 plants; 11.78%).

4.6.16 SPAD Chlorophyll Meter Reading (45 DAS)

TU-94-02 x LBG-752 registered more number of superior transgressive segregants (188 plants; 23.60%) for SCMR taken at 45 followed by LBG-787 x LBG-752 (166 plants; 20.78%) and TU-94-02 x KU-1006 (112 plants;

14.02%) while high inferior transgressive segregants were recorded in LBG-787 x LBG-752 (264 plants; 32.96%) followed by TU-94-02 x LBG-752 (206 plants; 25.81%) and TU-94-02 x KU-1006 (176 plants; 22.03%).

High percentage of desirable transgressive segregants for biomass were observed in cross TU-94-02 x LBG-752 (154 plants; 19.17%) followed by LBG-787 x LBG-752 (74 plants; 9.35%) and TU-94-02 x KU-1006 (52 plants; 6.55%) whereas, high percentage of negative transgressive segregants were noticed in TU-94-02 x KU-1006 (230 plants; 28.76%) followed by LBG-787 x LBG-752 (152 plants; 19.05%) and TU-94-02 x LBG-752 (98 plants; 12.24%).

4.6.18 Harvest Index

The number of transgressive segregants with harvest index higher than the higher parent value were high in cross TU-94-02 x LBG-752 (122 plants; 15.17%) for seed yield followed by LBG-787 x LBG-752 (78 plants; 9.65%) and TU-94-02 x KU-1006 (44 plants; 5.53%). The number of transgressive segregants with harvest index lower than the lower parent value were high in TU-94-02 x KU-1006 (398 plants; 49.76%), TU-94-02 x LBG-752 (338 plants; 42.24%) and LBG-787 x LBG-752 (248 plants; 31.05%).

4.6.19 Seed Yield per Plant

Among all the crosses, TU-94-02 x KU-1006 produced more number of positive transgressive segregants (268 plants; 33.60%) followed by TU-94-02 x LBG-752 (254 plants; 31.69%) and LBG-787 x LBG-752 (226 plants; 28.22%). In contrary, more number of negative transgressive segregants were registered in TU-94-02 x LBG-752 (136 plants; 17.02%) followed by LBG-787 x LBG-752 (92 plants; 11.60%) and TU-94-02 x KU-1006 (74 plants; 9.26%).

After studying the three crosses, a good number of transgressive segregants were observed for characters like plant height, number of clusters per plant, SLA (30 DAS), SLW (45 DAS), SCMR (30 DAS) and seed yield per plant in cross LBG-787 x LBG-752 and plant height, number of clusters per plant, number of seeds per pod, test weight, SLA (30 DAS), SLA (45 DAS), SLW (30 DAS) and seed yield per plant in cross TU-94-02 x KU-1006 whereas, in the cross TU-94-02 x LBG-752 plant height, test weight, SLA (30 DAS), SLA (45 DAS), SLW (30 DAS), SLW (45 DAS) and seed yield per plant were found with more number of positive transgressive segregants. Superior transgressive segregants identified in crosses, LBG-787 x LBG-752, TU-94-02 x KU-1006 and TU-94-02 x LBG-752 were presented in Plate 4.1, Plate 4.2 and Plate 4.3 respectively.

Among the three crosses studied, higher per cent of positive transgressive segregants for more number of traits were observed in the cross TU-94-02 x KU-1006 along with seed yield. This indicates the scope of evolving better genotypes with maximum number of beneficial alleles along with high seed yield in this cross.

Dhole and Reddy (2011) reported fifteen (4.79%) transgressive segregants for hundred seed weight and one (0.0027%) transgressive segregant for seed yield per plant in F_2 population of cross Rsel-247 x JL-781 of greengram. Kshirsagar *et al.* (2013) reported transgressive segregation for plant height, days to first flowering, yield per plant and harvesting duration in F_3 generation of two intervarietal crosses of tomato. 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. Shashikumar *et al.* (2016) observed 14% of transgressive segregation for pod yield per plant in F_3 population in KCG-6 x ICGV-9114 cross of groundnut. Showkath *et al.* (2016) observed 20 transgressive segregants in F_3 population of HA 10-8 x RIL 180 and 25 transgressive segregants in F_3 population of FPB 21 x RIL 180 for number of pods per plant. Kerem *et al.* (2017) evaluated F_2 and F_3 population derived from cross between *Cicer arietinum* and *Cicer reticulatum* of chickpea and observed highest number of transgressive segregants in seeds per plant (77%), number of pods per plant (83%), biological yield (86%) and seed yield (60%).

In brief, transgressive individuals with values exceeding the better parent were observed in all the three crosses *viz.,* LBG-787 x LBG-752, TU-94-02 x KU-1006, TU-94-02 x LBG-752 for all the nineteen 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, yield contributing and physiological characters are represented in Fig. 4.13 and Fig. 4.14 respectively. Promising progenies with high seed yield were represented in Plate 4.4.

LBG-787

LBG-752

Progeny 9

Progeny 4

Progeny 10

Progeny 2

Progeny 6

Plate 4.1 Transgressive segregants in F_3 generation of the cross LBG-787 x LBG-752

TU-94-02

KU-1006

Progeny 13

Progeny 12

Progeny 17

Progeny 15

Progeny 20

Plate 4.2 Transgressive segregants in F_3 generation of the cross TU-94-02 x KU-1006

TU-94-02

LBG-752

Progeny 23

Progeny 24

Progeny 21

Progeny 29

Progeny 22

Plate 4.3 Transgressive segregants in F_3 generation of the cross TU-94-02 x LBG-752

Progeny 4 (LBG-787 x LBG-752)

Progeny 20 (TU-94-02 x KU-1006)

Progeny 23 (TU-94-02 x LBG-752)

Progeny 24 (TU-94-02 x LBG-752)

Plate 4.4 Promising progenies identified in three crosses for seed yield

Chapter – V

Summary & Conclusions

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation entitled “Genetic analysis of grain yield and physiological attributes in F_3 generation of blackgram [*Vigna mungo* (L.) Hepper.]” was carried out at dry land farm, S. V. Agricultural College, Tirupati. The experimental material consisted of four parents viz., LBG–787, TU-94–02, LBG–752, KU–1006 and three F_3 populations of the crosses, LBG-787 x LBG–752, TU-94-02 x LBG–752 and TU-94-02 x KU-1006. The experiment was laid out in a Compact Family Block Design with three replications during *kharif,* 2018. The objectives of the investigation were to study the variability, heritability, genetic advance as per cent of mean, character association for different yield related, physiological characters and their direct and indirect effects on seed yield per plant and scoring of transgressive segregants for yield and physiological attributes *viz.,* days to 50% flowering, days to maturity, plant height, 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, test weight, SLA (30 DAS), SLA (45 DAS), SLW (30 DAS), SLW (45 DAS), SCMR (30 DAS), SCMR (45 DAS), biomass per plant, harvest index and seed yield per plant.

The analysis of variance between families revealed that the mean sum of squares due to crosses were significant for all the 19 characters studied. The Bartlett’s test for homogeneity of error variances for three crosses indicated that the error variances were homogeneous for all the characters except for number of clusters per plant, number of pods per plant, test weight, SLA (30 DAS), SLA (45 DAS), SLW (30 DAS) and SLW (45 DAS). The analysis of variance among progenies within each family indicated that there is significant difference between progeny means for all the characters studied in LBG-787 x LBG–752, except for test weight in TU-94-02 x LBG–752 and SLW (45 DAS) in TU-94-02 x KU-1006.

In the cross LBG-787 x LBG–752, progeny 2 showed low mean performance for the characters namely days to 50% flowering and days to maturity which is desirable. Progeny 4 showed high mean performance for most of the characters like plant height, number of branches per plant, number of clusters per plant, number of pods per plant, test weight and seed yield per plant. Progeny 6 showed high mean performance for pod length and number of seeds per pod. Progeny 4 showed high mean performance for physiological characters like SCMR (30 DAS), SCMR (45 DAS), biomass per plant and harvest index which is desirable. Therefore advancing progeny 2 and progeny 4 of cross LBG-787 x LBG-752 to further generations will help us in developing short duration and high yielding genotypes respectively.

Progeny 20 showed high mean performance for many characters like plant height, number of branches per plant, number of pods per cluster, number of pods per plant and seed yield per plant in TU-94-02 x KU-1006. Mean performance of pod length and number of seeds per pod is highest in progeny 17. Progeny 20 showed low mean performance for characters like SLA (30 DAS) and SLA (45 DAS). High mean performance for characters like SLW (30 DAS), SLW (45 DAS), SCMR (30 DAS), SCMR (45 DAS), biomass per plant and harvest index was highest in progeny 20. Therefore, among all the progenies evaluated in cross TU-94-02 x KU-1006, advancing progeny 20 to further generations will help in getting promising genotypes.

In the cross TU-94-02 x LBG-752, progeny 24 showed low mean performance for days to 50% flowering and days to maturity and high mean performance for number of clusters per plant, pod length and number of seeds per pod. Progeny 23 showed high mean performance for most of the yield contributing characters like plant height, number of branches per plant, number of pods per cluster, number of pods per plant and seed yield per plant. Progeny 23 showed low mean performance for characters like SLA (30 DAS) and SLA (45 DAS) and high mean performance for characters like SLW (30 DAS), SLW (45 DAS), SCMR (30 DAS), biomass per plant and harvest index. Therefore, advancing progeny 24 to further generations will help us in getting short duration and high yielding genotypes. Whereas, advancing progeny 24 help us in getting genotypes which are superior for both yield and physiological characters.

Among all the crosses, F_3 progenies of TU-94-02 x KU-1006 exhibited superiority for plant height, number of branches per plant, number of pods per cluster, number of pods per plant, SLW (30 DAS), SLW (45 DAS), SCMR (30 DAS), SCMR (45 DAS) and harvest index, whereas F_3 progenies of TU-94-02 x LBG-752 registered superior mean performance for number of clusters per plant, pod length, number of seeds per pod, test weight, seed yield per plant and biomass per plant. Therefore, it is concluded that among the three crosses studied, TU-94-02 x KU-1006 and TU-94-02 x LBG-752 are more desirable as per yield and physiological traits.

The studies on genetic parameters in three crosses revealed that estimates of phenotypic and genotypic coefficient of variation, heritability and genetic advance as per cent of mean were high for plant height, number of clusters per plant, number of pods per cluster, number of pods per plant, SLA (30 DAS) and seed yield per plant in cross LBG-787 x LBG-752. Similarly, high estimates of genetic parameters were also recorded for plant height, number of clusters per plant, number of pods per plant, biomass per plant and seed yield per plant in cross TU-94-02 x KU-1006 and SLA (45 DAS) in cross TU-94-02 x LBG-752. This suggests that these traits had sufficient amount of variability, operating in additive gene fashion with least influence of environment. Direct selection for these traits in these crosses *viz.,* LBG-787 x LBG-752, TU-94-02 x LBG-752, TU-94-02 x KU-1006 would result in further improvement of seed yield along with improved physiological traits. High heritability and genetic advance as per cent of mean were observed for seed yield per plant in all the three crosses, LBG-787 x LBG–752, TU-94-02 x LBG–752, TU-94-02 x KU-1006. This indicates that seed yield per plant governed by additive gene action and simple selection can be used to improve seed yield.

In all the crosses, among yield contributing traits, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length and number of seeds per pod showed significant positive association with seed yield per plant. In case of physiological traits, only biomass per plant and harvest index per plant showed significant positive association with seed yield per plant in all the three crosses. Therefore, improvement in these traits would result in increased seed yield per plant in all the three crosses *i.e.,* LBG-787 x LBG-752, TU-94-02 x LBG–752, TU-94-02 x KU-1006 and helps us to develop high yielding genotypes.

Path analysis revealed that in the cross LBG-787 x LBG-752, in case of yield contributing characters, number of pods per cluster exerted the high positive direct effect on seed yield per plant followed by plant height and test weight, whereas in case of physiological attributes, harvest index and biomass showed significant positive direct effect on seed yield per plant. Among yield contributing characters, number of clusters per plant has high positive direct effect on seed yield per plant followed by plant height and number of pods per cluster in cross TU-94-02 x KU-1006. In case of physiological characters of this cross SCMR (45 DAS) showed high direct effects on seed yield per plant. On contrary, in cross, TU-94-02 x LBG-752, among the yield contributing characters, number of clusters per plant exerted high positive direct effect on seed yield per plant followed by number of seeds per pod. As far as the physiological characters of this cross, harvest index had high positive direct effect on seed yield per plant followed by SLA (45 DAS). Hence, these traits can be used as selection criterion for the development of high yielding genotypes in their respective crosses.

Transgressive individuals with values exceeding the better parent were observed for all the characters in the three crosses studied. More number of transgressive segregants were observed for plant height, number of clusters per plant, SLA (30 DAS), SLW (45 DAS), SCMR (30 DAS) and seed yield per plant in the cross LBG-787 x LBG-752. Similarly, in the cross TU-94-02 x KU-1006, the characters *viz.,* plant height, number of clusters per plant, number of seeds per pod, test weight, SLA (30 DAS), SLA (45 DAS), SLW (30 DAS) and seed yield per plant showed more number of transgressive segregants. In cross TU-94-02 x LBG-752 more number of transgressive segregants were observed for traits namely plant height, test weight, SLA (30 DAS), SLA (45 DAS), SLW (30 DAS), SLW (45 DAS) and seed yield per plant. A track on these transgressive segregants should be maintained and forwarded to further generation till they reach nearly homozygous condition. Most promising one can be identified for evaluation at different levels in varietal identification to develop the genotype which is better than both the parents.

Based on the estimates of genetic parameters, selection for characters viz., plant height, number of clusters per plant, number of pods per cluster, number of pods pet plant, SLA (30 DAS) and seed yield per plant in cross LBG-787 x LBG-752; plant height, number of clusters per plant, number of pods pet plant, biomass per plant and seed yield per plant in cross TU-94-02 x KU-1006; plant height, number of branches per plant, number of pods per cluster, SLA (45 DAS) and seed yield per plant in cross TU-94-02 x LBG-752 improves yield.

Association studies suggest that prime importance should be given in selection of superior genotypes in their respective crosses as they are having high positive association and direct effects towards the seed yield per plant.

Number of transgressive segregants for seed yield, yield contributing and physiological attributes was high in cross TU-94-02 x KU-1006. Therefore, this cross can be exploited for developing superior genotypes.

Among all the three crosses studied, cross TU-94-02 x KU-1006 showed high progeny mean performance along with high estimates of heritability coupled with high genetic advance as per cent of mean for mostly yield and physiological traits viz., plant height, number of branches per plant, number of pods per cluster, number of pods per plant, seed yield per plant, SLW (45 DAS), SCMR (30 DAS), SCMR (45 DAS) and harvest index. Hence, this cross can be utilized for breeding high yielding varieties with good physiological characters through selection in further generations.

In cross LBG-787 x LBG–752, advancing progeny 2 and progeny 4 to further generations will help in developing short duration and high yielding genotypes respectively. In cross TU-94-02 x KU-1006, advancing progeny 20 to further generation will help in getting high yielding genotypes with good physiological characters. Promoting progeny 24 to the further generations will help in getting short duration and high yielding genotypes whereas, promoting progeny 23 will result in getting lines which are superior for both yield and physiological characters in cross TU-94-02 x LBG-752.

FUTURE LINE OF WORK:

1. Progeny 2 and progeny 24 of crosses LBG-787 x LBG-752 and TU-94-02 x LBG-752 respectively can be advanced to further generations to develop early maturing varieties as they have low mean performance for days to flowering and days to maturity in their respective crosses.
2. Progeny 4 in cross LBG-787 x LBG-752, progeny 20 in cross TU-94-02 x KU-1006 and progeny 23 in cross TU-94-02 x LBG-752 respectively have high mean performance for seed yield per plant, harvest index and low SLA with high SCMR. Therefore, selecting these progenies and promoting them to future generations will help in developing physiologically superior and high yielding genotypes coupled with drought tolerance.

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