

**Heterosis and Combining Ability Analysis for Seed
Yield and its Component Traits in Black gram
(*Vigna mungo* (L.) Hepper)**



THESIS

Submitted to the

Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya,
Gwalior

In partial fulfilment of the requirement for the degree of

MASTER OF SCIENCE

In

**AGRICULTURE
(PLANT BREEDING & GENETICS)**

By

NAKUL YADUVANSHI

Department of Plant Breeding and Genetics
Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya
R.A.K. College of Agriculture, Sehore (M.P.)

2016

CERTIFICATE – I

This is to certify that the thesis entitled “**Heterosis and combining ability analysis for seed yield and its component traits in black gram (*Vigna mungo* (L.) Hepper)**” submitted in partial fulfilment of the requirement of the degree of Master of Science in Agriculture (**Plant Breeding & Genetics**) of the Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior is a record of the bonafide research work carried out by **Shri Nakul Yaduwanshi** under my guidance and supervision. The subject of the thesis has been approved by Students Advisory Committee and the Director of Instruction. No part of the thesis has been submitted for any degree or diploma (Certificate/award etc.) or has been published. All the assistance and help received during the course of investigations have been duly acknowledged by him.

Place : Sehore

Date :

(Dr. A.K. Saxena)

Chairman
Advisory Committee

Thesis approved by the students advisory committee

Chairman Dr. A.K. Saxena

Member Dr.A.N.Tikle

Member Dr. M.Yasin

CERTIFICATE – II

This is to certify that the thesis entitled “**Heterosis and combining ability analysis for seed yield and its component traits in black gram (*Vigna mungo* (L.) Hepper)**” submitted by **Shri Nakul Yaduwanshi** to the **Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior** in partial fulfilment of the requirements for the degree of **M.Sc. (Ag.)** in the **Department of Plant Breeding & Genetics, RAK College of Agriculture, Sehore**, has after evaluation, been approved by the external examiner and by the Students Advisory Committee after an oral examination of same.

Place : Sehore
Date :

(Dr. A.K. Saxena)

Chairman
Advisory Committee

Members of the students advisory committee

Chairman Dr. A.K. Saxena

Member Dr.A.N.Tikle

Member Dr. M.Yasin

Head of the Department :.....

Dean of the collage

Director Instruction

.ACKNOWLEDGEMENT

The author of this manuscript praises the omniscient and almighty god and his parents, who provided him this opportunity of submitting the present thesis for M. Sc (Ag.). Degree.

The word can never express indebtedness but I can take this opportunity to express my deepest and heartfelt sense of gratitude to reverend, Chairman of Advisory Committee, Dr. Ashok Saxena (Legume Breeder), Department of Plant Breeding & Genetics, R.A.K. College of Agriculture, Sehore for suggesting the problem, providing necessary facilities and for his healthy criticisms in preparing the present manuscript of this thesis to make this task as success. He has been a constant source of inspiration and his love and affection to me will ever be remembered.

I wish to render my sincere thanks to the member of the thesis Advisory Committee Dr. A. N. Tikle (Senior Scientist) and Dr. M. Yasin (Principal Scientist) Department of Plant Breeding & Genetics, R.A.K. College of Agriculture, Sehore for their kind help and constant advisement.

I express my deep feelings of regards to Dr. (Smt.) S.B. Tambi, Dean, R.A.K. College of Agriculture, Sehore and Dr. S. R. Ramgiry, Head of Department of Plant Breeding & Genetics for his unique help and fruitful direction for the success of this study.

I cannot avoid expressing my sincere thanks to Mr. A. K. Shrivastava, Mr. R. D. Coukse, Mr. S. Dube, for their valuable help during the course of investigation.

I appreciate and express my cordial thanks to my collegians and friends, Mr. Bhojraj, Nikhil Kumar, Jivendra Singh, Anuj Kumar, Sagar Parmar, Mansingh Baghel, Sourav Gupta, Ravindra Kachave and kamlesh Bhadhekar for their friendly co operation and encouragement.

Lastly, but not the least I pay my dutiful thanks from the core of my heart to Father Shri Kanhaiya Yadavanshi, Mother Smt. Ramkali Elder Brother Gurunath Yadavanshi, Arjun , Jagdish , Kaliram Younger Sister Lalita and Lali Yadavanshi other loving family members and relatives for their love, affection, blessing and constant inspiration to continue my study.

I express my sincere thanks to Satish Singh, Sagar Computers, Sehore for all time help and excellent computer type setting of this manuscript

Place: Sehore

Date:

(Nakul Yaduvanshi)

List of Contents

Number	Title	Page
1.	Introduction	1-2
2.	Review of Literature	3-10
3.	Materials and Methods	11-19
4.	Results	20-36
5.	Discussion	37-48
6.	Summary, Conclusion and Suggestions	49-52
7.	Bibliography	i-iii
	Appendix	I
	vita	

List of Tables

Number	Title	Page.
3.1	List of testers and lines	11
3.2	List of hybrids	11
4.1	Analysis of variance showing mean squares for 11 characters in black gram	21
4.2	Estimates of general combining and specific combining ability variances for the 11 characters in black gram	22
4.3	Estimates of general combining ability (gca) effects of the 4 female and 3 male parents for 11 characters in black gram	25
4.4	Estimates of specific combining ability (sca) effects for 11 characters in black gram	28
4.5	Estimates of heterosis over mid-parent for eleven characters in black gram	32
4.6	Estimates of various parameters of genetic variability for different traits in black gram	36
5.1	Relationship between the best parents, best hybrids (per se performance), high heterotic crosses, best general and specific combiners	47-48

CHAPTER-I

INTRODUCTION

Blackgram, (*Phaseolus mungo* Linn. / *Vigna mungo* (L.) Hepper) is also known as urdbean, mash, black maple etc. It is self pollinated crop with very low percentage of natural out crossing. An important short-duration pulse crop grown in many parts of India, Black gram [*Vigna mungo* L] belongs to family Leguminosae. This crop is grown in cropping systems as a mixed crop, catch crop, sequential crop besides growing as sole crop under residual moisture conditions after the harvest of rice and also before and after the harvest of other summer crops under semi-irrigated and dryland conditions. Its seeds are highly nutritious with protein (25-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins. Seeds are used in the preparation of many popular dishes. It is one of the most important components in the preparation of famous south Indian dishes, e.g. dosa, idli, vada etc. besides, it adds about 42 kg Nitrogen per hectare in soil.

Black gram has been distributed mainly in tropical to sub-tropical countries where it is grown mainly in summer season. It is grown in India, Pakistan, Sri-Lanka, Burma, and some countries of South East Asia. Also it being a drought resistant crop, it is suitable for dry land farming and predominantly used as an inter-crop with other crops.

In India, it is cultivated in an area of 30.1 lakh ha with a total production of 14 lakh tones. Madhya Pradesh covers 18.55% area of India , it is cultivated in an area of 4.72 lakh ha with an annual production of 1.66 lakh tons (FAOSTAT, 2012) .

The combining ability analysis helps in selection of parents based on their performance in hybrid combination. The analysis also provides information on nature and magnitude of gene action involved in the inheritance of the different characters. It thus decides the selection criteria to practice in segregating generation. Some information on combining ability effects and variance for seed yield and its component characters are available in literature.

The magnitude of heterosis help to the breeders in isolating the high heterotic crosses which can be used either as a hybrid for isolation of transgressive segregate through different breeding techniques. Very limited

information is available on heterosis for seed yield and its determining characters in blackgram. Based on these criteria, present study was undertaken with the following objectives

1. To estimate different genetic parameters.
2. To determine the extent of heterosis for seed yield and its component characters.
3. To estimate general and specific combining ability for major yield traits.

CHAPTER-II

REVIEW OF LITERATURE

The literature pertaining to various aspects of the present investigation entitled “Heterosis and combining ability analysis for seed yield and its component traits in black gram (*Vigna mungo* (L.) Hepper)” has been reviewed under the following heads:

3.1 Combining Ability

3.2 Heterosis

3.3 Genetic parameters

3.1 Combining ability:

The concept of combining ability was proposed by Sprague and Tatum (1942) in which total genetic variation was partitioned into of general and specific combining ability effects. They defined general combining ability as the average performance of a line in hybrid combination (recognized as a measure of additive gene action) and specific combining ability better would be expected on the average performance of the line involved the crosses regarded as an estimates of the effect of non-additive gene action.

General combining ability involves additive genetic variance and additive X additive interaction variance, which specific combining ability includes non-additive genetic portion arising from dominance and epistatic deviation. Several workers have reported the relative importance of general combining ability and specific combining ability in crop plant. The breeder of a self pollinated crop can utilize the segment of the total genetic variability which results from the action of the additive gene and additive X additive interaction. Griffing (1956) explored the possibility of the application of general and specific combining ability analysis by using four methods and low models.

Dhaliwal and Singh (1970) carried out combining ability analysis in all possible crosses excluding reciprocals between six pure lines and significant recorded general combining ability effects for number of pods and clusters per plant, whereas specific combining ability effects were not significant.

Singh and Dhaliwal (1970) carried out combining ability in diallel analysis quantitative traits and recorded significant general combining ability effects for several characters such as seed yield per plant, pods per plant.

Singh and Dhaliwal (1971) studied combining ability in a diallel set of 6 pure breeding lines and reported that general combining ability variance were much large than the specific combining ability variance in black gram.

Singh and Srivastava (1982) studied general and specific combining ability variances of yield and yield related traits in ninety F₁ *Vigna mungo* hybrids. They observed that the significant general combining ability effects for seed yield per plant.

Sharma and Ahmed (1997) studied genetics and combining ability of quantitative characters in black gram in a 5×5 diallel cross excluding reciprocals during *kharif*, 1994. Combining ability analysis revealed that seed yield and its major attributes in black gram were either equally controlled by additive and gene actions.

Neog and talukdar (1999) reported that the parent KU91 was the best general combiner not only for yield per plant but also for five other components viz., days to maturity, plant height, number of secondary branches per plant, cluster per plant and 100-seed weight. Besides this parent, Pant U19 exhibited its potentiality as a good general combiner for early flowering and maturity and reduced plant height. Amongst the crosses, Pant U19×KU92-1 alone exhibited a high positive sca effects for yield per plant.

Santha and Veluswamy (1999) derived the information on combining ability and genetic variance from data on 9 yield related traits (viz., plant height , days to 50% flowering, primary branches per plant, cluster number, pods per plant, pod length, 100-seed weight, seed weight per pod and seed yield) in the parents and F₁ hybrids of a 10 line × 4tester black gram cross at Killikulam. The results indicated a preponderance of non-additive gene action for all the characters studied. Good cross combinations involved at least one parent with high or moderate gca effects.

Chand (2000) reported that both additive and dominance genetic variances were involved in the expression of most of the characters. However, additive genetic variance was higher in magnitude than dominance genetic variance for branches per plant, clusters per plant, pods per plant, 100-seed

weight and grain yield per plant. The degree of dominance revealed overdominance for all the characters except days to maturity and pod length, where partial dominance was recorded. Biparental mating or diallel selective mating system could be the best breeding method for more tangible advancement in black gram.

Ghafoor *et al.* (2000) reported the presence of both additive and non-additive genetic effects for seed yield and its components in black gram. Non-additive genetic effects were predominant for all the characters except seed weight.

Chand (2001) conducted an investigation to estimate the components of genetic variance for yield and related characters using NCD-II. The additive genetic variance was higher than the dominance genetic variance for all the characters studied. Days to maturity, plant height, cluster per plant, pods per plant and grain yield were governed by both additive and non-additive gene action. Biparental intermating may be suggested for exploiting both types of genetic variance.

Dana and Dasgupta (2001) reported in diallel crosses of black gram that general (gca) and specific (sca) combining ability were highly significant for all the traits (plant height, primary branches per plant, pods per plant, seeds per plant, 100-seed weight and seed yield per plant). No parent showed significantly positive gca effects for all 6 characters. The sca effects of the crosses exhibited no specific trend in cross combinations between parents having high, medium or low gca effects. No cross combination showed significantly positive sca effects and high *per se* performance along with parents having good gca effects for all the 6 characters.

Goindraj and Subramanian (2001) reported on the basis of combining ability analysis that all the studied 10 characters were predominantly under the control of non-additive genes.

Indrani and Dasgupta (2001) studied in 21 F₁ and 7 parents of blackgram and reported the mean squares due to general and specific combining ability were highly significant for all the traits viz. plant height, primary branches per plant, pods per plant, seeds per plant, 100 seed weight and seed yield per plant.

Neog and Talukdar (2001) reported that additive and dominant genes were important for days to maturity, clusters per plant, pods per plant and plant height. The magnitude of additive component of genetic variance was higher than non-additive component for all the characters. It revealed the major role of additive genetic variance in the expression of these characters in blackgram.

Thomas and Sreekumar (2001) reported that the best general combiners for important biological N fixation traits were COBG 305 and Pant U 19 among lines and T 9 among testers. Pant U 19×T 9 was the best specific cross combination for the above traits. For number of pods and grain yield per plant, WBG 13 and T9 were the best general combiners and hybrids LBG 17×VBN 1 and WBG n13 ×AKU 4 were the best specific combinations.

Chand and Rao (2002) reported that the additive genetic variances were higher in magnitude than the dominance genetic variances for cluster number, pods per plant and grain yield. Both additive and dominance genetic variances were significant for days to flowering, maturity, plant height, and cluster, pods and grain yield per plant. The dominance ratio and average degree of dominance were >1.0 for all the characters except days to flowering, suggesting the presence of interallelic interactions governing the expression of these characters and the possibility of obtaining transgressive segregants.

Vaithiyalingan *et al.* (2002) reported that non-additive gene action was predominant for all characters studied.

Krishna *et al.* (2003) reported that all the characters were predominantly under the control of non-additive gene action.

Chakroborty (2004) estimated components of genetic variance in 6 x 6 diallel cross and resulted that the distribution of gene with positive and negative effects was symmetrical in the parents for all the traits except primary branches per plant clusters per plant end seed yield per plant in blackgram.

Thangavel *et al.* (2004) estimated combining ability in 6 x 6 diallel cross and reported the additive and non-additive gene actions were important in the expression of plant height and seed yield per plant in blackgram.

Singh (2005) conducted a genetic analysis in F1 generation and reported that the lines HPBU 124, HPBU 125, HPBU 130 and Mx 17 were good general combiners for most of the growth parameter. Tester PDU 1 revealed good

general combiners for majority of the physiological traits including seed yield per plant. While Palampur 93 also performed good for leaf area per plant, leaf growth rate, net assimilation rate and crop growth rate.

Selvam and Elangaimannan (2010) reported in blackgram [*Vigna mungo*] that the parent ADT 3 recorded relatively high per se performance for seed yield, hundred seed weight, number of clusters per plant, number of pods per cluster, number of pods per plant and number of branches per plant with early flowering and short stature. Among the hybrids, ADT 3/99V48, ADT 3/LBG 645 and 2KU 53/LBG 645 were found to have high mean performance for almost all the yield component characters besides seed yield. The gca effect of the genotypes ADT 3, LBG 645 and 2 KU 53 was high and significant for the traits seed yield per plant besides number of pods per cluster, number of pods per plant and number of seeds per pod.

Ram *et al.* (2013) studied that the diallel set of 10 parents and their 45 f1 and 45 f2 hybrids were analyzed to estimate the magnitude of heterosis and to understand the nature and magnitude of gene action under different environments for seed yield and its component characters of blackgram [*Vigna mungo* (L.) Hepper]. As the genotype x environment interaction was significant for all the traits, hence the combining ability was carried out for each environment separately. The combining ability analysis revealed that the GCA and SCA variances were significant for all the characters in each of the three environments indicating the importance of both additive and non-additive genetic control of all the characters under study.

3.2 Heterosis:

Natrajan and Rathanasamy (1999) estimated heterosis (over better parent) for 9 biometrical traits (days to maturity, plant height, branches, clusters, pods and seed yield per plant, pod length, seeds per pod and 100-seed weight) among 50 black gram hybrids generated from 15 parents (10 lines and 5 testers) during the *kharif* season of 1996. Maximum heterobeltiosis was recorded from branches per plant (74.70), followed by pods per plant (67.37). The highest and lowest heterobeltiosis was recorded from PDU 10×WBG 57 (74.70) and Co 5×WBG 27 (-41.49), respectively.

Neog and Talukdar (1999) reported that the crosses pant U19×KU9201 and KU91×Pant U30 and KU92-1×KU91 exhibited high heterosis for reduced plant height.

Santha and Veluswamy (1999) observed the highest estimates of heterosis for primary branches number, cluster number, pod number and seed yield among the nine characters studied.

Sharma (2000) reported that the hybrids exhibited maximum heterosis for seed yield per plant followed by seeds per pod and pod clusters per plant. Highest value of heterosis over better parent (92.8%) was recorded for seed yield per plant in hybrids TPU-4×NP-21.

Krishna *et al.* (2003) reported highest heterosis and heterobeltiosis of 185.74 and 153.94 per cent, respectively for seed yield per plant in hybrid K-4686×HPU-7. High heterosis for seed yield was manifested through components heterosis, i.e. pods per plant and cluster per plant.

Singh *et al.* (2003) observed significant heterosis for seed yield in 30 cross combinations over the best control (UG-218). Heterosis for yield was generally accompanied by heterosis for yield components. Of 48 cross combinations, 26 and 45 crosses revealed significantly negative heterosis over the best control for days to 50% flowering and maturity.

Saravanan *et al.*, (2004) studied heterosis in 6×6 diallel, including reciprocals and found high heterosis over mid parent and better parent seed yield per plant. crosses between high × high and high × low general combining ability parents exhibited greater heterosis in blackgram.

Vaithiyalingam (2004) reported a pronounced hybrid vigour for yield and most of the yield components. Heterosis to the extent of 139.66 and 116.39 per cent over mid-parent and better parent, respectively, was recorded for seed yield per plant indicated that selected parents for study were genetically diverse.

3.3 Genetic parameters

Sharma and Ahmed (1997) reported that pods per plant exhibited the highest estimates of heritability indicating predominance of additive gene action. High heritability coupled with low or moderate genetic advance for plant height, seed density and seed yield per plant suggested the importance of non-additive gene action in the inheritance of these characters.

Sajikumar *et al.* (1998) reported that number of pods per plant showed high estimates of both heritability and genetic advance indicating additive nature of gene action and reliability of this character in selection.

Kumar *et al.* (2000) reported highest estimates of heritability for plant height (99.7%), followed by grain yield per plant (97.5%), number of branches per plant (97.1%) and 1000-seed weight (97.1%). High genetic advance estimates were obtained for number of clusters per plant, number of branches per plant and plant height (56.03, 50.65 and 43.39%, respectively). High heritability with high genetic advance was recorded for plant height followed by grain yield per plant, number of branches per plant, number of clusters per plant and number of pods per cluster. Thus, priority should be given to these plant characters during selection programme for crop improvement.

Yadav and Dahiya (2000) noted high heritability estimates for test weight, days to maturity, seed yield, plant height and pods per plant.

Neog and Talukdar (2001) reported that narrow sense heritability was relatively high for days to maturity, initiation of flowering and pods per cluster, indicating prevalence of high additive genetic variance.

Yadav *et al.* (2001) recorded high estimates of heritability and genetic advance for seed yield per plant, biological yield per plant, pods per plant and plant height.

CHAPTER-III

MATERIALS AND METHODS

The present investigation was carried out by conducting the field experiments at Research Area of MULLaRP, R.A.K. College of Agriculture, Sehore *kharif* season 2013-14. Four lines and three testers were crossed adopting line × tester mating scheme. These resulting 12 F1 hybrids and their parents were grown in a randomized Block Design with two replications. The details pertaining to experimental materials and methods along with the details of testers, lines and hybrids are described below.

Table 3.1: List of testers and lines

S. No.	Details of tester/line
Testers	
1.	AKU-01-11
2.	AKU-96-3
3.	NUL-7
Lines	
1.	JU-2
2.	JU-8-6
3.	RBU-38
4.	TPU-4

Table 3.2 List of hybrids

S.No.	Hybrids	S.No.	Hybrids
1	JU-2×AKU-O1-11	7	RBU-38×AKU-O1-11
2	JU-2×AKU-96-3	8	RBU-38×AKU-96-3
3	JU-2×NUL-7	9	RBU-38×NUL-7
4	JU-8-6×AKU-01-11	10	TPU-4×AKU-O1-11
5	JU-8-6×AKU -96-3	11	TPU-4×AKU-96-3
6	JU-8-6×NUL-7	12	TPU-4×NUL-7

The experimental material (12 F₁s and 7 parents) was planted in a Randomized Block Design with two replications fulfilling all recommended agronomical requirements. Each entry was planted in a single row plot of 4.0 m length. The distance maintained between plant to plant and row to row was 10 cm and 30 cm, respectively.

Observation recorded:

In order to record the observations, three competitive plants were selected at random from each plot in each replication. The following eleven observations were recorded on each plant, except for days to 50% flowering, days to maturity and 100 seed weight for which data were recorded on plot basis.

(i) Days to 50% flowering:

The number of days from sowing date to 50% of flowering was recorded.

(ii) Days to maturity:

Days taken from sowing to physiological maturity were worked out.

(iii) Plant height (cm):

Length of main stem from the ground level to the tip of the main stem was measured in cm at maturity.

(iv) Number of pods per plant:

Number of pods of the three selected plants were counted and averaged.

(v) Number of primary branches per plant:

Number of primary branches was counted on main stem of the plant.

(vi) Number of secondary branches per plant:

Number of secondary branches emerged from primary branches were recorded at maturity.

(vii) Pod length (cm):

Length of five randomly selected pods from each selected three plants/plot was measured and averaged.

(viii) 100 seed weight (g):

100 seed were taken from each plot randomly and weight was recorded in grams.

(ix) Biological yield per plant (g):

The biological yield per plant was calculated on the basis of following formula:

$$\text{Biological yield (g/plant)} = [\text{dry weight (g/3 plants)} - \text{seed weight (g/3plants)}]/3$$

(x) Harvest index:

Harvest index (%) was calculated by the formula:

$$\text{Harvest index} = \frac{\text{Economical yield}}{\text{Biological yield}} \times 100$$

(xi) Seed yield per plant (g):

Seed weight was measured in gm per plant and calculated on the basis of pooled weight of five plants.

Statistical analysis:

1. Analysis of variance:

The mean of each character were analyzed following the procedure given by Panse and Sukhatme (1967) for randomized block design.

2. Combining ability analysis:

When the data were found significant for a given character in randomized block design, it was subjected to combining ability analysis according to the procedure given by Kempthorne (1957).

The format for the analysis of variance along with the expectation of mean squares is given in the following table:

Format for line × tester analysis

Source	d.f.	M.S.	Expected mean square
Replications	r-1		
Genotypes	(fm+f+m)-1		
Parents	F+m-1		
F ₁ 's	fm-1		
Parents vs. F ₁ 's	1		
Lines	f-1	M1	$\sigma_e^2 + r(\text{Cov F.S.} - 2\text{Cov H.S.}) + rm(\text{Cov H.S.})$
Testers	m-1	M2	$\sigma_e^2 + r(\text{Cov F.S.} - 2\text{Cov H.S.}) + rf(\text{Cov H.S.})$
Line × Tester	(f-1)(m-1)	M3	$\sigma_e^2 + r(\text{Cov F.S.} - 2\text{Cov H.S.})$

Error	(r-1)(fm+f+m-1)	M4	σ_e^2
-------	-----------------	----	--------------

where,

r = number of replications

f = lines

m = testers

Cov H.S. = Covariance of Half-sibs

Cov F.S. = Covariance of Full-sibs

Significance of various sum of squares were tested by means of F test as given below.

Mean squares for line $\times$ tester was first tested against error mean square.

Thus,

$$F = \frac{M3}{M4}$$

If the mean sum of squares for line $\times$ tester was found non-significant, the sum of squares for error and line $\times$ tester were pooled accompanied by pooling of corresponding degree of freedom.

The new mean square was then used as denominator to test the significance of lines and testers. If the mean sum of squares for line $\times$ tester

was significant, it was employed as denominator for F test of lines and testers. Thus,

$$F \text{ test for lines} = \frac{M1}{M3}$$

$$F \text{ test for testers} = \frac{M2}{M3}$$

3. Estimation of covariance and variance components:

When the mean squares of the lines and testers were found significant, estimates of covariance of half-sibs were calculated as:

$$\text{Cov. (H.S.) lines} = \frac{M1 - M3}{rm}$$

$$\text{Cov. (H.S.) testers} = \frac{M2 - M3}{rf}$$

However, when the mean squares for both lines and testers were significant, average estimate of Cov. (H.S.) was calculated following King *et al.* (1961)

$$\text{Cov. (H.S.) average} = \frac{M1 + M2 - 2M3}{r(f + m)}$$

Covariance of full-sibs was calculated as:

$$\text{Cov. (F.S.)} = \frac{M1 + M2 - 3M4 + ry(6 - m - f)}{3r}$$

where,

y = average covariance half-sibs

The σ_{gca}^2 , σ_{sca}^2 , σ_A^2 and σ_D^2 were calculated as

$$\sigma_{gca}^2 = \text{Cov. H.S.}$$

$$\sigma_{sca}^2 = \text{Cov. F.S.} - 2 \text{ Cov. H.S.}$$

$$\sigma_A^2 = 4 (\sigma_{gca}^2)$$

$$\sigma_D^2 = 4 (\sigma_{sca}^2)$$

4. Estimation of general (gi and gj) and specific (sij) combining ability effects:

The general combining ability for i^{th} line or j^{th} tester and specific combining ability effects (for ij^{th} cross) were computed as shown below:

gca effects:

$$\text{gi (lines)} = \frac{y_{i.}}{rm} - \frac{y_{...}}{rfm}, \quad i = 1, 2, 3, 4$$

$$\text{gj (testers)} = \frac{y_{.j}}{rf} - \frac{y_{...}}{rfm}, \quad j = 1, 2, 3, \dots, 12$$

sca effects:

$$\text{sij} = \frac{y_{ij}}{r} - \frac{y_{i.}}{rf} - \frac{y_{.j}}{rm} + \frac{y_{...}}{rfm}$$

where,

$y_{..}$ = total of all hybrids

$y_{i.}$ = total of i^{th} female parent over all males and replications

$y_{.j}$ = total of j^{th} male parent over all females and replications

y_{ij} = $(ij)^{\text{th}}$ combination total over all replications

5. Standard errors for general and specific combining ability effects:

Standard errors required to test the significance of gca effects and sca effects were calculated as:

$$\text{S.E. (gi)} = \sqrt{\frac{M4}{rm}}$$

$$\text{S.E. (gj)} = \sqrt{\frac{M4}{rf}}$$

The significance of g_i and g_j was tested by means of 't' test using the following formula.

$$t \text{ (for } g_i) = \frac{g_i - 0}{S.E.(g_i)}$$

$$t \text{ (for } g_j) = \frac{g_j - 0}{S.E.(g_j)}$$

The values of the ratio so obtained were referred to 't' table at error degrees of freedom.

The significance of difference between gca effects of two lines (or testers) was tested against the standard error for difference as:

$$S.E. (g_i - g_j) \text{ for tester} = \sqrt{\frac{2M4}{r_f}}$$

$$S.E. (g_i - g_j) \text{ for line} = \sqrt{\frac{2M4}{r_m}}$$

The standard error for specific combining ability is calculated as below:

$$S.E. (s_{ij}) = \sqrt{\frac{M4}{r}}$$

Significance of difference between sca effects of two crosses was tested against the standard error which was computed as:

$$S.E. (s_{ij} - s_{ki}) = \sqrt{\frac{M4}{r}}$$

6. Estimation of phenotypic and genotypic coefficients of variation:

The phenotypic and genotypic coefficients of variation in per cent were computed by the following formulae given by Burton (1952).

$$\text{Phenotypic Coefficient of Variation (PCV)} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{Genotypic Coefficient of Variation (GCV)} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

The coefficient of variation were categorized as proposed by Sivasubramanian and Madhava Menon (1973)

Percent of variability	Category
<10	Low
10-20	Moderate
>20	High

7. Estimation of heritability and genetic advance:

Heritability in broad sense was estimated as the ratio of genotypic to the phenotypic variance and was expressed in percentage. Heritability in per cent in broad sense was estimated by the following formula given by Singh and Choudhary (1977):

$$\text{Heritability (h}^2\text{)} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

The range of heritability was categorized as suggested by Robinson *et al.* (1949)

Low	-	<30
Moderate	-	30-60
High	-	>60

The estimates of expected genetic advance from selection, G(s), was obtained by the formula suggested by Robinson *et al.* (1949).

$$G(s) = k \times h^2 \times \sigma_p$$

where,

k = Selection differential in standard deviation units which is 2.06 for 5% selection intensity,

h^2 = Heritability in broad sense, and

σ_p = Phenotypic standard deviation

Genetic advance was expressed as percentage of mean by using the formula suggested by Johnson *et al.* (1955).

$$\text{Genetic advance as percentage of mean} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

The following classification was utilized in the study.

GA Percent value	Category
<10	Low
10-20	Moderate
>20	High

8. Heterosis:

This has been expressed as percentage increase or decrease in the mean value of the F₁ hybrid over its mid parental value.

$$\text{Thus } H_1 = \frac{F_1 - \text{M.P.}}{\text{M.P.}} \times 100$$

Where

F₁ = mean of the F₁ hybrid

M.P. = mean of the two parents of that particular cross.

Significance of heterosis was tested by t test.

$$t = \frac{F_1 - M.P.}{S.E.(H_1)}$$

Where S.E. (H_1) is the standard error of heterosis and is given by

$$S.E. (H_1) = \sqrt{S_i^2 (1/2 + 1/4)}$$

S_i^2 = error mean square obtained from the general analysis of variance of parents and F_1 's

The calculated 't' value was compared with table value of 't' at respective error d.f. for 5 per cent and 1 per cent levels of significance.

CHAPTER-IV

RESULTS

The investigation was carried out to identify superior parental lines in terms of their combining ability as well as superior cross combinations and also to study the heterosis in 12 crosses for 11 quantitative characters of black gram. The results obtained from the study are presented under the following headings.

4.1 Analysis of variance

Mean squares for genotypes were highly significant for all the attributes (except pod length) being investigated (Table 4.1). There were significant differences among the parental lines for all the characters except characters like days to 50% flowering, pod length and 100 seed weight. This gave the inference that there was no genetic diversity for the above mentioned attributes. The crosses showed significant to highly significant differences for all the characters except days to 50% flowering and pod length. Significance of mean squares for parent vs crosses is taken to be an indication of existence of heterosis. Mean squares for parent vs crosses comparison were highly significant for number of pods per plant, 100 seed weight, biological yield per plant, harvest index and seed yield per plant and significant for days to 50% flowering and number of secondary branches per plant. Mean squares due to females and males were significant for number of pods per plant and days to 50% flowering, respectively. Mean squares due to female $\times$ male were highly significant for all the characters studied except, three characters, viz., days to 50% flowering, pod length and 100 seed weight which suggested that male performed consistently over different females for these later attributes, For rest of the characters male lines exhibited differential behaviour over the females.

Estimated values of general combining and specific combining ability variances for the 11 characters in black gram (Table 4.2) showed that the sca variance was higher than the gca variance *i.e.*, variance ratio was less than unity for most of the characters, indicating predominance of dominance variance. Dominance variance was more than additive variance for all the characters studied.

Table 4.1. Analysis of variance showing mean squares for 11 characters in black gram

Source	d.f.	Mean sum of squares										
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of pods /plant	Number of primary branches/ plant	Number of secondary branches /plant	Pod length (cm)	100 seed weight (g)	Biological yield /plant	Harvest index (%)	Seed yield/ plant (g)
Replications	1	3.789*	1.297	1.492	9.344	0.124	0.059	1.34**	0.013	17.047	5.002	1.924**
Treatments	18	12.222**	7.632**	8.631**	2036.6**	0.993**	0.13**	0.0749	0.423**	463.76**	60.75**	18.18**
Parents	6	1.571	6.118**	85.892**	183.2**	1.227**	0.018**	0.0803	0.517	139.22**	528.52**	0.729**
Crosses	11	0.773	8.859**	94.377**	2506.7**	0.94**	0.194**	0.076	0.232*	625.51**	66.595**	16.12**
Parents Vs Crosses	1	4.072*	3.211	0.077	7986.3**	0.164	0.095*	0.032	1.953**	631.79**	43.828**	145.5**
Females (lines)	3	0.167	9.04	103.22	6723.2*	1.575	0.276	0.099	0.405	1225.1	32.677	19.02
Males (testers)	2	3.50**	11.289	36.608	843.71	0.825	0.301	0.106	0.146	268.38	57.745	3.422
Female × Male	6	0.167	7.959**	109.21**	952.77**	0.662**	0.117**	0.054	0.175	444.73**	86.504**	18.91**
Error	18	0.5673	0.789	1.344	13.277	0.1123	0.019	0.059	0.07	6.613	2.171	0.192

*, **: Significant at 5% and 1%, respectively

Table 4.2. Estimates of general combining and specific combining ability variances for the 11 characters in black gram

Source	Characters										
	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of pods /plant	Number of primary branches/ plant	Number of secondary branches /plant	Pod length (cm)	100 seed weight (g)	Biological yield /plant	Harvest index (%)	Seed yield/ plant (g)
σ_{gca}^2	0.24	0.31	-5.61	404.38	0.077	0.024	0.007	0.014	43.15	-5.90	-1.09
σ_{sca}^2	-0.18	3.52	54.17	467.45	0.31	0.05	0.00	0.06	220.91	42.25	9.31
$\frac{\sigma_{gca}^2}{\sigma_{sca}^2}$	-1.33	0.09	-0.10	0.87	0.25	0.48	-	0.23	0.20	-0.14	-0.12

4.2 Combining ability effects

Parental strains for hybridization may be selected or chosen on the basis of their combining ability effects rather than their *per se* performance. Hence general combining ability effects of females as well as males were estimated and presented in Table 4.3.

4.2.1 Days to 50 per cent flowering

Strains with negative general combining ability were preferred because early genotypes are generally desirable in crop like black gram. Male parent NUL-7 (-0.75) showed significant negative gca effect. Among the female parents, none of the parents depicted significant negative gca effects.

4.2.2 Days to maturity

Among the four female parents, the gca effects were significant for two female lines. Among these, TPU-4 had positive and RBU-38 had negative gca effects. Two testers exhibited significant gca effects for days to maturity. The tester AKU-01-11 had negative while the tester AKU-96-3 had positive gca effects.

4.2.3 Plant height

The female parent JU-2 (-3.80) showed highest significant negative gca effect followed by JU-8-6 (-2.10). However, the one other line TPU-4 showed significant positive gca effects. Among the male parents, AKU-01-11 (-2.47) recorded significantly high negative gca effect for this trait. While, NUL-7 and AKU-96-3 were exactly in the opposite end with gca effect of 1.32 and 1.14, respectively.

4.2.4 Number of pods per plant

Significant gca effect in positive direction among the testers was observed for AKU-96-3 (11.75) whereas significant gca effects in negative direction was observed for AKU-01-11 (-7.27) and NUL-7 (-4.48). Similarly, among the female parents TPU-4 (48.98) recorded significant positive gca effect for the trait while JU-8-6 (-25.45), JU-2 (-16.12) and RBU-38 (-7.41) showed significant gca effects in negative direction.

4.2.5 Number of primary branches per plant

Significant gca effect in positive direction among the testers was observed for AKU-96-3 (0.27) whereas significant gca effects in negative direction was observed for NUL-7 (-0.35). Similarly, among the female parents

JU-2 (0.60) recorded significant positive gca effect for the trait while RBU-38 (-0.64) showed significant gca effects in negative direction.

4.2.6 Number of secondary branches per plant

The female parent RBU-38 (0.31) showed significant positive gca effect. However, the line TPU-4 (-0.17) showed significant negative gca effects. As compared to this, among the male parents AKU-96-3 (0.19) recorded significantly positive gca effect for this trait. While, AKU-01-11 was exactly in the opposite end with gca effect of -0.20.

4.2.7 Pod length

None of the female as well as male parents showed significant gca effects.

4.2.8 100 seed weight

Among the female lines TPU-4 (0.37) showed highly significant positive gca effect for 100 seed weight. Among male parents, none of them exhibited significant gca effects.

4.2.9 Biological yield per plant

Female parent TPU-4 (21.36) showed highly significant positive gca effect. However, the other female parents JU-2, JU-8-6 and RBU-38 showed significant gca effects in negative direction. Among the male parents AKU-96-3 (3.95) followed by NUL-7 (2.70) exhibited significantly high positive gca effects. Compared to this, AKU-01-11 (-6.65) showed significant gca effect in the negative direction.

4.2.10 Harvest index

Significant gca effects in the positive direction was recorded by RBU-38 (2.08) among the female parents, while JU-8-6 (-3.35) showed significant negative gca effects. Among the male parents, AKU-96-3 (2.32) showed significant positive gca effects for the trait. Whereas, the male parent NUL-7 (-2.94) recorded significant but negative gca effects.

4.2.11 Seed yield per plant

Male parent AKU-96-3 (0.71) showed highly significant positive gca effect. However, the other male parent AKU-01-11 (-0.58) showed significant gca effect in negative direction. Among the female parents TPU-4 (2.57) exhibited significantly high positive gca effects. Compared to this, JU-2 (-1.36) followed by JU-8-6 (-1.01) showed significant gca effects in the negative direction.

Table 4.3. Estimates of general combining ability (gca) effects of the 4 female and 3 male parents for 11 characters in black gram

Parents	Characters										
	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of pods /plant	Number of primary branches/ plant	Number of secondary branches /plant	Pod length (cm)	100 seed weight (g)	Biological yield /plant	Harvest index (%)	Seed yield/ plant (g)
Female parents											
JU-2	-0.08	-0.71	-3.80**	-16.12**	0.60**	-0.11	-0.08	-0.13	-8.54**	0.60	-1.36**
JU-8-6	0.25	-0.21	-2.10**	-25.45**	-0.03	-0.02	-0.10	-0.03	-7.25**	-3.35**	-1.01**
RBU-38	-0.08	-0.88*	0.18	-7.41**	-0.64**	0.31**	0.18	-0.21	-5.56**	2.08**	-0.21
TPU-4	-0.08	1.79**	5.72**	48.98**	0.12	-0.17*	0.01	0.37**	21.36**	0.68	2.57**
S.E. (g_i) female	0.31	0.36	0.47	1.49	0.14	0.06	0.10	0.11	1.05	0.60	0.18
Male parents											
AKU-01-11	0.50	-1.17**	-2.47**	-7.27**	0.08	-0.20**	-0.13	-0.13	-6.65**	0.63	-0.58**
AKU-96-3	0.25	1.21**	1.14*	11.75**	0.27*	0.19**	0.05	0.17	3.95**	2.32**	0.71**
NUL-7	-0.75*	-0.04	1.32**	-4.48**	-0.35**	0.01	0.08	0.00	2.70**	-2.94**	-0.13
S.E. (g_i) male	0.27	0.31	0.41	1.29	0.12	0.05	0.09	0.09	0.91	0.52	0.15

*, **: Significant at 5% and 1%, respectively

4.3 Specific combining ability effects

Estimates of sca effects on 12 hybrid combinations for eleven quantitative traits are presented in Table 4.4.

4.3.1 Days to 50 per cent flowering

None of the crosses exhibited significant sca effects for this trait.

4.3.2 Days to maturity

Two hybrids showed significant positive sca effects (undesirable direction). But two hybrids namely JU-2×AKU-O1-11 and RBU-38×AKU-96-3 recorded significant negative sca effects.

4.3.3 Plant height

Of the 12 crosses, the sca effects were significant for 7 crosses. Of these, 3 crosses had positive and 4 had negative sca effects. The hybrid JU-8-6×AKU-01-11 (12.03) registered the maximum positive sca effect followed by RBU-38×AKU-96-3 (5.35) and TPU-4×NUL-7 (4.25). While, the cross RBU-38×AKU-O1-11 (-6.10) documented the highest negative sca effect followed by JU-8-6×NUL-7 (-6.02), JU-8-6×AKU -96-3 (-6.01) and TPU-4×AKU-O1-11 (-4.84).

4.3.4 Number of pods per plant

Significant sca effects for number of pods per plant were exhibited by 9 hybrids. Out of these, 5 had positive and 4 had negative sca effects. The hybrid JU-8-6×AKU-01-11 (26.00) followed by RBU-38×NUL-7 (22.25) expressed the highest positive sca effect, while cross JU-8-6×AKU -96-3 (-23.03) recorded highest significant negative sca effect.

4.3.5 Number of primary branches per plant

About one third of the crosses (4) were exhibited significant sca effects for number of primary branches per plant. Of these, 2 crosses had positive and 2 crosses had negative sca effects. The hybrid RBU-38×NUL-7 (0.57) registered the maximum positive sca effect followed by JU-8-6×NUL-7 (0.52). While, the cross JU-2×NUL-7 (-0.57) documented the highest negative sca effect followed by TPU-4×NUL-7 (-0.52).

4.3.6 Number of secondary branches per plant

Only one hybrid out of 12 had desirable significant positive sca effects for number of secondary branches per plant. The hybrid JU-8-6×AKU -96-3 (0.26) displayed highest significant positive sca effect, whereas, hybrid JU-8-6×NUL-7 (-0.36) recorded the significant negative sca effects.

4.3.7 Pod length

None of the crosses exhibited significant sca effects for this trait.

4.3.8 100 seed weight

None of the crosses exhibited significant sca effects for this trait.

4.3.9 Biological yield per plant

Significantly higher sca effects in the positive direction were recorded in 6 hybrids. TPU-4×AKU-96-3 (21.50), JU-8-6×AKU-01-11 (7.58), JU-8-6×NUL-7 (6.03) and JU-2×NUL-7 (5.84) were the top four hybrids, which have displayed highest sca effects for biological yield per plant. While, 5 hybrid combinations were recorded significant sca effect in negative direction for biological yield per plant.

4.3.10 Harvest index

Eight crosses exhibited significant sca effects. Among these, 4 crosses had positive and 4 had negative sca effects. The hybrid JU-2×AKU-96-3 (7.23) recorded the highest positive sca effect followed by TPU-4×NUL-7, JU-8-6×AKU -96-3 and RBU-38×AKU-01-11 recording 6.68, 4.71 and 3.86 sca effects, respectively. Whereas, the cross TPU-4×AKU-96-3 (-6.52) depicted highest negative sca effect followed by JU-2×NUL-7 (6.24) and RBU-38×AKU-96-3 (-5.42).

4.3.11 Seed yield per plant

Out of 12 crosses, the sca effects were significant for 10 crosses. Among these, 5 crosses had positive and also 5 crosses had negative of sca effects. The hybrid JU-2×AKU-96-3 (4.09) expressed highest positive sca effects followed by JU-8-6×NUL-7 (2.08), JU-8-6×AKU-01-11 (1.65), TPU-4×AKU-96-3 (1.56) and RBU-38×NUL-7 (1.31), whereas, the cross JU-8-6×AKU -96-3 (-3.74) depicted highest negative sca effects followed by JU-2×NUL-7 (-2.81) and RBU-38×AKU-96-3 (-1.91).

Table 4.4. Estimates of specific combining ability (sca) effects for 11 characters in black gram

Crosses	Characters										
	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of pods /plant	Number of primary branches/ plant	Number of secondary branches /plant	Pod length (cm)	100 seed weight (g)	Biological yield /plant	Harvest index (%)	Seed yield/ plant (g)
JU-2×AKU-O1-11	-0.17	-3.17**	-1.09	5.63*	0.45	-0.02	-0.16	-0.06	5.43**	-0.98	-1.28**
JU-2×AKU-96-3	0.08	2.46**	0.06	9.90**	0.13	-0.15	-0.05	-0.12	-11.27**	7.23**	4.09**
JU-2×NUL-7	0.08	0.71	1.03	-15.52**	-0.57*	0.17	0.20	0.19	5.84**	-6.24**	-2.81**
JU-8-6×AKU-01-11	0.50	0.83	12.03**	26.00**	-0.12	0.10	0.08	0.37	7.58**	-2.72*	1.65**
JU-8-6×AKU -96-3	-0.25	-0.04	-6.01**	-23.03**	-0.41	0.26*	0.00	-0.14	-13.61**	4.71**	-3.74**
JU-8-6×NUL-7	-0.25	-0.79	-6.02**	-2.97	0.52*	-0.36**	-0.08	-0.23	6.03**	-1.99	2.08**
RBU-38×AKU-O1-11	-0.17	1.00	-6.10**	-20.98**	-0.38	-0.18	-0.10	-0.33	-8.17**	3.86**	0.60
RBU-38×AKU-96-3	0.08	-1.38*	5.35**	-1.27	-0.19	0.03	0.15	0.37	3.38	-5.42**	-1.91**
RBU-38×NUL-7	0.08	0.38	0.75	22.25**	0.57*	0.15	-0.05	-0.04	4.78*	1.56	1.31**
TPU-4×AKU-O1-11	-0.17	1.33*	-4.84**	-10.65**	0.05	0.10	0.17	0.02	-4.85*	-0.16	-0.98**
TPU-4×AKU-96-3	0.08	-1.04	0.60	14.41**	0.47	-0.14	-0.11	-0.10	21.50**	-6.52**	1.56**
TPU-4×NUL-7	0.08	-0.29	4.25**	-3.76	-0.52*	0.04	-0.07	0.08	-16.66**	6.68**	-0.58
	0.53	0.63	0.82	2.58	0.24	0.10	0.17	0.19	1.82	1.04	0.31

*, **: Significant at 5% and 1%, respectively

4.4 Heterosis:

The magnitude of heterosis expressed as percentage increase or decrease over mid-parent (economic heterosis) was studied for seed yield per plant and ten yield attributes viz., days to 50% flowering, days to maturity, plant height, number of pods per plant, number of primary branches per plant, number of secondary branches per plant, pod length, 100 seed weight, biological yield per plant and harvest index. The estimates are presented in Table 4.5.

4.4.1 Days to 50% flowering

When compared to the mid-parent, only one hybrid was earlier in days to 50% flowering than their respective mid-parent, but the negative heterosis was not significant. When compared to the mid parent, a range from -0.61 to 4.29 per cent was found for days to 50% flowering and the maximum negative value was for the cross, JU-2×NUL-7, while the maximum positive value was for the cross, JU-8-6×AKU-01-11.

4.4.2 Days to maturity

The F1 hybrids were earlier than the mid-parents in half of the crosses but the heterosis was significant in 4 crosses. The range of heterosis varied from -7.83 to 1.84 per cent. The crosses JU-2×AKU-O1-11 exhibited highest negative and significant heterosis (-7.83%) followed by RBU-38×AKU-O1-11, RBU-38×AKU-96-3 (-2.42%, each) and JU-8-6×AKU-01-11 (-2.11%).

4.4.3 Plant height

Five crosses exhibited significant negative heterosis over mid-parents. The range of heterosis varied from -42.96 to 56.77 per cent, the highest negative and positive values were noted in crosses, RBU-38×AKU-O1-11 and TPU-4×NUL-7, respectively. The cross RBU-38×AKU-O1-11 exhibited the highest and significant negative heterosis (-42.96) followed by JU-2×AKU-O1-11 (-30.06), JU-8-6×AKU -96-3 (-12.25%), JU-2×AKU-96-3 (-11.58%) and TPU-4×AKU-O1-11 (-9.07%). However, the crosses viz., TPU-4×NUL-7, JU-8-6×AKU-01-11 and TPU-4×AKU-96-3 showed significant positive value of heterosis.

4.4.4 Number of pods per plant

Most of the F1 hybrids were produced more number of pods per plant than mid-parent but the heterosis was significant in 7 crosses. The cross TPU-4×AKU-96-3 (280.78%) followed by TPU-4×NUL-7 (150.24%), JU-2×AKU-96-3 (114.48%), RBU-38×AKU-96-3 (114.47%), TPU-4×AKU-O1-11 (104.47%), RBU-38×NUL-7 (98.80%) and JU-8-6×AKU-O1-11 (51.24%) showed maximum heterosis over mid-parent in positive direction. Only one cross, RBU-38×AKU-O1-11 exhibited significant negative heterosis over their respective parents.

4.4.5 Number of primary branches per plant

Out of 12, only 4 hybrids showed significant values of heterosis. The crosses, TPU-4×AKU-96-3, TPU-4×NUL-7 and JU-2×AKU-96-3 exhibited positive and significant value of heterosis while significant and negative value of heterosis was exhibited by RBU-38×AKU-O1-11. The cross TPU-4×AKU-96-3 showed maximum positive heterosis over mid-parent.

4.4.6 Number of secondary branches per plant

When compared to the mid-parent, 7 out of 12 crosses exhibited positive heterosis. The range of heterosis varied from -12.62 (JU-8-6×NUL-7) to 24.75 (RBU-38×AKU-96-3) per cent. The F1 was found to be significantly superior in 3 crosses exhibiting positive heterosis. The cross RBU-38×AKU-96-3 exhibited the highest positive and significant heterosis over mid parent followed by JU-8-6×AKU -96-3 (24.49%) and RBU-38×NUL-7 (16.98%).

4.4.7 Pod length

None of the crosses exhibited significant heterosis over their respective mid parents. However, its varied from -11.08% (JU-2×AKU-O1-11) to 9.74% (RBU-38×AKU-96-3).

4.4.8 100 seed weight

The F1 hybrids, in general, were superior to their corresponding mid-parent values in respect of all of the cross combinations, except some few crosses like JU-2×AKU-O1-11 and RBU-38×AKU-O1-11 which showed negative heterosis. Six crosses exhibited positive and significant values of heterosis, when compared to the mid-parent. The heterosis ranged from -13.47 to 53.61 per cent. The highest and significantly positive value of heterosis was shown by TPU-4×AKU-96-3 followed by JU-8-6×AKU -96-3, RBU-38×AKU-96-3, JU-8-

6×AKU-01-11, TPU-4×NUL-7 and TPU-4×AKU-O1-11 the values being 53.61, 52.93, 39.65, 38.93, 31.73 and 26.50 per cent, respectively.

4.4.9 Biological yield per plant

The crosses, JU-2×NUL-7, JU-8-6×NUL-7, RBU-38×AKU-96-3, RBU-38×NUL-7, TPU-4×AKU-O1-11, TPU-4×AKU-96-3 and TPU-4×NUL-7 showed significant heterosis in positive direction when compared to the respective mid-parent. The cross JU-2×AKU-O1-11 and RBU-38×AKU-O1-11 exhibited negative and significant value of heterosis over mid-parent. The range of heterosis varied from –59.49 to 321.57 per cent over mid-parents. The highest value of heterosis was shown by the cross TPU-4×AKU-96-3.

4.4.10 Harvest index

Six out of 12 crosses exhibited positive heterosis when compared to the mid-parent. The range of heterosis varied from -38.60% (JU-8-6×NUL-7) to 109.03% (RBU-38×AKU-O1-11). The F1 was found to be significantly superior in 6 crosses exhibiting positive heterosis. The cross RBU-38×AKU-O1-11 exhibited the highest positive and significant heterosis over mid parent followed by TPU-4×AKU-O1-11 (48.52%), JU-2×AKU-O1-11 (47.89%), TPU-4×NUL-7 (41.80%), JU-2×AKU-96-3 (38.39%) and RBU-38×NUL-7 (30.59%).

4.4.11 Seed yield per plant

When compared to the respective mid-parent, most of the crosses, except JU-2×AKU-O1-11, JU-2×NUL-7 and JU-8-6×AKU -96-3, showed significant heterosis in positive direction. The cross JU-2×NUL-7 exhibited negative and non significant value of heterosis over mid-parent. The range of heterosis varied from –6.86 to 240.31 per cent over mid-parents. The highest value of heterosis was shown by the cross TPU-4×AKU-96-3 followed by JU-2×AKU-96-3 (227.57%), JU-8-6×NUL-7 (142.16%), RBU-38×NUL-7 (134.36%), TPU-4×NUL-7 (134.35%), JU-8-6×AKU-O1-11 (103.43%), TPU-4×AKU-O1-11 (101.35%), RBU-38×AKU-96-3 (93.48%) and RBU-38×AKU-O1-11 (90.65%).

Table 4.5. Estimates of heterosis over mid-parent for eleven characters in black gram

Cross	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of pods /plant	Number of primary branches/ plant	Number of secondary branches /plant	Pod length (cm)	100 seed weight (g)	Biological yield /plant	Harvest index (%)	Seed yield/ plant (g)
JU-2×AKU-O1-11	0.61	-7.83**	-30.06**	13.32	4.53	-7.07	-11.08	-8.19	-25.51**	47.89**	13.33
JU-2×AKU-96-3	0.00	1.81	-11.58**	114.48**	16.22*	4.08	0.00	12.75	-4.20	38.39**	227.57**
JU-2×NUL-7	-0.61	0.62	4.05	-15.44	-12.44	4.85	6.22	3.19	39.41**	-33.53**	-6.86
JU-8-6×AKU-O1-11	4.29*	-2.11**	46.52**	51.24**	-3.99	1.01	-1.97	38.93**	-10.82	-7.68	103.43**
JU-8-6×AKU -96-3	1.22	-0.30	-12.25*	12.63	10.92	24.49**	5.05	52.93**	-2.17	-0.49	20.37
JU-8-6×NUL-7	0.62	-0.31	2.11	3.64	34.90**	-12.62*	2.43	17.48	54.82**	-38.60**	142.16**
RBU-38×AKU-O1-11	2.47	-2.42*	-42.96**	-22.06**	-28.06**	0.00	-4.94	-13.47	-59.49**	109.03**	90.65**
RBU-38×AKU-96-3	1.84	-2.42*	4.25	114.47**	-0.70	24.75**	9.74	39.65**	81.35**	-10.40	93.48**
RBU-38×NUL-7	1.25	0.62	0.19	98.80**	15.35	16.98**	4.19	0.44	42.15**	30.59**	134.36**
TPU-4×AKU-O1-11	3.75*	0.00	-9.07*	104.47**	-1.29	-5.05	3.27	26.50**	33.63**	48.52**	101.35**
TPU-4×AKU-96-3	3.11	0.00	25.43**	280.78**	35.25**	2.04	4.76	53.61**	321.57**	-27.56**	240.31**
TPU-4×NUL-7	2.53	1.84	56.77**	150.24**	-7.91	-2.91	5.52	31.73**	67.24**	41.80**	134.35**
S.E. (Het.)	0.65	0.77	1.00	3.16	0.29	0.12	0.21	0.23	2.23	1.28	0.38

*, **: Significant at 5% and 1%, respectively

4.5. Variability parameters:

Variability was measured by estimation of coefficient of variation (genotypic and phenotypic), heritability, genetic advance and genetic gain. Environment plays an important role in the expression of phenotype and genotype facts, which are inferred, from phenotypic observations. Hence, variability can be observed through biometric parameters like genotypic coefficient of variation, heritability (broad sense) and genetic advance. This would be of great help to breeder in evolving a selection programme for gene. The estimates of coefficient of variation, heritability and genetic advance for all the eleven characters studied (Table 4.6) explained here as under:

4.5.1. Phenotypic and genotypic coefficients of variation

In general estimates of PCV were higher than their corresponding GCV however good correspondence was observed between GCV and PCV for all characters (Table 4.6). A wide range of phenotypic coefficient of variation (PCV) was observed for traits ranging from 2.31% for days to 50% flowering to 52.36% for number of pods per plant. Higher magnitude of phenotypic coefficient of variation was recorded for number of pods per plant (52.36%), biological yield per plant (49.94%), seed yield per plant (47.08%), harvest index (30.23%), number of primary branches per plant (22.39%) and plant height (24.23%). Moderate estimates of PCV were observed for 100 seed weight (16.95%) followed by number of secondary branches per plant (10.56%) while low estimate of phenotypic coefficient of variation was observed for days to 50% flowering, days to maturity and pod length the values being 2.31, 2.51 and 6.68 per cent, respectively.

Genotypic coefficient of variation (GCV) ranged from 1.40% to 52.05%. Higher magnitude of genotypic coefficient of variation was recorded for number of pods per plant (52.02%), biological yield per plant (49.24%), seed yield per plant (46.58%), harvest index (29.17%) and plant height (23.86%). Moderate estimates of genotypic coefficient of variation were recorded for number of primary branches per plant (19.98%) followed by number of 100 seed weight (14.34%) while low estimates of genotypic coefficient of variation was observed in days to 50% flowering (1.40%) followed by days to maturity (2.26%), pod length (2.28%) and number of secondary branches per plant (9.09%).

Relatively low magnitudinal differences were observed between genotypic coefficient of variation and phenotypic coefficient of variation for days

to maturity, number of pods per plant, plant height, seed yield per plant, biological yield per plant, days to 50% flowering and harvest index indicates less environmental influence in the expression of these attributes. Relatively high differences between genotypic coefficient of variation and phenotypic coefficient of variation were observed for pod length, 100 seed weight, number of primary branches per plant and number of secondary branches per plant. These findings suggested that greater influence of the environment in the expression of these traits.

4.5.2. Heritability (broad sense) and genetic advance:

Heritability is a measure of the extent of phenotypic variation caused by the action of genes. For making effective improvement in the character for which selection is practiced, heritability has been adopted by large number of workers as a reliable indicator. The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability. According to Lush (1949) heritability in broad sense is the ratio of total genotypic variance to phenotypic variance, expressed in percentage. The estimates of heritability are more advantageous when expressed in terms of genetic advance. Johnson *et al.* (1955) suggested that heritability and genetic advance when calculated together would prove more useful in predicting the resultant effect of selection on phenotypic expression, without genetic advance the estimates of heritability will not be of practical value and emphasized the concurrent use of genetic advance along with heritability. High heritability alone is not enough to make sufficient improvement though selection in genetic advance generation.

The estimates of heritability and genetic advance for all the characters are presented in Table 4.6. The estimates of heritability (broad sense) for most of the characters under study were high. Highest estimate of heritability was observed for number of pods per plant (98.7%) followed by seed yield per plant (97.9%), biological yield per plant (97.2%), plant height (96.9%), harvest index (93.1%), days to maturity (81.3%), number of primary branches per plant (79.7%), number of secondary branches per plant (74.2%) and 100 seed weight (71.6%). The moderate heritability was observed for days to 50% flowering (36.6%) while low for pod length (11.7%).

The genetic advance as per cent of mean for all the characters have been studied based on the classification by Johnson *et al.* (1955) and the estimated values are given in Table 4.6.

The characters which recorded high (>20 percent) genetic advance as per cent of mean were number of pods per plant (106.47%) followed by biological yield per plant (99.98%), seed yield per plant (94.91%), harvest index (58.00%), plant height (48.39%), number of primary branches per plant (36.74%) and 100 seed weight (24.92%).

The character that recorded moderate (10 to 20 percent) level of genetic advance as per cent of mean was number of secondary branches per plant (16.24%) while low estimates of genetic advance as per cent of mean were recorded by followed by pod length (1.55%), days to 50% flowering (1.73%) and days to maturity (4.20%).

High heritability with high genetic advance as per cent of mean was observed for number of pods per plant, biological yield per plant, seed yield per plant, harvest index, plant height, number of primary branches per plant and 100 seed weight. High heritability with moderate genetic advance as per cent of mean was observed for number of secondary branches per plant.

Table 4.6: Estimates of various parameters of genetic variability for different traits in black gram

S. No	Characters	PCV (%)	GCV (%)	Heritability (Broad sense) (%)	Genetic advance	Genetic advance as % of mean
1	Days to 50% flowering	2.31	1.40	36.6	0.71	1.73
2	Days to maturity	2.51	2.26	81.3	3.43	4.20
3	Plant height (cm)	24.23	23.86	96.9	13.22	48.39
4	Number of pods /plant	52.36	52.02	98.7	65.10	106.47
5	Number of primary branches/plant	22.39	19.98	79.7	1.22	36.74
6	Number of secondary branches /plant	10.56	9.09	74.2	0.42	16.24
7	Pod length (cm)	6.68	2.28	11.7	0.06	1.55
8	100 seed weight (g)	16.95	14.34	71.6	0.73	24.92
9	Biological yield /plant	49.94	49.24	97.2	30.70	99.98
10	Harvest index (%)	30.23	29.17	93.1	10.76	58.00
11	Seed yield/ plant (g)	47.08	46.58	97.9	6.11	94.91

CHAPTER-V

DISCUSSION

The choice of the suitable parents for evolving better varieties is a matter of constant concern to the plant breeder. Some idea of the usefulness of the parents could be obtained from their direct performance, particularly for components of the yield. However, the nature of gene action may vary with the genetic structure and divergence between populations involved in hybridization. Consequently, a high yielding line may not necessarily be able to transmit its superiority in cross combinations and vice-versa. It is, therefore, necessary to assess the genetic potential of the parents by estimating their combining ability before they are used in a hybridization programme. The hybrids and their parents in the present study were evaluated by Line $\times$ Tester analysis (Kempthorne, 1957). The method is effective in determining the relative efficiency of male and female parents in hybrids. It also enables one to predict the performance of parents and relative magnitude and direction of GCA and SCA effects. The results from this experiment are discussed under the following headings.

5.1.1 Analysis of variance

5.1.2 *Per se* performance with respect to seed yield and its related traits

5.1.3 General combining ability effects

5.1.4 Specific combining ability effects

5.1.5 Heterosis

5.1.6 Heritability and genetic advance

5.1.1 Analysis of variance

Variation among the parental lines is a basic prerequisite for developing the experimental material for estimation of genetic parameters using any mating design. With the major objective being study of inheritance of productivity and its related traits, ensuring variability for these traits is essential. In the present studies significant mean square for parents indicated that there was considerable genetic diversity among the parental lines for the

characters days to maturity, plant height, number of pods per plant, number of primary branches per plant, number of secondary branches per plant, biological yield per plant, harvest index and seed yield per plant. Mean Squares for F_1 s were highly significant for most of the traits except days to maturity and pod length suggesting significant genetic differences among the crosses for these traits. This is in agreement with the expectations because parental lines had already revealed significant genetic differences for most of these traits. Present studies revealed that there were significant differences among the mean of parents as a group versus F_1 s as a group for days to 50% flowering, number of pods per plant, number of secondary branches per plant, 100 seed weight, biological yield per plant, harvest index and seed yield per plant. This strongly pointed to the existence of heterosis for these traits.

Mean squares for Line $\times$ tester interactions were highly significant for characters like days to maturity, plant height, number of pods per plant, number of primary branches per plant, number of secondary branches per plant, biological yield per plant, harvest index and seed yield per plant. It, therefore, suggested differential behaviour of male lines over different female lines and vice-versa. These mean squares also enable the measurement of non-additive genetic components. Since these mean squares were significant for the above mentioned characters, non-additive variance was responsible for part of the variation observed for these traits. Role of non-additive variance in the expression of quantitative characters was reported by Santha and Veluswamy (1999), Ghafoor *et al.* (2000), Goindraj and Subramanian (2001), Vaithiyalingam *et al.* (2002) and Krishna *et al.* (2003).

Sca variance was higher than gca for all the studied traits except days to 50% flowering indicating preponderance of non-additive gene action in the expression of these traits. Similar results were reported by Santa and Veluswamy (1999), Govindraj and Subramanian (2001), Vaithiyalingam *et al.* (2002) and Krishna *et al.* (2003). The results clearly reflected that heterosis breeding would be rewarding for the commercial exploitation of yield in the present set of material.

5.1.2 *Per se* performance

The *per se* performance was considered as an important criterion for evaluation. The results (Appendix I) indicated that tester AKU-01-11 recorded the superior value for seed yield per plant along with highest number of pods per plant, number of primary branches per plant, pod length, number of secondary branches per plant, 100 seed weight and biological yield per plant and required less time for 50% flowering. Furthermore, tester AKU-96-3 for harvest index; and NUL-7 for days to 50% flowering, days to maturity, plant height, number of secondary branches per plant, pod length, 100 seed weight and also for seed yield per plant were recorded desirable mean.

Among the lines TPU-4 recorded highest *per se* performance for number of pods per plant, number of secondary branches per plant, pod length, biological yield per plant, harvest index and seed yield per plant and required less times for days to 50% flowering. The line JU-2 for days to maturity, number of pods per plant, number of primary branches per plant, number of secondary branches per plant, pod length, 100 seed weight, biological yield per plant and seed yield per plant; JU-8-6 for days to 50% flowering, days to maturity, plant height, number of secondary branches per plant and harvest index; and RBU-38 for x1n days to maturity, number of primary branches per plant, number of secondary branches per plant, pod length, 100 seed weight and biological yield per plant recorded desirable mean.

Among the hybrids TPU-4×AKU-96-3 recorded the superior value for seed yield per plant along with higher number of pods per plant, biological yield per plant, number of primary branches per plant, pod length and 100 seed weight and require lesser time for days to 50% flowering. Hybrids RBU-38×AKU-96-3 recorded higher number of secondary branches per plant, pod length and 100 seed weight while hybrid JU-2×AKU-01-11 recorded desirable values for days to maturity, plant height and number of primary branches per plant.. Hybrid TPU-4×NUL-7 was recorded highest value for 100 seed weight and lowest desirable value for days to 50% flowering while JU-2×AKU-96-3 recorded highest value for harvest index.

5.1.3 General combining ability effects

The second criterion for selection is by considering general combining ability effects (gca) of the parents. Since the parents with high mean values may not necessarily be able to transmit their superior traits into their progenies, it become necessary to access their compatibility to express their own high performance to the hybrids involving them.

The parents with significant negative gca effects for days to 50% flowering, days to maturity and plant height are desirable. Therefore, the parents with significant negative gca estimates for days to 50% flowering, days to maturity and plant height and with significant positive gca effects for the remaining characters are considered as good general combiners. The parents with positive and non-significant or negative significant and non-significant gca effects for number of pods per plant, number of primary branches per plant, number of secondary branches per plant, pod length, 100 seed weight, biological yield per plant, harvest index and seed yield per plant are rated as poor general combiners.

The estimates of gca effects revealed that the one line TPU-4 recorded positive and significant gca for seed yield per plant. In addition, TPU-4 also recorded desirable gca for number of pods per plant, 100 seed weight and biological yield per plant.

On the basis of gca effects of testers, the good general combiners were AKU-96-3 for seed yield per plant, number of pods per plant, number of primary branches per plant, number of secondary branches per plant, biological yield per plant and harvest index; AKU-01-11 for days to maturity and plant height; and NUL-7 for days to 50% flowering and biological yield per plant. The high gca is due to additive and additive $\times$ additive gene effects (Griffing, 1956) which are the fixable components of genetic variation. Therefore, it would be worthwhile to use above lines and testers in hybridization programme.

Tester AKU-96-3 possessed desirable gca and superior *per se* performance for harvest index while tester NUL-7 possessed desirable gca and superior *per se* performance for days to 50% flowering. Similarly the line

TPU-4 exhibited desirable gca effects and superior *per se* performance for number of pods per plant, biological yield per plant and seed yield per plant. Line RBU-38 exhibited significant positive gca effects and superior *per se* performance for days to maturity and number of secondary branches per plant. Similarly, line JU-2 possessed desirable gca and superior *per se* performance for number of primary branches per plant while line JU-8-6 exhibited significant positive gca effects and superior *per se* performance for plant height. But there was, in general, no correspondence between *per se* performance and combining availability effects.

5.1.4 Specific combining ability effects:

The estimates of sca effects revealed that, out of 12, 5 cross combinations exhibited significant and positive sca effects for seed yield per plant. The cross with highest sca effects for seed yield per plant was JU-2×AKU-96-3. This cross has also showed significant sca effects in the desirable direction for number of pods per plant and harvest index. The another important cross was JU-8-6×NUL-7 where the sca effects were significant in desirable direction for plant height, number of primary branches per plant and biological yield per plant. The cross JU-8-6×AKU-01-11 exhibited significant sca effects for seed yield per plant, number of pods per plant and biological yield per plant; TPU-4×AKU-96-3 number of pods per plant and biological yield per plant; and RBU-38×NUL-7 for seed yield per plant, number of pods per plant, number of primary branches per plant and biological yield per plant.

Out of 12, 2 crosses for days to maturity; 4 crosses for plant height; 5 crosses for number of pods per plant; 3 crosses for number of primary branches per plant; 1 cross for number of secondary branches per plant; 6 crosses for biological yield per plant; and 4 crosses for harvest index exhibited significant sca effects in desirable direction.

Study of the relationship of sca effects and *per se* performance of crosses revealed that there was close agreement between sca effects and *per se* performance of few cross combinations for example 1 cross for days to maturity, number of pods per plant, biological yield per plant, harvest index

and seed yield per plant; and 2 crosses for plant height but there was no agreement between the sca effects and the *per se* performance of crosses for days to 50% flowering.

Study of the relationships of sca effects of crosses and gca effects of parents revealed that most of the good specific combinations for various characters involved parents with low×low or high × low/ low ×high or high x high gca effects. For example out of all 5 crosses, which recorded significant sca effects for seed yield per plant, 2 crosses viz., JU-8-6×AKU-01-11 and JU-8-6×NUL-7 resulted from low × low general combiners, 2 crosses viz., JU-2×AKU-96-3 and RBU-38×NUL-7 resulted from high × low/low × high and one cross, TPU-4×AKU-96-3 resulted from high x high general combiners. High sca effects of low × high gca combinations might be due to complementary non-additive interallelic interactions and hence could be used in heterosis breeding. Similarly, an appreciable portion of heterosis expressed by low gca × low gca crosses might be ascribed to dominance × dominance type of non allelic gene action- registering over dominance and were non-fixable. Thus, it is clear that the superior performance of these hybrids was largely due to epistatic interaction. To harness this type of gene action in these cross combinations, selection has to be postponed to later generations for realization of superior segregants. In these crosses a suitable population improvement programme such as intermating of F₂ segregants followed by recurrent selection would be appropriate to exploit the non-additive gene action.

5.1.5 Heterosis

Result from this study showed that heterosis occurred for most of the characters studied. However, the degree of heterosis varied considerably depending upon the character.

Desirable significant heterosis over mid parent occurred in four crosses viz., JU-2×AKU-01-11, JU-8-6×AKU-01-11, RBU-38×AKU-01-11 and RBU-38×AKU-96-3 for days to maturity. Heterosis was also observed for days to 50% flowering in positive direction, but significant desirable negative heterosis over mid-parent did not occur for a single cross.

Five crosses showed significant negative heterosis over mid-parent for plant height. For number of pods per plant, significant positive heterosis over mid-parent was expressed in JU-2×AKU-96-3, JU-8-6×AKU-01-11, RBU-38×AKU-96-3, RBU-38×NUL-7, TPU-4×AKU-01-11, TPU-4×AKU-96-3 and TPU-4×NUL-7, while for number of primary branches per plant, significant positive heterosis over mid-parent was in 3 crosses viz., JU-2×AKU-96-3, JU-8-6×NUL-7 and TPU-4×AKU-96-3. Significant positive heterosis over mid parent was also observed in JU-8-6×AKU -96-3, RBU-38×AKU-96-3 and RBU-38×NUL-7 for number of secondary branches per plant.

Heterosis effects were evident in most of the crosses for 100 seed weight and harvest index. For both the characters the positive heterosis was observed in 6 crosses. Crosses, JU-8-6×AKU-01-11, JU-8-6×AKU -96-3, RBU-38×AKU-96-3, TPU-4×AKU-01-11, TPU-4×AKU-96-3 and TPU-4×NUL-7 for 100 seed weight and the crosses, JU-2×AKU-01-11, JU-2×AKU-96-3, RBU-38×AKU-01-11, RBU-38×NUL-7 TPU-4×AKU-01-11 and TPU-4×NUL-7 for harvest index showed significant positive heterosis over mid parent. Similarly, seven crosses viz., JU-2×NUL-7, JU-8-6×NUL-7, RBU-38×AKU-96-3, RBU-38×NUL-7, TPU-4×AKU-01-11, TPU-4×AKU-96-3 and TPU-4×NUL-7 exhibited positive and significant heterosis over mid parent for biological yield per plant. None of the crosses exhibited significant positive heterosis for pod length.

The value of heterosis over mid-parent ranged from –0.61 to 4.29 per cent for days to 50% flowering, from –7.83 to 1.84 per cent for days to maturity, from –46.96 to 56.77 per cent for plant height, from –22.06 to 280.78 per cent for number of pods per plant, from –28.06 to 35.25 per cent for number of primary branches per plant, from -11.08 to 9.74 per cent for pod length, from -13.47 to 53.61 per cent for 100 seed weight, and from –59.49 to 32.51 per cent for biological yield per plant and from –38.60 to 109.03 per cent for harvest index.. Sharma (2000), Krishna *et al.* (2003), Singh *et al.* (2003), Saravanan *et al.*,(2004) and Vaithiyalingam (2004) observed heterosis for number of seed yield.

In the present material, 9 crosses exhibited significant positive heterosis for seed yield per plant. The range of heterosis was from -6.86 to

240.31 per cent. The highest heterosis was observed for the cross TPU-4×AKU-96-3 followed by JU-2×AKU-96-3, JU-8-6×NUL-7, TPU-4×NUL-7, RBU-38×NUL-7, JU-8-6×AKU-01-11, TPU-4×AKU-01-11, RBU-38×AKU-96-3 and RBU-38×AKU-01-11. Heterosis for seed yield in black gram has been reported by Santa and Veluswamy (1999), Sharma (2000), Krishna *et al.* (2003), Singh *et al.* (2003) and Vaithiyalingam (2004).

Hybrid, TPU-4×AKU-96-3 recorded highest heterosis for seed yield also expressed heterosis for number of pods per plant, number of primary branches per plant, 100 seed weight and biological yield per plant in desirable direction. Similarly, JU-2×AKU-96-3 exhibited desirable heterosis for plant height, number of pods per plant, number of primary branches per plant and harvest index. The cross JU-8-6×NUL-7 also expressed desirable heterosis for number of primary branches per plant and biological yield per plant while TPU-4×NUL-7 exhibited desirable heterosis for number of pods per plant, 100 seed weight, biological yield per plant and harvest index. The cross RBU-38×NUL-7 expressed desirable heterosis for number of pods per plant, number of secondary branches per plant, biological yield per plant and harvest index while JU-8-6×AKU-01-11 exhibited desirable heterosis for days to maturity, number of pods per plant and 100 seed weight. The cross TPU-4×AKU-01-11 expressed desirable heterosis for plant height, number of pods per plant, 100 seed weight, biological yield per plant and harvest index while RBU-38×AKU-96-3 exhibited desirable heterosis for days to maturity, number of pods per plant, number of secondary branches per plant, 100 seed weight and biological yield per plant. Hybrid RBU-38×AKU-01-11 exhibited desirable heterosis for days to maturity, plant height and harvest index. Thus, the results of the present investigation clearly showed that heterosis was manifested in intervarietal crosses of black gram for most of the characters studied. Maximum extent of desirable heterosis, over all the crosses, was observed for seed yield per plant (240.31%), which was followed by biological yield per plant (321.57%), number of pods per plant (280.78%), harvest index (109.03%), 100 seed weight (53.61%), plant height (-46.96%), number of primary branches per plant (35.25%), number of secondary branches per plant (24.75%), pod length (9.74%), days to maturity (-7.83%) and days to

50% flowering (-0.61%). Thus, it is obvious that increase in seed yield in F_1 hybrids is the result of increase in value of yield components.

The overall relationship of *per se* performance of parents with gca, *per se* performance of hybrids with sca and heterosis (over mid-parent) with sca effects (Table 5.1) revealed that the parents with high *per se* performance for most of the characters also exhibited high gca effects indicating *per se* performance was a good indicator of its general combining ability. In most of the cases, the hybrid exhibiting high *per se* performance also recorded high sca effects similarly the cross combinations which are showing high sca effects also showed heterotic performance implying the role of specific combining ability effects in hybrids vigour or heterotic performance.

5.1.6 Genetic parameters

The study pertaining to generic parameters showed that phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters revealing the significant effect of environment. Substantial values of genotypic coefficient of variation were in line with phenotypic coefficient of variation. The high phenotypic coefficient of variation was observed for number of pods per plant, biological yield per plant, seed yield per plant, harvest index, number of primary branches per plant and plant height which suggested that selection may be effective for these traits.

The magnitude of genotypic coefficient of variation suggested that number of pods per plant, biological yield per plant, seed yield per plant, harvest index and plant height which showed high heritability coupled with high genetic advance as per cent of mean had better chance for improvement. Besides this, all these characters also had narrow differences between the values of PCV and GCV showing least influence of environment.

Heritability provides the information about the degree of inheritance of a particular character. Broad sense heritability, which is the proportion of genotypic variance to the phenotypic variance, is a useful estimate since selections have to make on the phenotypic values of the characters, which are the results of breeding values and their interplay with environmental

values. Traits with high heritability and high desirable correlation would yield correlated response and thus ease the task of the plant breeder.

Since heritability estimates are influenced by environmental, genetic material and also other factors hence their utility will be restricted. Thus, heritability in conjunction with genetic advance as per cent of mean would give a more reliable index of selection value (Johnson *et al.*, 1995).

The high heritability together with high genetic advance as per cent of mean was observed for plant height, number of pods per plant, number of primary branches per plant, 100 seed weight, biological yield per plant, harvest index and seed yield per plant which pointed to the fact that phenotypic variability for these traits was largely determined by genetic cause hence simple selection could lead to substantial improvement in these characters. These results were in accordance with the reports of Kumar *et al.* (2000) and Yadav *et al.* (2001) for plant height; Sajikumar *et al.* (1998) and Yadav *et al.* (2001) for number of pods per plant; Kumar *et al.* (2000) for number of primary branches per plant and 100 seed weight; Yadav *et al.* (2001) for biological yield per plant; and of Kumar *et al.* (2000) and Yadav *et al.* (2001) for seed yield per plant.

High heritability with moderate genetic advance was recorded for number of secondary branches per plant indicating that these characters were less influenced by environment but governed by both additive and non-additive gene action.

From the foregone discussion, it can be concluded that plant height, number of pods per plant, biological yield per plant, harvest index and seed yield per plant recorded high PCV and GCV, high heritability and genetic advance as per cent of mean indicating prevalence of additive gene action in the control of these characters and simple selection may be effective to improve these characters.

Table 5.1. Relationship between the best parents, best hybrids (*per se* performance), high heterotic crosses, best general and specific combiners

Characters	Best parent (<i>per se</i>)	Best hybrids (<i>per se</i>)	Best heterotic crosses	Best general combiners	Best specific combiners
Days to 50% flowering	TPU-4	JU-2×NUL-7	-	NUL-7	-
	RBU-38	JU-8-6×NUL-7			
	NUL-7	RBU-38×NUL-7			
	AKU-01-11	TPU- 4×NUL-7			
Days to maturity	RBU-38	JU-2×AKU-O1-11	JU-2×AKU-O1-11	RBU-38	JU-2×AKU-O1-11
	JU-8-6		JU-8-6×AKU-01-11	AKU-01-11	RBU-38×AKU-96-3
	NUL-7		RBU-38×AKU-O1-11		
			RBU-38×AKU-96-3		
Plant height	JU-8-6	RBU-38×AKU-O1-11	JU-2×AKU-O1-11	JU-2	RBU-38×AKU-O1-11
	NUL-7	JU-2×AKU-O1-11	JU-2×AKU-96-3	JU-8-6	JU-8-6×NUL-7
			JU-8-6×AKU -96-3	AKU-01-11	JU-8-6×AKU -96-3
			RBU-38×AKU-O1-11		TPU-4×AKU-O1-11
			TPU-4×AKU-O1-11		
Number of pods /plant	TPU-4	TPU-4×AKU-96-3	JU-2×AKU-96-3	TPU-4	JU-8-6×AKU-01-11
	AKU-01-11		JU-8-6×AKU-01-11	AKU-96-3	RBU-38×NUL-7
			RBU-38×AKU-96-3		TPU-4×AKU-96-3
			RBU-38×NUL-7		JU-2×AKU-96-3
			TPU-4×AKU-O1-11		JU-2×AKU-O1-11
			TPU-4×AKU-96-3		
			TPU-4×NUL-7		
Number of primary branches/plant	JU-2	JU-2×AKU-O1-11	JU-2×AKU-96-3	JU-2	RBU-38×NUL-7
	AKU-01-11	JU-2×AKU-96-3	JU-8-6×NUL-7	AKU-96-3	JU-8-6×NUL-7
		TPU-4×AKU-96-3	TPU-4×AKU-96-3		
Number of secondary branches /plant	RBU-38	RBU-38×AKU-96-3	JU-8-6×AKU -96-3	RBU-38	JU-8-6×AKU -96-3
	TPU-4	RBU-38×NUL-7	RBU-38×AKU-96-3	AKU-96-3	

	NUL-7	JU-8-6×AKU -96-3	RBU-38×NUL-7		
Pod length (cm)	RBU-38	RBU-38×AKU-96-3	-	-	-
	AKU-01-11	RBU-38×NUL-7			
		JU-2×NUL-7			
100 seed weight (g)	JU-2	TPU-4×NUL-7	JU-8-6×AKU-01-11	TPU-4	-
	RBU-38	TPU-4×AKU-96-3	JU-8-6×AKU -96-3		
	NUL-7	RBU-38×AKU-96-3	RBU-38×AKU-96-3		
			TPU-4×AKU-O1-11		
			TPU-4×AKU-96-3		
			TPU-4×NUL-7		
Biological yield /plant	RBU-38	TPU-4×AKU-96-3	JU-2×NUL-7	TPU-4	TPU-4×AKU-96-3
	TPU-4		JU-8-6×NUL-7	AKU-96-3	JU-8-6×AKU-01-11
	AKU-01-11		RBU-38×AKU-96-3	NUL-7	JU-8-6×NUL-7
			RBU-38×NUL-7		JU-2×NUL-7
			TPU-4×AKU-O1-11		JU-2×AKU-O1-11
			TPU-4×AKU-96-3		RBU-38×NUL-7
			TPU-4×NUL-7		
Harvest index (%)	JU-8-6	JU-2×AKU-96-3	JU-2×AKU-O1-11	RBU-38	JU-2×AKU-96-3
	TPU-4		JU-2×AKU-96-3	AKU-96-3	TPU-4×NUL-7
	AKU-96-3		RBU-38×AKU-O1-11		JU-8-6×AKU -96-3
			RBU-38×NUL-7		RBU-38×AKU-O1-11
			TPU-4×AKU-O1-11		
			TPU-4×NUL-7		
Seed yield/ plant (g)	TPU-4	TPU-4×AKU-96-3	JU-2×AKU-96-3	TPU-4	JU-2×AKU-96-3
	JU-2		JU-8-6×AKU-01-11	AKU-96-3	JU-8-6×NUL-7
	AKU-01-11		JU-8-6×NUL-7		JU-8-6×AKU-01-11
	NUL-7		RBU-38×AKU-O1-11		TPU-4×AKU-96-3
			RBU-38×AKU-96-3		RBU-38×NUL-7
			RBU-38×NUL-7		

			TPU-4×AKU-O1-11		
			TPU-4×AKU-96-3		
			TPU-4×NUL-7		

CHAPTER-VI

SUMMARY, CONCLUSION AND SUGGESTIONS

Four lines and three testers were crossed adopting line × tester mating scheme. These resulting 12 F1 hybrids and their parents were grown in a randomized Block Design with two replications at Research Area of MULLaRP, R.A.K. College of Agriculture, Sehore during Kharif season 2013-14. Observations were recorded on three randomly chosen competitive plants. The eleven quantitative characters studied were days to 50% flowering, days to maturity, plant height, number of pods per plant, number of primary branches per plant, number of secondary branches per plant, pod length, 100 seed weight, biological yield per plant, harvest index and seed yield per plant. The data were analyzed according to the method given by Kempthorne (1957). Results obtained are summarized as under:

- The analysis of variance revealed significant differences among the parents for most of the characters except days to 50% flowering, pod length and 100 seed weight. Female parent showed significant variation for number of pods per plant while male parents exhibited significant variation for days to 50% flowering. The female × male interaction was significant for all the characters except days to 50% flowering, pod length and 100 seed weight. The results indicated significance of non-additive genetic variance for the characters.
- In the present investigation non-additive genetic variance played a predominant role for most of the characters like days to maturity, plant height, number of pods per plant, number of primary branches per plant, number of secondary branches per plant, pod length, 100 seed weight, biological yield per plant, harvest index and seed yield per plant as sca variance was higher than gca variance for these characters. Therefore, superior hybrids can be developed by exploitation of heterosis.
- The estimates of combining ability effects indicated that the tester AKU-96-3 and line TPU-4 were good general combiners for seed yield

per plant. In addition to this AKU-96-3 was a good general combiner for number of pods per plant, number of primary branches per plant, number of secondary branches per plant, biological yield per plant and harvest index, while TPU-4 was a good combiner for number of pods per plant, 100 seed weight and biological yield per plant.

- The estimates of sca effects revealed that the crosses, JU-2×AKU-96-3, JU-8-6×AKU-01-11, JU-8-6×NUL-7, RBU-38×NUL-7 and TPU-4×AKU-96-3 exhibited good specific combining ability for seed yield per plant. Out of these crosses, JU-8-6×NUL-7 and RBU-38×NUL-7 also exhibited good specific combining ability for 3 yield attributing traits while JU-2×AKU-96-3, JU-8-6×AKU-01-11 and TPU-4×AKU-96-3 exhibited good specific combining ability for 2 yield attributing traits along with seed yield.
- Most of the good specific combinations for various traits involved parents with low × low, high × low, low × high or high × high gca effects.
- Significant values of heterosis were observed for 10 characters. Significant desirable heterosis over mid parent was observed in 9 crosses for seed yield per plant; in 4 crosses for days to maturity; in 5 crosses for plant height; in 3 crosses for number of primary branches per plant and number of secondary branches per plant; in 7 crosses for number of pods per plant and biological yield per plant; and in 6 crosses for 100 seed weight and seed yield per plant. The heterosis over mid-parent ranged from –0.61 to 4.29 per cent for days to 50% flowering, from –7.83 to 1.84 per cent for days to maturity, from –46.96 to 56.77 per cent for plant height, from –22.06 to 280.78 per cent for number of pods per plant, from –28.06 to 35.25 per cent for number of primary branches per plant, from –11.08 to 9.74 per cent for pod length, from –13.47 to 53.61 per cent for 100 seed weight, from –59.49 to 32.51 per cent for biological yield per plant and from –38.60 to 109.03 per cent for harvest index, and from –6.86 to 240.31 per cent for seed yield per plant. The most of the cross combinations which are showing high sca effects also showed heterotic performance.

- High heritability estimates coupled with high genetic advance as per cent of mean was observed for plant height, number of pods per plant, number of primary branches per plant, 100 seed weight, biological yield per plant, harvest index and seed yield per plant. High heritability combined with moderate genetic advance as per cent of mean was observed for number of secondary branches per plant while high heritability with low genetic advance as per cent of mean was noted for days to maturity.

Conclusions:

1. Most of the studied traits are under the influence of non-additive gene action.
2. AKU-96-3 was the desirable tester parent with significant positive gca effect for seed yield per plant along with number of pods per plant, number of primary branches per plant, number of secondary branches per plant, biological yield per plant and harvest index while lines, TPU-4 was good general combiner for number of pods per plant, 100 seed weight and biological yield per plant along with seed yield.
3. Hybrids JU-2×AKU-96-3, JU-8-6×AKU-01-11, JU-8-6×NUL-7, RBU-38×NUL-7 and TPU-4×AKU-96-3 recorded desirable sca effects for seed yield per plant. Out of these hybrids, three crosses, JU-2×AKU-96-3, JU-8-6×AKU-01-11 and TPU-4×AKU-96-3 for two traits; and two crosses viz., JU-8-6×NUL-7 and RBU-38×NUL-7 for three traits also recorded significant sca effects.
4. On the basis of *per se* performance of parents and hybrids, heterosis and gca and sca effects of yield and its component characters in the 12 cross combinations under study, TPU-4×AKU-96-3 cross combination appeared to be suitable for exploitation in future plant breeding programme.
5. The traits viz., plant height, number of pods per plant, number of primary branches per plant, 100 seed weight, biological yield per plant, harvest index and seed yield per plant possessing high genetic

advance as per cent of mean coupled with high heritability may be further improved through simple selection.

Suggestions:

A methodology, based on the principles and techniques of biometrical genetics, has been suggested for use in future in black gram breeding programme.

REFERENCES

- Burton, G.M. (1952). Quantitative inheritance in grasses. *In: Sixth Intl. Grassland Cong.* 1: 227-285.
- Chakaraborty, S. (2004). Diallel analysis for components of genetic variation on some metric traits in black gram. *Annals Agric. Res.* 25:135-138.
- Chand, Pooran (2000). Analysis of gene effects for yield determining factors in black gram [*Vigna mungo* (L.) Hepper]. *Leg. Res.* 23 (3): 180-182.
- Chand, Pooran (2001). Studies on gene action for yield and its components in urd bean [*Vigna mungo* (L.) Hepper]. *Leg. Res.* 24 (2): 121-123.
- Chand, Pooran and C.R. Rao (2002). Studies on gene action in a biparental cross in black gram [*Vigna mungo* (L.) Hepper]. *Indian J. Gen. & Pl. Breed.* 62 (4): 347-348.
- Dana, Indrani and T. Dasgupta (2001). Combining ability in black gram. *Indian J. Gen. and Pl. Breed.* 61 (2): 170-171.
- Dhalival, H.S. and K.B. Singh (1970). combining ability inheritance of pod and clusters number in *Phaseolus mungo* L. Hepper. *Theor. Appl. Genet.* 40:117-120.
- Ghafoor, A., Z. Ahmad, M. Afzal and A.S. Qureshi (2000). Influence of genetic diversity and combining ability in determining hybrid vigour in black gram *Vigna mungo* (L.) Hepper]. *J. Gen. & Breed.* 54 (2): 125-131.
- Govindraj, P and M. Subramanian (2001). Combining ability analysis in black gram (*Vigna mungo* L.). *Madras Agric. J.* 84 (4-6): 237-240.
- Indrani, D. and T. Dasgupta (2001). Combining ability in blackgram. *Indian J. Genet.* 61:170-171.
- Johnson, H.W.; Robinson, H.E. and Comstock, R.E. (1955). Estimation of genetic and environmental variability in soybean. *Agron J.* 47: 314-318.
- Kempthorne, O. (1957). An introduction of Genetic Statistics. New York: John Wiley and Sons. Inc; London: Chapman & Hall Ltd.
- King J.G., J.R. Quinby, J.C. Stephens, N.W. Kramer and K.A. Lahr (1961). An evaluation of parents of grains sorghum hybrids. *Bull. Texas Agric. Exp. Stn. M.P.* 510.
- Krishnan, A.G., M. Reddissekhar, K.R. Reddy and K.S. Reddy (2003). Heterosis and combining ability studies in urd bean [*Vigna mungo* (L.) Hepper]. *Leg. Res.* 26 (4): 280-283.
- Kumar, Rajendra, Avdesh Singh and A.S. Rath (2000). Estimating genetic parameters in urd bean. *Ann. Agric. Res.* 21 (3): 335-337.

- Natrajan, C. and R. Rathanasamy (1999). Heterosis and inbreeding depression in black gram. *Madras Agric. J.* 86 (7-9): 447-450.
- Neog, S.B. and P. Talikdar (2001). Genetic analysis in black gram [*Vigna mungo* (L.) Hepper]. *J. Intracademia* 5 (4): 432-437.
- Neog, S.B. and P. Talukdar (1999). Combining ability and heterosis in black gram. *J. Agric. Sci. Soc. North East India.* 12 (2): 210-216.
- Panse, V.G. and Sukhatme, P.V. (1967). *Statistical Method for Agricultural Workers.* ICAR, New Delhi, pp- 97-151.
- Panse, V.G. and Sukhatme, P.V. (1967). *Statistical Method for Agricultural Workers.* ICAR, New Delhi, pp- 97-151.
- Ram, B. Tikka, S. B. S. and Acharya, A.(2013). Heterosis and combining ability in blackgram (*Vigna mungo*) under different environments. *Indian Journal of Agricultural Sciences*; **83** (6):611-616.
- Robinson, H.F., Comstock, R.E. and Harvey. P.H. (1949). Estimates of heritability and the degree of dominance in Corn. *Agron. J.* 41: 353-359.
- Robinson, H.F., Comstock, R.E. and Harvey. P.H. (1949). Estimates of heritability and the degree of dominance in Corn. *Agron. J.* 41: 353-359.
- Sajikumar, K.R., D.I.S. Bai and P. Saraswathy (1998). Genetic variability of black gram genotypes. *J. Trop. Agric.* 36 (1-2): 18-20.
- Santha, S. and P. Veluswamy (1999). Combining ability studies for biometrical traits in urd bean (*Vigna mungo* L.). *J. Ecobiol.* 11 (1): 29-34.
- Santha, S. and P. Veluswamy (1999). Heterosis for yield and yield attributes in black gram. *J. Ecobiol.* 11 (1): 65-70.
- Saravanan, K. Sabeson, T. Thangavel, P., siddesh kumar, J and J. Ganeshun (2004). Heterosis for yield and yield components in blackgram (*Vigna mungo* L. Hepper). *Legume Res.* 27:209-212.
- Sharma, Debojit and N.U. Ahmad (1997). Genetics and combining ability studies for yield and its components in black gram [*Vigna mungo* (L.) Hepper]. *J. Agric. Sci. Soc. North East India.* 10 (1): 19-24.
- Sharma, R.N. (2000). Exploitation of heterosis in urd bean [*Vigna mungo* (L.) Hepper]. *J. Interacademia.* 4 (1)L 9-12.
- Singh K.B. and H.S. Dhaliwal (1970). Combining ability and in heritance of pod and cluster number in phaseolus mungo. *Theoretical Applaid Genet.* 40:117-120.

- Singh K.B. and H.S. Dhaliwal (1971). Combining ability and genetics of day to 50% flowering in black gram. *Indian J. Agril. Sci.* 41:719-723.
- Singh, M. (2005). A study of combining ability for physiological traits in urdbean (*Vigna mungo* L. Hepper). *Legume Res.*, 50:683-684.
- Singh, Mohar, S.K. Sharma and R.K. Chahota (2003). Heterosis in urd bean [*Vigna mungo* (L.) Hepper]. *Crop Res.* 26 (1): 131-134.
- Singh, R.K. and Chaudhary, B.D. (1977). *Biometrical methods in quantitative genetic analysis*. Kalyani Publishers, New Delhi. 318 p.
- Singh, R.K. and Chaudhary, B.D. (1977). *Biometrical methods in quantitative genetic analysis*. Kalyani Publishers, New Delhi. 318 p.
- Singh, P. and A.N. Shrivastava (1982) Combining ability for yield components in black gram . *Science and Culture*. 48:185-186.
- Thangavel, P., Sabeson, T., Saravanan, K., Vermani, N. And J. Ganesh (2004). Combining ability studies in blackgram (*Vigna mungo* L.Hepper). *Legume Res.* 27:216-216.
- Thomas, B. and S.G. Sreekumar (2001). Combining ability for biological nitrogen fixation traits and yield coponents in black gram [*Vigna mungo* (L.) Hepper]. *J. Trop. Agric.* 39 (2): 93-97.
- Vaithiyalingam, M. (2004). Heterosis for yield yield components in black gram (*Vigna mungo*). *J. Ecobiol.* 16 (2): 87-91.
- Vaithiyalingan, M., S. Chidambaran, P. Vivekanandan and C. Vanniarajan (2002). Combining ability studies in black gram [*Vigna mungo* (L.) Hepper]. *Crop Res.* 24 (1): 81-85.
- Yadav, G.C., P.K. Singh, B.B. Singh and Ritu Verma (2001). Genetic variability and path coefficients in urdbean. *Indian J Pulses Res.* 14 (2): 143-144.
- Yadav, O.P. and B.N. Dahiya (2000). Contribution of some agronomic traits towards seed yield in black gram [*Vigna mungo* (L.) Hepper]. *Int. J. Trop. Agric.* 18 (3): 291-294.
- Griffing, B. (1956b). Concept of general and specific combining ability in relation to diallel crossing system. *Aust. J. Bio. Sci.* 9: 463-493.

Appendix-I: Mean performance of parents and F₁'s in respect of 11 characters in black gram

Parents/ Crosses	Days to 50% flowe- ring	Days to maturity	Plant height (cm)	No. of pods /plant	No. of primary branches/p lant	No. of secondary branches /plant	Pod length (cm)	100 seed weight (g)	Biological yield /plant	Harvest index (%)	Seed yield/ plant (g)
JU-2	42.00	81.50	29.86	48.06	4.50	2.50	4.01	3.42	27.35	15.34	4.17
JU-8-6	41.00	81.00	20.31	38.56	2.66	2.50	3.70	2.14	24.43	19.01	3.70
RBU-38	40.50	80.50	39.14	45.76	2.66	2.65	4.17	2.98	29.13	13.64	3.97
TPU-4	39.50	82.50	29.40	52.96	3.24	2.50	3.72	2.69	28.13	16.45	4.73
AKU-01-11	40.50	84.50	27.13	48.06	4.11	2.45	3.93	2.63	37.25	11.18	4.17
AKU-96-3	41.00	84.50	26.01	24.44	3.02	2.40	3.63	1.88	10.13	27.32	2.78
NUL-7	39.50	80.50	19.82	37.32	2.46	2.65	3.71	2.70	21.18	17.10	3.63
JU-2×AKU-O1-11	41.50	76.50	19.93	54.46	4.50	2.30	3.53	2.78	24.06	19.61	4.72
JU-2×AKU-96-3	41.50	84.50	24.70	77.75	4.37	2.55	3.82	2.99	17.95	29.52	11.38
JU-2×NUL-7	40.50	81.50	25.85	36.10	3.05	2.70	4.10	3.16	33.83	10.78	3.63
JU-8-6×AKU-01-11	42.50	81.00	34.75	65.50	3.25	2.50	3.74	3.31	27.50	13.94	8.00
JU-8-6×AKU -96-3	41.50	82.50	20.32	35.48	3.15	3.05	3.85	3.07	16.90	23.05	3.90
JU-8-6×NUL-7	40.50	80.50	20.49	39.32	3.45	2.25	3.80	2.84	35.30	11.09	8.88
RBU-38×AKU-O1-11	41.50	80.50	18.90	36.56	2.44	2.55	3.85	2.43	13.45	25.94	7.75
RBU-38×AKU-96-3	41.50	80.50	33.96	75.28	2.82	3.15	4.28	3.39	35.59	18.35	6.53
RBU-38×NUL-7	40.50	81.00	29.54	82.58	2.95	3.10	4.11	2.85	35.75	20.07	8.90
TPU-4×AKU-O1-11	41.50	83.50	25.70	103.28	3.63	2.35	3.95	3.37	43.68	20.52	8.95
TPU-4×AKU-96-3	41.50	83.50	34.75	147.36	4.23	2.50	3.85	3.51	80.63	15.85	12.77
TPU-4×NUL-7	40.50	83.00	38.58	112.96	2.62	2.50	3.92	3.55	41.23	23.78	9.79
C.D. (5%)	1.79	1.87	2.34	7.66	0.70	0.29	0.51	0.56	5.40	3.10	0.92

VITA

Name of Author : **Mr. Nakul Yaduvanshi**
Mother's Name : Smt. Ramkali Yaduvanshi
Father's Name : Shri Kanhaiya Yaduvanshi
Date of Birth : 15 / 02 / 2015
E-mail : 90nakul@gmail.com
Mobile No. : 8103194916
Permanent Address : Vill.-Bamla , Post.- Bordehi ,
Teh.-Amla ,Dist.- Betul, (mp).
Pincode-460544 .

Educational Qualification:

Name of examination	Board/University	Year of passing	Mark Obtained	Division
High School	M.P., Board Bhopal	2005	335	1 st .
Higher Secondary	M.P., Board Bhopal	2007	301	1 st
B.Sc. (Ag.)	RVSKVV, Indore (M.P.)	2012	1132.7	1 st
M.Sc. (Ag.)	RVSKVV, Gwalior (M.P.)	2016	-	1 st

I have submitted my thesis in 2016, during his course work in partial fulfilment of the requirement for the degree of M.Sc. in Plant Breeding & Genetics

Place : Sehore

Date : **(Nakul Yaduvanshi)**