COMBINING ABILITY FOR BIOLOGICAL NITROGEN FIXATION TRAITS AND YIELD COMPONENTS IN BLACKGRAM (*Vigna mungo* (L.) Hepper)

BY

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THESIS
SUBMITTED IN PARTIAL FULFILMENT OF
THE REQUIREMENT FOR THE DEGREE
MASTER OF SCIENCE IN AGRICULTURE
FACULTY OF AGRICULTURE
KERALA AGRICULTURAL UNIVERSITY

DEPARTMENT OF PLANT BREEDING AND GENETICS
COLLEGE OF AGRICULTURE
VELLAYANI, THIRUVANANTHAPURAM

1996

DECLARATION

I hereby declare that this thesis entitled **"Combining ability for biological nitrogen fixation traits and yield components in blackgram [*Vigna mungo* (L.) Hepper]"** is a bonafide record of research work done by me during the course of research and that the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title, of any other University or Society.

Beena Thomas

Vellayani,
4-11-1996.

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CERTIFICATE

Certified that this thesis entitled **"Combining ability for biological nitrogen fixation traits and yield components in blackgram [*Vigna mungo* (L.) Hepper]"** is a record of research work done independently by **Miss. Beena Thomas** under my guidance and supervision and that it has not previously formed the basis for the award of any degree, fellowship or associateship to her.

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ACKNOWLEDGEMENT

I am gratefully indebted to Dr. S.G. Sreekumar, Associate Professor, Department of Plant Breeding and Genetics and Chairman of Advisory Committee for his meticulous guidance, timely suggestions, unfailing patience and constant encouragement during the conduct of this research work and preparation of thesis.

I place on record my sincere gratitude to Dr. R. Gopimony, Professor and Head, Department of Plant Breeding and Genetics for his generous help throughout the course of work and critical scrutiny of the manuscript.

I express my deep sense of reverence and immense thanks to Dr. Sasikumar Nair, Professor, Department of Plant Pathology for his timely help and valuable suggestions.

I extend my sincere thanks to Dr. (Mrs.). P. Saraswathy, Professor and Head Department of Agricultural Statistics, for her expert advice and keen interest renderd to me in formulating this thesis.

I wish to record my thanks to Dr.(Mrs.) Sumabai, D.I., Associate Professor, Department of Plant Breeding and Genetics, Prof. P. Reghunath, Department of Entomology, Dr. B.R. Reghunath, Associate Professor, Department of Horticulture and Prof. Abdul Hameed, Department of Soil Science and Agricultural Chemistry for their sincere help at various stages of the study.

My profound thanks to the Professor and Head, National Pulses Research Centre, Vamban, TNAU for providing required seed materials.

I acknowledge Mr. C. E. Ajithkumar, Junior Programmer for rendering his help in the computer analysis of the data.

Thanks to M/s. Athira Computers, Kesavadasapuram, Thiruvananthapuram, for the whole-hearted effort in preparing the graphs and type-setting the manuscript.

Help extended by the staff members of the Department of Plant Breeding is worth mentioning and I express my thanks to them.

I remember with gratitude Mr. S. Sreekumar, Department of Plant Breeding and Genetics for his invaluable assistance rendered during the course of work.

My heartiest thanks to all my friends, who had helped me at various stages of the work, especially Anitha, Sangeetha, Reena, Sindhu, Sophia, Roy and Prashant.

I am deeply obliged to my parents and Binu for all their support and encouragement given throughout the research work.

Above all, I bow myself to God Almighty for his blessings showered upon me.

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INTRODUCTION

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India being primarily an agricultural country, major share of the protein requirements in diet is contributed by grain legumes. Blackgram (*Vigna mungo* (L.) Hepper), one of the most important grain legumes of Kerala, is cultivated in uplands during rabi season and in summer rice fallows during the third crop season. The cultivation of legumes was reported to be beneficial to the succeeding cereal crop, by Nambiar *et al.* (1988). Particularly, in the rice based cropping system, they have a significant role. The nitrogen fixation and legume productivity are greatly influenced by interactions between the legume host, *Rhizobium* and the above ground and below ground environments (Herridge *et al.*, 1994). Alexander (1977) estimated the quantity of nitrogen fixed per hectare per year as 125-335 kg for alfalfa, 80-150 kg for pea, 65-115 kg for soybean and 65-130 kg for cowpea.

The nitrogen fixing capacity of legume - *Rhizobium* symbionts is of immense value. Application of nitrogenous fertilizers, eventhough increases grain production, is very expensive. Therefore; exploitation of nitrogen fixing potential of leguminous crops through genetic manipulation and cultivation has much practical significance in enriching the soil fertility. There is possibility of breeding legumes for increased nitrogen fixation capacity by improving nitrogen fixation traits (Singh and Murthy, 1988). Genetic information on combining ability of parents and the nature of gene action involved in the inheritance of biological nitrogen fixation traits and yield components is very relevant in the choice of suitable parents for improving blackgram genotypes for increased nitrogen fixation capacity and yield.

The present research project was carried out with the objective of assessing the general and specific combining abilities and gene action involved in the inheritance of biological nitrogen fixation traits and yield components in blackgram. This will help in developing varieties with good biological nitrogen fixation capacity combined with reasonable yield potential.

REVIEW OF LITERATURE

REVIEW OF LITERATURE

The genetic studies on nitrogen fixation of legume crops are of recent origin. Works done on blackgram are scanty. Hence, the review on the genetic studies on nitrogen fixation is extended to major legume crops of India.

2.1. Combining ability and gene action

The combining ability and gene action for biological nitrogen fixation traits and yield components in different pulses, have been estimated by several workers. A brief review of such studies are presented here.

2.1.1. Nitrogen fixation traits

Significant gca and sca effects for nitrogen fixation traits such as total nitrogen content per plant, and nodule fresh weight were observed by Hely (1972) in *Trifolium ambiguum.*

In spanish clover, Pinchbeck *et al.* (1980) found the importance of additive gene effects alone, for biological nitrogen fixation traits such as nitrogen content per plant, nodule fresh weight and plant dry weight.

Tan (1981) reported the significance of gca and sca effects for total nitrogen content, nodule fresh weight and nodule dry weight in alfalfa.

Combining ability studies for biological nitrogen fixation traits in crimson clover revealed that both gca and sca effects were significant. For total nitrogen content per plant and nodule fresh weight additive and non-additive gene effects were important (Smith *et al.*, 1982).

From a diallel analysis in cowpea, Miller *et al.* (1986) showed the significance of SCA variance for nitrogenase activity, nodule weight and nodule number. The GCA was significant only for nodule weight. They also suggested the prominance of additive gene action for nodule number and nitrogenase activity and non-additive gene action for nodule weight.

Singh and Murthy (1988) while analysing the combining ability in greengram in a diallel cross involving eight varieties found significant gca and sca effects for total nitrogen content per plant and nodule fresh weight indicating the importance of both additive and non-additive gene effects in the control of nitrogen fixation traits.

Sreekumar (1993) in a line x tester analysis of greengram observed the presence of both GCA and SCA variances and predominance of non-additive gene action for the expression of root/shoot ratio.

A line x tester analysis of cowpea varieties indicated the significance of both GCA and SCA variances and predominance of non-additive gene action for total weight of nodules, weight of effective nodules and nitrogen content in the plant at 50 per cent flowering (Sreekumar, 1995).

2.1.2. Yield and yield components

2.1.2.1. Plant height

In blackgram, Sagar and Chandra (1977) suggested that the variance due to GCA was much larger than SCA variance indicating the predominance additive gene action for plant height.

Pillai (1980) in blackgram observed that GCA variance was higher for plant height suggesting additive gene action for the trait.

The variance due to SCA was of greater magnitude than GCA suggesting non-additive gene action for plant height in blackgram (Rajarathinam and Rathnaswamy, 1990).

Jayarani (1993) in cowpea reported that the character plant height might be governed by both general and specific combining ability effects.

2.1.2.2. Dry weight of plants

Significant gca and sca effects for dry weight of the plant was reported by Hely (1972) in *Trifolium ambiguum*.

In spanish clover, Pinchbeck *et al.* (1980) observed the importance of additive gene effects alone, for dry weight.

Tan (1981) reported the significance of gca and sca effects for dry weight in alfalfa.

Combining ability studies in crimson clover done by Smith *et al.* (1982) revealed that additive and non-additive gene effects were important for dry weight.

Miller *et al.* (1986) from a diallel analysis in cowpea, showed that SCA variance for dry weight was non-significant. Non-additive gene action was found to be important for the trait.

From a line x tester analysis of cowpea varieties, Sreekumar (1995) suggested the significance of both GCA and SCA variances and predominance of non-additive gene action for dry weight of plant at 50 per cent flowering.

2.1.2.3. Number of pods

In blackgram high amount of non-additive gene action for number of pods was reported by Singh and Singh (1971) and Singh and Dhaliwal (1972).

A study on 6 x 6 diallel cross of blackgram conducted by Sagar and Chandra (1977) revealed that the magnitude of SCA variance was very high suggesting the predominance of non-additive gene action for number of pods per plant, though both the variances due to GCA and SCA were significant.

Pillai (1980) in blackgram reported that SCA variance was more important indicating the predominance of non-additive genetic variance for pod number.

In greengram, Deshmukh and Manjare (1980) while estimating combining ability in a diallel cross observed highly significant variances due to GCA and SCA for number of pods per plant and reported non-additive gene action.

A half diallel cross of eight cowpea varieties, along with their parents were evaluated by Chauhan and Joshi (1981). The results indicated that both general and specific combining ability variances were important for number of pods per plant and there was a predominance of additive gene action.

The GCA variance was found to be higher than SCA variance for number of pods per plant indicating the predominance of additive gene action in greengram (Wilson *et al.*, 1985).

Significant GCA and SCA variances for number of pods per plant was reported by Chowdhury (1986) in an analysis of half diallel cross with eight greengram varieties.

Dasgupta and Das (1987) in blackgram observed that both additive and non-additive genetic variances were significant for number of pods, with higher magnitude of non-additive component.

Combining ability analysis in blackgram conducted by Singh *et al.* (1987) revealed that both GCA and SCA variances were highly significant for pods per plant. Predominance on non-additive gene action was also found.

Saxena and Sharma (1989) derived information from a diallel cross of greengram and suggested the significance of GCA mean square for number of pods per plant in F_1. Both GCA and SCA mean squares were found significant in F_2. Mean square due to GCA were larger in magnitude indicating the predominance of additive gene action for this trait.

In cowpea, the combining ability was estimated in a diallel cross by Thiyagarajan *et al.* (1990). They reported the importance of both additive and non-additive gene effects for number of pods per plant.

The importance of both additive and non-additive gene actions for number of pods was observed by Natarajan *et al.* (1990) in a 7 x 7 diallel cross in greengram.

A line x tester analysis in blackgram by Rajarathinam and Rathnaswamy (1990) revealed that the variance due to SCA was greater than GCA for number of pods indicating the preponderance of non-additive gene action.

Based on the combining ability studies in blackgram, Kalia *et al.* (1991) indicated significant mean mean squares due to SCA for number of pods per plant.

Anilkumar (1993) observed significant GCA variance and predominance of non-additive gene action for number of pods per plant in a line x tester analysis with greengram.

In cowpea, from a line x tester analysis Sreekumar (1995) reported the significance of both GCA and SCA variances for number of pods per plant and the importance of non-additive gene action in controlling this character.

2.1.2.4. Number of seeds per pod

While analysing combing ability in greengram in a diallel cross involving eight varieties, Deshmukh and Manjare (1980) found highly significant variances due to GCA and SCA and preponderance of non-additive gene action for number of seeds per pod.

Eight cowpea varieties crossed in a half diallel fashion along with their parent were evaluated by Chauhan and Joshi (1981) and reported the importance of both GCA and SCA variances for number of seeds per pod. Additive gene action was involved in the inheritance of this trait.

A diallel analysis in blackgram by Malhotra (1983) revealed the significance of GCA variance and additive gene effect for number of seeds per pod.

Information on combining ability was derived from a diallel cross of five greengram varieties by Wilson *et al.* (1985). They have suggested the existence of both additive and non-additive gene action for number of seeds per pod with a predominance of additive gene action.

A diallel analysis in greengram revealed the significances of both GCA and SCA mean squares and predominance of additive gene action (Saxena and Sharma, 1989).

Combining ability studies in blackgram conducted by Kalia *et al.* (1991) indicated significant mean squares due to SCA for number of seeds per pod.

Anilkumar (1993) estimated combining ability in greengram from a line x tester analysis and reported the significance of gca effect alone for number of seeds per pod. Additive gene action was observed for this trait.

A line x tester analysis in cowpea conducted by Sreekumar (1995) revealed significant GCA and SCA variances and a predominance of non-additive gene action for number of seeds per pod.

2.1.2.5. 100 grain weight

In blackgram, the study of gene action for various characters by Pillai (1980) revealed that the GCA variance was higher for hundred seed weight indicating preponderance of additive gene action for this trait.

A half diallel cross of eight cowpea varieties along with parents carried out by Chauhan and Joshi (1981) revealed that both general and specific combining variances were important for hundred seed weight. The GCA variance was higher in magnitude than SCA variance indicating the predominant role of additive gene action in the inheritance of hundred seed weight.

Malhotra (1983) in a diallel analysis of blackgram found the importance of both GCA and SCA variances for hundred seed weight. Both additive and non-additive gene effects were significant and important for this yield component.

Combining ability studies with 5 x 5 diallel cross in greengram indicated the existence of both additive and non-additive gene action for hundred seed weight. The variance due to GCA was found to be much higher than that due to SCA, suggesting additive gene action for this character (Wilson *et al.*, 1985).

Importance of both additive and non-additive gene effects and preponderance of non additive gene action for hundred seed weight was reported by Thiyagarajan *et al.* (1990) in cowpea form a diallel analysis with six parents.

A line x tester analysis in greengram revealed the importance of GCA variance alone for hundred grain weight. The character was under the control of additive gene action (Anil kumar, 1993).

Combining ability studies in cowpea carried out by Sawant (1995) indicated that both GCA and SCA variances were highly significant for hundred seed weight. Additive gene effect was predominant for the trait.

Sreekumar (1995) in cowpea observed significant GCA and SCA variances for hundred seed weight indicating the presence of additive and non-additive genetic components. A predominant role of non-additive gene action was also reported.

2.1.2.6. Grain yield per plant

Combining ability studies in greengram by Deshmukh and Manjare (1980) revealed the significance of both GCA and SCA variances and non-additive gene action for grain yield per plant.

In blackgram, Pillai (1980) observed that the SCA variance was more important for seed yield indicating the predominance of non-additive gene action.

The combining ability analysis of eight cowpea varieties in a half diallel cross conducted by Chauhan and Joshi (1981) suggested the significance of both GCA and SCA variances for grain yield per plant. But the magnitude of GCA variance was found to be higher indicating the additive gene action.

Malhotra (1983) from a diallel cross in blackgram reported that both the additive and non-additive gene effects were significant for seed yield, with the predominance of additive gene effects.

A diallel analysis of five greengram varieties conducted by Wilson *et al.* (1985) showed the existence of both additive and non-additive gene actions for seed yield per plant. The variance due to GCA was observed to be more than SCA suggesting the predominance of additive gene action.

Chowdhury (1986) reported significant GCA and SCA variances for seed yield per plant based on the combining ability analysis using eight parent half diallel cross in greengram.

In blackgram, Dasgupta and Das (1987) observed that both additive and non-additive variances were significant with predominance of non-additive component, for seed yield.

A line x tester analysis by Mishra *et al.* (1987) involving four testers and ten lines of cowpea indicated the importance of both GCA and SCA variances for seed yield.

Combining ability studies in blackgram done by Singh *et al.*, (1987) revealed that for grain yield per plant both GCA and SCA variances were highly significant and non-additive gene action was prominent.

Haque *et al.* (1988) observed higher sca effect for yield in the cross PLV 652 x T_9 in a line x tester analysis with six blackgram lines and four testers.

In greengram, Saxena and Sharma (1989) reported that both GCA and SCA mean squares were significant for yield per plant.

Rajarathinam and Rathnaswamy (1990) conducted a line x tester analysis in blackgram and observed that for seed yield per plant the variance due to SCA was greater than GCA suggesting the predominance of non-additive gene action.

Thiyagarajan *et al.* (1990) reported both additive and non-additive gene effects and preponderance of non-additive gene effects for yield per plant in a diallel cross in cowpea.

Kalia *et al.* (1991) observed significant mean squares due to SCA for seed yield, while estimating combining ability for seed yield and its components over environments in blackgram.

Significance of both GCA and SCA variances and the involvement of additive and non-additive gene actions with the predominance of non-additive gene action for the expression of grain yield per plant in greengram were reported by Anilkumar (1993) from a line x tester analysis.

In cowpea, Sreekumar (1995) observed significant GCA and SCA variances and preponderance of non-additive gene action for grain yield per plant.

2.2. Heterosis

Various workers have reported the presence of heterosis in pulses.

In blackgram, Sagar and Chandra (1977) observed heterosis for plant height and pod number per plant

Pillai (1980) found heterosis in yield and its components such as pod number, 100 seed weight and plant height, over mid parent, better parent and standard parent in blackgram.

According to Dasgupta and Das (1987), the degree and direction of heterosis varied greatly for different crosses in blackgram. Two crosses viz., Mash 1 x LU272 and Mash 1 x LU241 exhibited significantly positive heterosis.

Haque *et al.* (1988) noticed maximum heterosis for yield in the cross between the blackgram varieties PLU200B and T9.

Heterosis for seed yield in blackgram was studied by Kalia *et al.* (1988) and they have observed significant heterosis over the mid parent value in a few crosses, viz. CO4 x UG170, CO4 x HPU433 and HPU433 x HPU617.

In a study of heterosis for dry matter components in greengram, four hybrids, all with CO4 as one parent were shown to have positive, highly significant heterosis over the better parent for grain yield and pod weight, but negative heterosis for total dry matter and harvest index (Natarajan, 1989).

Information on heterosis in blackgram derived from data on 11 yield related characters by Shinde and Deshmukh (1989) revealed that the cross between the parental varieties Sindkheda 1-1 and T9 recorded the maximum heterosis for yield.

Verma *et al.* (1991) studied heterosis and inbreeding in blackgram and reported that the highest yielding hybrid (PS1 x RU4) surpassed its better parent by 31 per cent. It was also reported that the crosses showing high hybrid vigour also generally showed high inbreeding depression.

The highest value of heterosis over the better parent was shown by pods per plant followed by seed yield per plant and pod weight per plant, in greengram (Patil *et al.*, 1992).

From a study of 11 characters, in 90 F_1 hybrids of greengram, Singh and Pathak (1992) reported heterosis over the better parent for yield and many yield components.

Hazra *et al.* (1993) analysed heterosis for pod yield and its components in cowpea and suggested that the frequency and level of heterosis was related more to specific combining ability than to the genetic divergence of the parents.

Heterosis and inbreeding depression for yield and yield components in greengram was studied by Naidu and Sathyanarayana (1993) and they showed that the average relative heterosis and heterobeltiosis were high for seed yield, shoot dry weight and pods per plant. The average inbreeding depression was also found to be high for shoot dry weight, seed yield and pods per plant.

Nodulation and yield traits in greengram were studied from a diallel crossing programme and the highest heterosis over better parent or mid parent was seen in the crosses T44 x ML80 for all nodulation traits HG19 x T44 for 100 seed weight and T44 x Black Neelalu for seed yield per plant (Singh and Singh, 1993).

Sawant *et al.* (1994) in cowpea found that highest positive heterosis over mid parent was for seed yield per plant followed by inflorescence per plant, pods per plant, branches per plant and plant height. A similar trend over better parent was observed except for branches per plant and plant height. Average heterosis was maximum for seed yield per plant followed by pods per plant and inflorescence per plant.

In cowpea, significant and positive standard heterosis was observed for weight of nodules and nitrogen content at 50 per cent flowering. For number of pods and grain yield per plant relative heterosis, heterobettiosis and standard heterosis were significant and positive (Sreekumar, 1995).

MATERIALS AND METHODS

MATERIALS AND METHODS

The research programme was carried out at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, Thiruvananthapuram, during 1995-'96.

Materials

The experimental material comprised of eight black gram varieties as parents and their 15 hybrids. The parents consisted of five lines and three testers. The lines having high nitrogen fixation capacity already identified from a PG project implemented earlier at the Kerala Agricultural University were used as female parents (Thomas, 1994). The testers were the recommended high yielding varieties. The details of genetic materials are presented in Table 1.

Experiment I

A. Selfing

The lines and testers were raised in pots during April to June 1995 and allowed for self pollination. To prevent any chance cross pollination mature flower buds were covered with tissue paper bags on the previous day of opening and retained for two days. The selfed pods were harvested, seeds extracted and collected separately.

Table 1. Details of genetic materials included in the study

Sl. No.	Genetic materials		Attribute
I.	Parents		
i.	Lines :	5	High nitrogen fixing capacity
	L_1	LBG17	
	L_2	LBG622	
	L_3	WBG13	
	L_4	COBG305	
	L_5	Pant U19	
ii.	Testers :	3	High yielding
	T_1	AKU4	
	T_2	T9	
	T_3	VBN1	
II.	Hybrids :	15	
	$L_1 \times T_1$	LBG17 x AKU4	
	$L_1 \times T_2$	LBG17 x T9	
	$L_1 \times T_3$	LBG17 x VBN1	
	$L_2 \times T_1$	LBG622 x AKU4	
	$L_2 \times T_2$	LBG622 x T9	
	$L_2 \times T_3$	LBG622 x VBN1	
	$L_3 \times T_1$	WBG13 x AKU4	
	$L_3 \times T_2$	WBG13 x T9	
	$L_3 \times T_3$	WBG13 x VBN1	
	$L_4 \times T_1$	COBG305 x AKU4	
	$L_4 \times T_2$	COBG305 x T9	
	$L_4 \times T_3$	COBG305 x VBN1	
	$L_5 \times T_1$	Pant U19 x AKU4	
	$L_5 \times T_2$	Pant U19 x T9	
	$L_5 \times T_3$	Pant U19 x VBN1	

B. Line x Tester hybridization programmes

Lines and testers were raised in pots and hybridization was done during August-November 1995, in three sets (Plate 1).

To obtain synchronised flowering lines and testers were sown on different dates. Emasculation was done in the evening (4 to 6 p.m.), in the flower buds of the lines, which were likely to open on the next day morning and protected with tissue paper bags. The emasulated flower buds were pollinated on the next day morning (8 to 10 a.m.) using pollen collected from the tester plants. The artificially pollinated flowers were labelled and protected with paper cover. The covers were retained for two days. The mature pods were collected separately, seeds extracted and used for field evaluation.

Experiment II

Evaluation of lines, testers and L x T combinations

The five lines, three testers and their fifteen F_1 combinations were evaluated in $6m^2$ plots, adopting a randomised block design with three replications, in the summer rice fallow, at the College of Agriculture, Vellayani, during January to March 1996 (Plate 2).

Seed treatment using *Rhizobium* culture KAU-BG-2 was done. For that, the inoculant was mixed uniformly with the seeds by using 2.5% starch solution. The inoculated seeds were dried under shade over a gunny bag and sown immediately at a spacing of 25 x 15cm. The cultural and

Plate 1. Line x Tester hybridization

Plate 2. Field experiment for the evaluation of lines, testers and their 15 hybrids

management practices were followed as per the Package of Practices Recommendations Crops'-93 (KAU, 1993). Data on various characters were recorded replication wise, from a random sample of five plants per treatment by completely excluding the border rows and the mean values were used for statistical analysis.

Traits studied from the field experiment

1. Length of primary root

Plants were uprooted carefully at harvest and length of tap root measured in centimeters.

2. Number of secondary roots

Number of secondary roots were counted on each uprooted sample plants.

3. Shoot/root ratio

From each sample plant shoot and root portions were separately taken, sundried for two days, oven dried at 60-70°C for one day, dry weights recorded and the ratio computed.

4. Weight of nodules

Nodules were separated out from the roots of sample plants at 50% flowering, fresh weight recorded and expressed in milligrams.

5. Nitrogen content at 50% flowering

Sample plants were uprooted at 50% flowering, sundried for two days and then ovendried at 60-70°C for one day. Properly dried plants were powdered and from this 0.1g was taken for the nitrogen estimation by Microkjeldahl method.

6. Nitrogen content at maturity

Nitrogen content of the plants at maturity was also estimated using Microkjeldahl method as in the previous case.

7. Plant height

Height of the plant was measured in centimeters from the base of the main shoot to the tip, at harvest.

8. Dry weight of plants

Observational plants along with the separated nodules were sundried for two days and then ovendried at 60-70°C for 24 hours and dry weight recorded.

9. Number of pods

Total number of pods from the observational plants were counted and the mean calculated.

10. Number of seeds per pod

Number of seeds from ten randomly selected pods of observational plants was counted and averaged.

11. 100 grain weight

A random sample of 100 grains was collected from the observational plants, weighed and the mean weight was expressed in grams.

12. Grain yield per plant

Grain yield from the sample plants was recorded and the average expressed in grams.

Statistical analysis

i. ANOVA

Analysis of variance was employed to test for the significance of genotypic differences, for a l x t mating design using the linear model.

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + r_k + e_{ijk}$$

where, μ = population mean effect

g_i = effect of female parent (line)
(gca effect of i^{th} line) $i = 1, 2, \ldots\ldots l$

g_j = effect of male parent (tester)
(gca effect of j^{th} tester) $j = 1, 2, \ldots\ldots t$

s_{ij} = combined effect of i^{th} line and j^{th} tester (sca effect of i x j cross)

r_k = replication effect k = 1, 2, ..., r

e_{ijk} = environment effect, and

Y_{ijk} = any character measured on i x j cross in k^{th} replication

(Arunachalam, 1974)

With l lines, t testers and l x t hybrids so that $g = l + t + lt$ genotypes raised in a RBD with r replications, the split up of the degrees of freedom due to various components of variation is given below in Table 2.

Table 2. ANOVA for modified line x tester

Sl. No.	Source	df	SS	MS	Expected mean square
1	Replication	(r – 1)			
2	Genotypes	(g – 1)			
(a)	Parents	(l + t) – 1			
(i)	Lines	(l – 1)			
(ii)	Testers	(t – 1)			
(iii)	Lines vs. Testers	1			
(b)	Hybrids	lt – 1	SSH		
(i)	Lines	(l – 1)	SSL	ML	$\sigma^2_e + r\,\sigma^2_{sca} + rt\,\sigma^2_{gca}$
(ii)	Testers	(t – 1)	SST	MT	$\sigma^2_e + r\,\sigma^2_{sca} + rl\,\sigma^2_{gca}$
(iii)	Lines x Testers	(l – 1) (t – 1)	SSLT	MLT	$\sigma^2_e + r\,\sigma^2_{sca}$
(c)	Parents vs. Hybrids	1			
3	Error	(r – 1) (g – 1)		Me	σ^2_e

(ii) Combining ability analysis

The gca effects of lines, testers and sca effects of hybrids are estimated as follows

$$g_i = \frac{Y_{i..}}{rt} - \frac{Y_{...}}{rlt}, \quad i = 1, 2, \ldots\ldots., l$$

$$g_j = \frac{Y_{.j.}}{rl} - \frac{Y_{...}}{rlt}, \quad j = 1, 2, \ldots\ldots., t$$

$$s_{ij} = \frac{Y_{ij.}}{r} - \frac{Y_{i..}}{rt} - \frac{Y_{.j.}}{rl} + \frac{Y_{...}}{rlt}$$

where,

$Y_{i..}$ = sum of the crosses involving i^{th} line as one parent over all the testers and replication

$Y_{.j.}$ = sum of the crosses involving j^{th} tester as one parent over all the lines and replication

$Y_{ij.}$ = sum of all the genotypes (lt) over the replication

$Y_{...}$ = grand total

The significance of gca effects of lines, testers and their within differences, sca effects of crosses and within their differences are tested using 't' test as given below.

Effect	't'	SE
gca		
g_i (lines)	$\mid g_i \mid / SE(g_i)$	$(Me / rt)^{1/2}$
g_j (testers)	$\mid g_j \mid / SE(g_j)$	$(Me / rl)^{1/2}$
$g_i - g_j$ (lines)	$\mid g_i - g_j \mid / SE(g_i - g_j)$	$[(2Me) / rt]^{1/2}$
$g_i - g_j$ (tester)	$\mid g_i - g_j \mid / SE(g_i - g_j)$	$[(2Me) / rl]^{1/2}$
sca		
s_{ij}	$\mid s_{ij} \mid / SE(s_{ij})$	$(Me/r)^{1/2}$
$s_{ij} - s_{kl}$	$\mid s_{ij} - s_{kl} \mid / SE(s_{ij} - s_{kl})$	$[(2Me) / r]^{1/2}$

(iii) Estimation of genetic components of variance

$$\sigma^2_{gca} = \frac{(1+F)^2}{4} \sigma^2_A$$

$$\sigma^2_{sca} = \left[\frac{1+F}{2}\right]^2 \sigma^2_D$$

when $F = 1$

$$\sigma^2_{gca} = \sigma^2_A$$

$$\sigma^2_{sca} = \sigma^2_D$$

where F = coefficient of inbreeding

σ^2_A = additive genetic variance

σ^2_D = dominance genetic variance

(iv) Heterosis

Types of heterosis	Formulae	SE_d
Relative heterosis (RH)	$\frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$	$\left[\frac{3\ Me}{2r}\right]^{½}$
Heterobeltiosis (HB)	$\frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$	$\left[\frac{2\ Me}{r}\right]^{½}$
Standard heterosis (SH)	$\frac{\overline{F_1} - \overline{SP}}{\overline{SP}} \times 100$	$\left[\frac{2\ Me}{r}\right]^{½}$

where, $\overline{F_1} = F_1$ mean, $\overline{MP}$, $\overline{BP}$, $\overline{SP}$ respectively the mean of mid parent, better parent and standard parent.

The parent expressing maximum value for a trait is considered as standard parent for that trait.

RESULTS

RESULTS

The data on various characters in blackgram recorded from the experiment were statistically analysed. The results obtained are presented below.

4.1. Mean performance

Mean value of twelve characters are presented in table 3 and 4. Length of primary root was minimum among lines in LBG622 (10.50cm) and in VBN1 (10.70cm) among the testers. It was maximum in WBG13 (18.70cm) among lines and in AKU4 (13.40cm) among testers. Among hybrids the lowest and highest values were recorded for Pant U19 x VBN1 (11.87cm) and WBG13 x AKU4 (23.17cm) respectively.

Minimum number of secondary roots was observed among lines in Pant U19 (8.63) and among testers in VBN1 (9.43). The maximum value for this character was shown by WBG13 (12.97) among lines and AKU4 (15.93) among testers. It was lowest for LBG17 x VBN1 (8.67) and highest for WBG13 x AKU4 (18.43) among hybrids.

Shoot/root ratio was lowest for WBG13 (17.23) among lines and for VBN1 (17.03) among testers. This ratio was highest for Pant U19 (30.73)

Table 3. Mean of various nitrogen fixation traits in black gram.

Sl. No.		Length of primary root (cm)	Number of secondary roots	Shoot/root ratio	Weight of nodules (mg)	Nitrogen content (at 50% flowering) (%)	Nitrogen content (at maturity) (%)
Lines (Female parents)							
1	L_1	12.87	12.40	19.17	216.67	3.47	2.67
2	L_2	10.50	9.07	18.77	119.17	5.17	3.47
3	L_3	18.70	12.97	17.23	59.17	4.17	3.03
4	L_4	10.93	8.63	30.73	248.33	4.73	3.10
5	L_5	10.93	8.63	30.73	248.33	4.73	3.10
Testers (Male parents)							
6	T_1	13.40	15.93	24.83	29.83	4.27	3.03
7	T_2	12.87	10.10	29.43	200.83	4.40	3.13
8	T_3	10.70	9.43	17.03	19.17	3.47	2.87
Hybrids							
9	$L_1 \times T_1$	15.07	18.03	22.50	217.50	5.00	3.63
10	$L_1 \times T_2$	15.27	14.33	21.97	204.17	5.20	3.43
11	$L_1 \times T_3$	14.50	8.67	24.07	188.33	4.57	3.03
12	$L_2 \times T_1$	12.73	15.80	21.93	217.50	5.33	3.53
13	$L_2 \times T_2$	13.83	13.00	21.47	242.83	5.20	3.20
14	$L_2 \times T_3$	12.27	8.77	22.30	168.17	4.20	3.13
15	$L_3 \times T_1$	23.17	18.43	24.70	232.33	5.23	3.23
16	$L_3 \times T_2$	22.67	16.77	23.33	186.83	4.40	3.10
17	$L_3 \times T_3$	13.20	12.23	20.20	216.83	5.37	3.63
18	$L_4 \times T_1$	15.37	15.23	20.90	257.00	5.67	3.63
19	$L_4 \times T_2$	14.93	13.70	29.13	313.50	6.00	3.80
20	$L_4 \times T_3$	13.30	9.80	21.30	228.83	5.43	3.57
21	$L_5 \times T_1$	14.13	14.83	32.67	223.67	5.50	3.53
22	$L_5 \times T_2$	12.90	11.97	33.90	394.67	6.23	3.87
23	$L_5 \times T_3$	11.87	9.13	23.80	185.17	4.27	3.17
	$F_{22,44}$	164.49^{**}	358.71^{**}	342.04^{**}	14.14^{**}	172.67^{**}	40.61^{**}
	SEm	0.26	0.17	0.25	22.08	0.06	0.05

* Significant at 1% level

** Significant at 5% level

Table 4. Mean of various yield contributing characters in blackgram

Sl. No.		Dry weight of plants (g)	Plant height (cm)	Number of pods	Number of seeds/pod (g)	100 grain weight (g)	Grain yield/plant (g)
Lines							
1	L_1	8.97	34.13	18.13	6.27	4.52	4.88
2	L_2	7.00	32.57	15.53	6.00	4.17	4.01
3	L_3	10.93	47.73	23.73	6.77	4.16	6.91
4	L_4	5.10	20.77	22.33	6.60	4.01	6.33
5	L_5	3.07	20.77	16.93	5.43	4.17	3.92
Testers							
6	T_1	16.97	43.03	29.27	6.10	4.38	7.67
7	T_2	9.03	26.07	35.20	5.87	4.27	8.26
8	T_3	4.63	21.17	20.47	5.60	3.92	4.58
Hybrids							
9	$L_1 \times T_1$	18.00	41.23	32.33	6.30	4.45	8.15
10	$L_1 \times T_2$	10.13	44.27	46.13	6.00	4.41	11.07
11	$L_1 \times T_3$	10.70	37.90	46.53	6.13	4.71	11.41
12	$L_2 \times T_1$	21.30	56.20	36.27	6.87	4.30	9.93
13	$L_2 \times T_2$	11.03	42.47	47.87	6.23	4.48	11.92
14	$L_2 \times T_3$	11.97	34.77	39.53	6.53	4.30	10.33
15	$L_3 \times T_1$	23.03	60.53	59.73	7.13	5.00	18.32
16	$L_3 \times T_2$	9.53	52.83	60.47	6.13	4.46	15.95
17	$L_3 \times T_3$	8.10	48.63	52.53	6.27	4.36	13.17
18	$L_4 \times T_1$	16.17	35.37	39.07	7.03	4.60	10.99
19	$L_4 \times T_2$	8.59	41.17	43.27	6.33	4.40	12.01
20	$L_4 \times T_3$	5.97	31.37	40.60	6.47	4.47	10.5
21	$L_5 \times T_1$	13.63	37.57	43.27	5.73	4.54	9.92
22	$L_5 \times T_2$	5.03	32.27	48.93	5.90	4.57	11.55
23	$L_5 \times T_3$	4.90	33.27	36.73	5.73	4.13	8.42
	$F_{22,44}$	1538.62**	1883.30**	2897.62**	41.04**	30.70**	177.0**
	SEm	0.14	0.25	0.24	0.07	0.04	0.27

* Significant at 1% level ** Significant at 5% level

among lines and for T9 (29.43) among testers. Among the F_1s minimum and maximum values were observed for WBG13 x VBN1 (20.20) and Pant U19 x T9 (33.90) respectively.

For weight of nodules value was minimum among lines in WBG13 (59.17mg) and among testers in VBN1 (19.17mg). Maximum value for this trait was shown by Pant U19 (248.33mg) among lines and T9 (200.00mg) among testers. LBG622 x VBN1 (168.17mg) and Pant U19 x T9 (394.67mg) exhibited lowest and highest values respectively among hybrids.

Nitrogen content at fifty per cent flowering was lowest for LBG17 (3.47%) among lines and VBN1 (3.47%) among testers. This was highest for LBG622 (5.17%) among lines and T9 (4.40%) among testers. Minimum and maximum values among hybrids were recorded in LBG622 x VBN1 (4.20%) and Pant U19 x T9 (6.23%) respectively.

In the case of nitrogen content at maturity, the value was minimum for LBG17 (2.67%) among lines and VBN1 (2.87%) among testers. Maximum value was for LBG622 (3.47% among lines and T9 (3.13%) among testers. This was lowest for LBG17 x VBN1 (3.03%) and highest for Pant U19 x T9 (3.87%) respectively among hybrids.

Minimum plant height was observed in COBG305 and Pant U19 (20.77cm) among lines and VBN1 (21.17cm) among testers. This was maximum for WBG13 (47.73cm) among lines and AKU4 (43.03cm) among testers. Lowest and highest values for this trait was shown by COBG305 x VBN1 (31.37cm) and WBG13 x AKU4 (60.53cm) respectively among hybrids.

Dry weight of plants was minimum for Pant U19 (3.07g) among lines and for VBN1 (4.63g) among testers. Maximum value for this character was expressed by WBG13 (10.93g) among lines and AKU4 (16.97g) among testers. Among F_1s, Pant U19 x VBN1 (4.90g) exhibited lowest dry weight and WBG13 x AKU4 (2303g) recorded highest dry weight.

Number of pods was lowest for Pant U19 (16.93) among lines VBN1 (20.47) among testers. It was highest for WBG13 (23.73) among lines and T9 (35.20) among testers. Lowest value was for LBG17 x AKU4 (32:33) and highest value was for WBG13 x T9 (60.47) among hybrids.

Lowest number of seeds per pod was found in Pant U19 (5.43) among lines and in VBN1 (5.60) among testers. Highest value for this trait was observed in WBG13 (6.77) among lines and in AKU4 (6.10) among testers. Among F1s lowest number was for Pant U19 x AKU4 and Pant U19 x VBN1 (5.73). Highest value among hybrids was shown by WBG13 x AKU4 (7.13).

For 100 grains weight minimum value was expressed by COBG305 (4.01g) among lines and VBN1 (36.92g) among testers. It was maximum for LBG17 (4.52g) among lines and AKU4 (4.38g) among testers. Among hybrids minimum value was observed in Pant U19 x VBN1 (4.13g) and maximum value WBG13 x AKU4 (5.00g).

Grain yield per plant was minimum among lines in Pant U19 (3.92g) and among testers in VBN1 (4.58g). It was maximum in WBG13 (6.91g) among lines and in T9 (8.26g) among testers. Among hybrids the lowest and highest values were recorded for LBG17 x AKU4 (8.15g) and WBG13 x AKU4 (18.32g) respectively.

4.2. Combining ability

The analysis of variance for various characters studied are presented in table 5.

Significant treatment effects were observed among genotypes for all the characters. Hence subjected to combining ability analysis in a line x tester model and results are presented below.

Among the parents and among the crosses there were significant differences for all the characters studied. On further analysis there were no significant differences among lines for the traits like weight of modules, nitrogen content at 50 per cent flowering, nitrogen content at maturity and 100 grain weight. The analysis revealed that among testers there were no significant differences for characters such as length of primary root, shoot/root ratio, weight of nodules, nitrogen content at 50 per cent flowering, nitrogen content at maturity, 100 grain weight and grain yield per plant.

Table 5. ANOVA for various characters in blackgram

		Mean squares											
Source	df	Length of primary root	Number of secondary roots	Shoot/ root ratio	Weight of nodules	Nitrogen content at 50% flowering	Nitrogen content at maturity	Plant height	Dry weight of plants	Number of pods	Number of seeds/ pod	100 grain weight	Grain yield/ plant
Replication	2	0.04	0.19	0.08	1499.75	0.002	0.02	0.004	0.04	0.05	0.02	0.004	0.07
Treatments	22	32.89**	29.68**	65.23**	20681.47**	1.610**	0.29**	2348.10**	87.05**	520.15**	0.60**	0.17**	39.66**
Parents	7	21.78**	18.31**	87.43**	24174.60**	1.010**	0.16**	328.78**	58.17**	133.30**	0.63**	0.11**	8.62**
Crosses	14	34.50**	31.90**	55.02**	9763.75**	1.080**	0.22**	242.14**	92.86**	200.50**	0.55**	0.12**	21.00**
Parent Vs Cross	1	88.044**	78.13**	52.67**	149077.60**	13.100**	2.25**	1966.81**	207.73**	7703.21**	0.91**	1.225**	18.35**
Lines (female parents)	4	68.54**	20.07**	99.67**	9446.19	1.050	0.22	552.51**	68.93**	458.51**	1.09**	0.08	52.43**
Testers (male parents)	2	44.51	174.39**	53.20	18923.75	1.87	0.180*	307.50**	479.01*	226.82**	1.01	0.13	11.40
Lines x Testers	8	14.98**	2.20**	33.15**	7632.53**	0.910**	0.22**	70.62**	8.29**	64.92**	0.17**	0.14**	7.67**
Error	44	0.20	0.08	0.19	1462.82	0.010	0.01	0.18	0.06	0.18	0.01	0.01	0.22

* Significant at 1% level ** Significant at 5% level

The general combining ability effects of parents and specific combining ability effects of hybrids for twelve characters are given in Table 6 and 7 respectively.

4.2.1. Length of primary root

The combining ability analysis revealed that length of primary root differed significantly among lines and line x tester. Among lines only one genotype viz., WBG13 showed highly significant positive gca effects ie., 4.66. Lines COBG305, Pant U19 and LBG622 recorded significant negative gca effects of -0.48, -2.05 and -2.07 respectively. LBG17 exhibited non-significant negative gca of -0.07. Among testers, only VBN1 showed significant negative gca of -1.99 while it was positive and significant for AKU4 (1.08) and T9 (0.91). The sca effect was positive and significant for hybrids like LBG17 x VBN1 (1.54), LBG622 x VBN1 (1.31), WBG13 x AKU4 (2.41), WBG13 x T9 (2.08), COBG305 x VBN1 (0.75) and Pant U19 x VBN1 (0.89). Significant negative sca was shown by LBG17 x AKU4, LBG17 x T9 (-0.59), LBG622 x AKU4 (-1.29), WBG13 x VBN1 (-4.49) and Pant U19 x T9 (-0.97).

4.2.2. Number of secondary roots

Number of secondary root differed significantly among lines, testers and F_1s. Among lines only two genotypes ie., WBG13 (2.43) and LBG17 (0.30) showed significant and positive general combining ability. The other

Table 6. gca effects of lines and testers

	Length of primary root	Number of secondary roots	Shoot root ratio	Weight of nodules	Nitrogen content (at 50% flowering)	Nitrogen content (at maturity)	Plant height	Dry weight of plants	Number of pods	Number of seeds/ pod	100 grain weight	Grain yield/ plant
Lines												
L_1	-0.07	0.30*	-1.47*	-28.49*	-0.25*	-0.07*	-0.86*	1.09*	-3.22*	-0.18*	0.04	-1.37*
L_2	-2.07*	-0.86*	-2.42*	-22.32	-0.26*	-0.14*	2.49*	2.82*	-3.66*	0.22*	-0.12*	-0.85*
L_3	4.66*	2.43*	-1.57*	-19.82	-0.17*	-0.11*	12.01*	1.70*	12.69*	0.19*	0.13*	4.24*
L_4	-0.48*	-0.47*	-0.34*	34.62*	0.53*	0.23*	-6.02*	-1.61*	-3.91*	0.29*	0.01	-0.41*
L_5	-2.05*	-1.40*	-5.80*	36.01*	0.16*	0.09*	-7.62*	-4.00*	-1.91*	-0.53*	-0.07	-1.61*
SE	0.15	0.10	0.15	12.75	0.03	0.03	0.14	0.08	0.14	0.04	0.02	0.16
Testers												
T_1	1.08*	3.09*	0.22	-2.22	0.17*	0.08*	4.19*	6.52*	-2.75*	0.29*	0.10*	-0.11*
T_2	0.91*	0.57*	1.76*	36.58*	0.05*	0.23*	0.61*	-2.99*	4.45*	-0.20*	-0.01	0.92*
T_3	-1.99*	-3.66*	-1.98*	-34.36*	-0.41*	-0.13*	-4.80*	-3.53*	-1.70*	-0.09*	-0.09*	-0.81*
SE	0.12	0.07	0.11	9.88	0.02	0.02	0.11	0.06	0.11	0.03	0.02	0.12

* Significant at 1% level

Table 7. sca effects of hybrids for various characters.

Crosses	Length of primary root	Number of secondary roots	Shoot / root ratio	Weight of nodules	Nitrogen content (at 50% flowering)	Nitrogen content (at maturity)	Plant height	Dry weight of plants	Number of pods	Number of seeds/ pod	100 grain weight	Grain yield / plant
L_1 x T_1	-0.96*	1.27*	-0.57*	16.39	-0.10	0.19*	-4.09*	-1.46*	-6.58*	-0.14	-0.17*	-1.95*
L_1 x T_2	-0.59*	0.08	-2.64*	-35.74	0.04	0.02	2.52*	0.18	0.02	0.06	-0.10*	-0.06*
L_1 x T_3	1.54*	-1.35*	3.21*	19.36	0.05	0.21*	1.57*	1.28*	6.56*	0.08	0.27*	2.01*
L_2 x T_1	-1.29*	0.19	-0.19	10.22	0.25*	0.16*	7.53*	-0.16	-2.20*	0.03	-0.16*	-0.69*
L_2 x T_2	-0.02	-0.10	-2.20*	-3.24	0.06	-0.14*	-2.62*	-0.66*	2.20*	-0.11	0.14*	0.27
L_2 x T_3	1.31*	-0.10	2.38*	-6.98	-0.30*	-0.03	-4.91*	0.82*	0.01	0.08	0.02	0.42
L_3 x T_1	2.41*	-0.46*	1.73*	22.56	0.06	-0.17*	2.34*	2.96*	4.91*	0.33*	0.29*	2.62*
L_3 x T_2	2.08*	0.38*	-1.17*	-61.74*	-0.83*	-0.27*	-1.78*	-1.03*	-1.56*	-0.18*	-0.13*	-0.79*
L_3 x T_3	-4.49*	0.08	-0.56*	39.19	0.77*	0.44*	-0.56*	-1.93*	-3.35*	-0.15*	-0.16*	-1.84*
L_4 x T_1	-0.25	-0.76*	-3.30*	-7.22	-0.21*	-0.11*	-4.79*	-0.60*	0.84*	0.13	0.01	-0.06
L_4 x T_2	-0.51	0.22	3.99*	10.48	0.07	0.09	4.59*	1.34*	-2.16*	-0.08	-0.08	-0.08
L_4 x T_3	0.75*	0.55*	-0.69*	-3.26	0.14*	0.03	0.20	-0.75*	1.32*	-0.05	0.06	0.14
L_5 x T_1	0.09	-0.23	2.32*	-41.94	-0.01	-0.07	-0.99*	-0.74*	3.04*	-0.35*	0.03	0.07
L_5 x T_2	-0.97*	-0.58*	2.02*	90.26*	0.67*	0.30*	-2.71*	0.17	1.51*	0.31*	0.17*	0.66
L_5 x T_3	0.89*	0.82*	-4.34*	-48.31*	-0.66*	-0.23*	3.70*	0.57*	-4.55*	-0.04	-0.20*	-0.74*
SE	0.26	0.17	0.25	22.08	0.06	0.05	0.25	0.14	0.24	0.07	0.04	0.27

* Significant at 1% level

lines viz., LBG622, COBG305 and Pant U19 expressed significant negative gca effects of -0.86, -0.47 and -1.40 respectively. Among testers AKU4 (3.09) and T9 (0.57) recorded significant and positive gca effects. VBN1 showed significant and negative gca effect of -3.66. Positive and significant sca effects were expressed by hybrids LBG17 x AKU4 (1.27), WBG13 x T9 (0.38), COBG305 x VBN1 (0.55) and Pant U19 x VBN1 (0.82). The sca effect was significant and negative for the hybrids LBG17 x VBN1 (-1.35), WBG13 x AKU4 (-0.46), COBG305 x AKU4 (-0.76) and Pant U19 x T9 (0.58).

4.2.3. Shoot/root ratio

Shoot/root ratio varied significantly among lines and line x tester. Significant and positive gca effect was exhibited by Pant U19 (5.80) among lines LBG17 (-1.47), LBG622 (-2.42), WBG13 (-1.57) and COBG305 (-0.34) recorded significant negative gca for this trait. Among testers gca effect was positive and significant for T9 (1.76). Negative and significant gca effect was shown by VBN1 (-1.98). AKU4 (0.22) recorded non-significant value. Among hybrids positive and significant sca effect was exhibited by LBG17 x VBN1 (3.21), LBG622 x VBN1 (2.38), WBG13 x AKU4 (1.73), COBG305 x T9 (3.99), Pant U19 x AKU4 (2.32) and Pant U19 x T9 (2.02). The sca effect was negative and significant for hybrids such as LBG17 x AKU4 (-0.57), LBG17 x T9 (-2.64), LBG622 x T9 (-2.20), WBG13 x T9 (-1.17), WBG13 x VBN1 (-0.56), COBG305 x AKU4 (-3.30), COBG305 x VBN1 (-0.69) and Pant U19 x VBN1 (-1.34).

4.2.4. Weight of nodules

For this trait there was no significant difference among lines, testers and line x tester. Among lines significant and positive gca effect was shown by COBG305 (34.62) and Pant U19 (36.01). LBG17 expressed significant negative gca effect of -28.49 WBG13 and COBG305 displayed non-significant gca effect. Positive and significant gca effect was exhibited by T9 (36.58) among testers. Significant and negative gca was observed in the case of VBN1 (-34.36). Among hybrids only one viz., Pant U19 x T9 (90.26) showed significant and positive sca effect. Negative and significant sca effect was recorded by WBG13 x T9 (-61.74) and Pant U19 x VBN1 (-48.31). All other hybrids showed non-significant sca effects.

4.2.5. Nitrogen content at 50 per cent flowering

Nitrogen content at 50 per cent flowering did not varied significantly among lines, testers and line x tester.

Positive and significant gca effect was shown by COBG305 (0.53) and Pant U19 x T9 (0.16), among lines. The gca effect was negative and significant for LBG17 (-0.25), LBG622 (-0.26) and WBG13 (-0.17). Among testers AKU4 (0.17) and T9 (0.23) displayed positive and significant gca effects. VBN1 exhibited negative and significant gca effects of -0.41. Out of the fifteen hybrids, only four viz., LBG622 x AKU4 (0.25), WBG13 x VBN1 (0.77), COBG305 x VBN1 (0.14) and Pant U19 x T9 (0.67) expressed significant and positive sca effect. Significant and negative sca effect was recorded by hybrids such as LBG622 x VBN1 (-0.30), WBG13 x T9 (-0.83), COBG305 x AKU4 (-0.21) and Pant U19 x T9 x VBN1 (-0.66).

4.2.6. Nitrogen content at maturity

No significant difference was recorded among lines, testers and line x tester for this character. Positive and significant gca effect was displayed by COBG305 (0.23) and Pant U19 (0.09) among lines LBG17 (-0.07), LBG622 (-0.14) and WBG13 (-0.11) showed negative and significant gca effects. Among testers, significant positive gca effect was exhibited by AKU4 (0.08) and T9 (0.05). In the case of VBN1 (-0.13) gca effect was significant and negative. Hybrids like LBG17 x AKU4 (0.19), LBG622 x AKU4 (0.16), WBG13 x VBN1 (0.44) and Pant U19 x T9 (0.30) expressed significant and positive sca effect. Negative and significant sca effect was displayed by LBG17 x VBN1 (-0.21), LBG622 x T9 (-0.14), WBG13 x AKU4 (-0.17), WBG13 x T9 (-0.27), COBG305 x AKU4 (-0.11) and Pant U19 x VBN1 (-0.23).

4.2.7. Plant height

The combining ability analysis for plant height displayed that lines, testers and line x tester differed significantly. Two genotypes such as LBG622 and WBG13 recorded significant and positive gca effects among lines with values 2.49 and 12.01 respectively. LBG17 (-0.86), COBG305 (-6.02), and

Pant U19 (-7.62) showed significant negative gca effect. Among testers gca effect was significant and positive for AKU4 (4.19) and T9 (0.61). It is negative and significant for VBN1. Hybrids like LBG17 x T9 (2.52), LBG17 x VBN1 (1.57), LBG622 x AKU4 (7.53), WBG13 x AKU4 (2.34), COBG305 x T9 (4.59) and Pant U19 x VBN1 (3.70) displayed significant and positive sca effect. Negative and significant sca effect was shown by LBG17 x AKU4 (-4.09), LBG622 x T9 (-2.62), LBG622 x VBN1 (-4.91), WBG13 x T9 (-1.78), WBG13 x VBN1 (-0.56), COBG305 x AKU4 (-4.79), Pant U19 x AKU4 (-0.99) and Pant U19 x T9 (-2.71).

4.2.8. Dry weight of plants

Dry weight of plants showed significant difference among lines, tester and line x tester. Three of the lines exhibited positive and significant gca effect ie., LBG17 (1.09), LBG622 (2.82) and WBG13 (1.70). Significant and negative gca effect was observed in COBG305 (-1.61) and Pant U19 (-4.00). Among testers only one viz., AKU4 (6.52) expressed significant and positive gca effect. T9 (-2.99) and VBN1 (-3.53) showed significant negative gca effect. Five hybrids such as LBG17 x VBN1 (1.28), LBG622 x VBN1 (0.82), WBG13 x AKU4 (2.96), COBG305 x T9 (1.34) and Pant U19 x VBN1 (0.57)displayed significant and positive sca effect. Negative and significant sca effect was recorded by LBG17 x AKU4 (-1.46), LBG622 x T9 (-0.66), WBG13 x T9 (-1.03), WBG13 x VBN1 (-1.93), COBG305 x AKU4 (-0.60), COBG305 x VBN1 (-0.75) and Pant U19 x AKU4 (-0.74).

4.2.9. Number of pods

Number of pods varied significantly among lines, testers and line x tester. WBG13 (12.69) alone recorded significant and positive gca effect among the line. Other four genotypes viz., LBG17 (-3.22), LBG622 (-3.66), COBG305 (-3.91) and Pant U19 (-1.91) showed significant negative gca effect. Among testers T9, exhibited positive and significant gca effect with a value of 4.45. AKU4 (-2.75) and VBN1 (-1.70) expressed significant and negative gca effect. Hybrids such as LBG17 x VBN1 (6.56), LBG622 x T9 (2.20), WBG13 x AKU4 (4.91), COBG305 x AKU4 (0.84), COBG305 x VBN1 (1.32), Pant U19 x AKU4 (3.04) and Pant U19 x T9 (1.51) displayed significant and positive sca effect. Among hybrids negative and significant sca effect was shown by LBG17 x AKU4 (-6.58), LBG622 x AKU4 (-2.20), WBG13 x T9 (-1.56), WBG13 x VBN1 (-3.35), COBG305 x T9 (-2.16) and Pant U19 x VBN1 (-4.55).

4.2.10. Number of seeds per pod

Number of seeds per pod exhibited significant difference among lines, testers and line x tester. Positive and significant gca effect was expressed by LBG622 (0.22), WBG13 (0.19) and COBG305 (0.29) among lines LBG17 and Pant U19 displayed significant and negative gca effects of -0.18 and -0.53 respectively. Among testers only on viz., AKU4 (0.29) recorded positive and significant gca effect. For T9 (-0.20) and VBN1 (-0.09) gca effect was negative and significant. Only two hybrid combinations such as WPG13 x

AKU4 (0.33) and Pant U19 x T9 (0.31) exhibited positive and significant sca effects. Three hybrids viz., WBG13 x T9 (-0.18), WBG13 x VBN1 (-0.15) and Pant U19 x AKU4 (-0.35) showed significant and negative sca effects.

4.2.11. 100 grain weight

No significant difference was noticed among lines, testers and line x tester for this trait. Only one genotype among lines displayed positive and significant gca effect ie., WBG13 (0.13). Negative and significant gca effect was shown by LBG622 (-0.12) and Pant U19 (-0.007). Among testers positive and significant gca effect was recorded by AKU4 (0.10). Significant and negative gca effect was observed in the case of VBN1 (-0.09). Out of the fifteen hybrids only four viz., LBG17 x VBN1 (0.27), LBG622 x T9 (0.14), WBG13 x AKU4 (0.29) and Pant U19 x T9 (0.17) exhibited positive and significant sca effects. Hybrid combinations such as LBG17 x AKU4 (-0.17), LBG17 x T9 (-0.10), LBG622 x AKU4 (-0.16), WBG13 x T9 (-0.13), WBG13 x VBN1 (-0.16) and Pant U19 x VBN1 (-0.20) recorded significant and negative sca effects.

4.2.12. Grain yield per plant

Grain yield per plant varied significantly among lies and line x tester. Among the lines only one viz., WBG13 (4.24) showed significant and positive gca effects. LBG17 (-1.37), LBG622 (-0.85), COBG305 (0.41) and Pant U19 (-1.61) displayed significant and negative gca effect. Among testers T9 (0.92) recorded significant and positive gca effect AKU4 (-0.11) and VBN1 (-0.81) exhibited negative and significant gca effect. Only two hybrids viz., LBG17 x VBN1 (2.01) and WBG13 x AKU4 (2.62) expressed significant and positive sca effect. For other hybrids viz., LBG17 x AKU4 (-1.95), LBG622 x AKU4 (-0.69), WBG13 x T9 (-0.79), WBG13 x VBN1 (-1.84) and Pant U19 x T9 x VBN1 (-0.74) sca effect was negative and significant.

4.3. Proportional contribution

Proportional contribution of lines, testers and line x testers to total variance was estimated and they are presented in table 8 and Fig. 1. Among different characters the proportional contribution of lines ranged from a minimum of 17.98% for number of secondary roots to a maximum of 71.35% for grain yield per plant. In testers also proportional contribution varied very widely from a minimum of 7.76% for grain yield per plant to a maximum of 78.09% for number of secondary roots. In line x tester hybrids range was from 3.94% for number of secondary roots to 64.98% for 100 grain weight.

Contribution of lines to total variance was high for characters shoot/ root ratio, number of seeds per pod, length of primary root, plant height, number of pods and grain yield per plant having values 51.76%, 56.26%, 56.76%, 65.19%, 65.34% and 71.35% respectively.

Contribution of testers to total variance was high for traits dry weight of plant (73.69%) and number of secondary roots (78.09%).

Table 8. Proportional contribution of line, tester and line x tester to the total variance

Sl. No.	Character	Line (%)	Tester (%)	Line x Tester (%)
1.	Length of primary root	56.76	18.43	24.81
2.	Number of secondary roots	17.98	78.09	3.94
3.	Shoot/root ratio	51.76	13.81	34.43
4.	Weight of nodules	27.64	27.69	44.67
5.	Nitrogen content (at 50% flowering)	27.57	24.70	47.73
6.	Nitrogen content (at maturity)	29.80	12.23	57.97
7.	Plant height	65.19	18.14	16.67
8.	Dry weight of plant	21.21	73.69	5.10
9.	Number of pods	65.34	16.16	18.50
10.	Number of seeds/pod	56.26	26.07	17.67
11.	100 grain weight	19.37	15.65	64.98
12.	Grain yield/plant	71.35	7.76	20.89

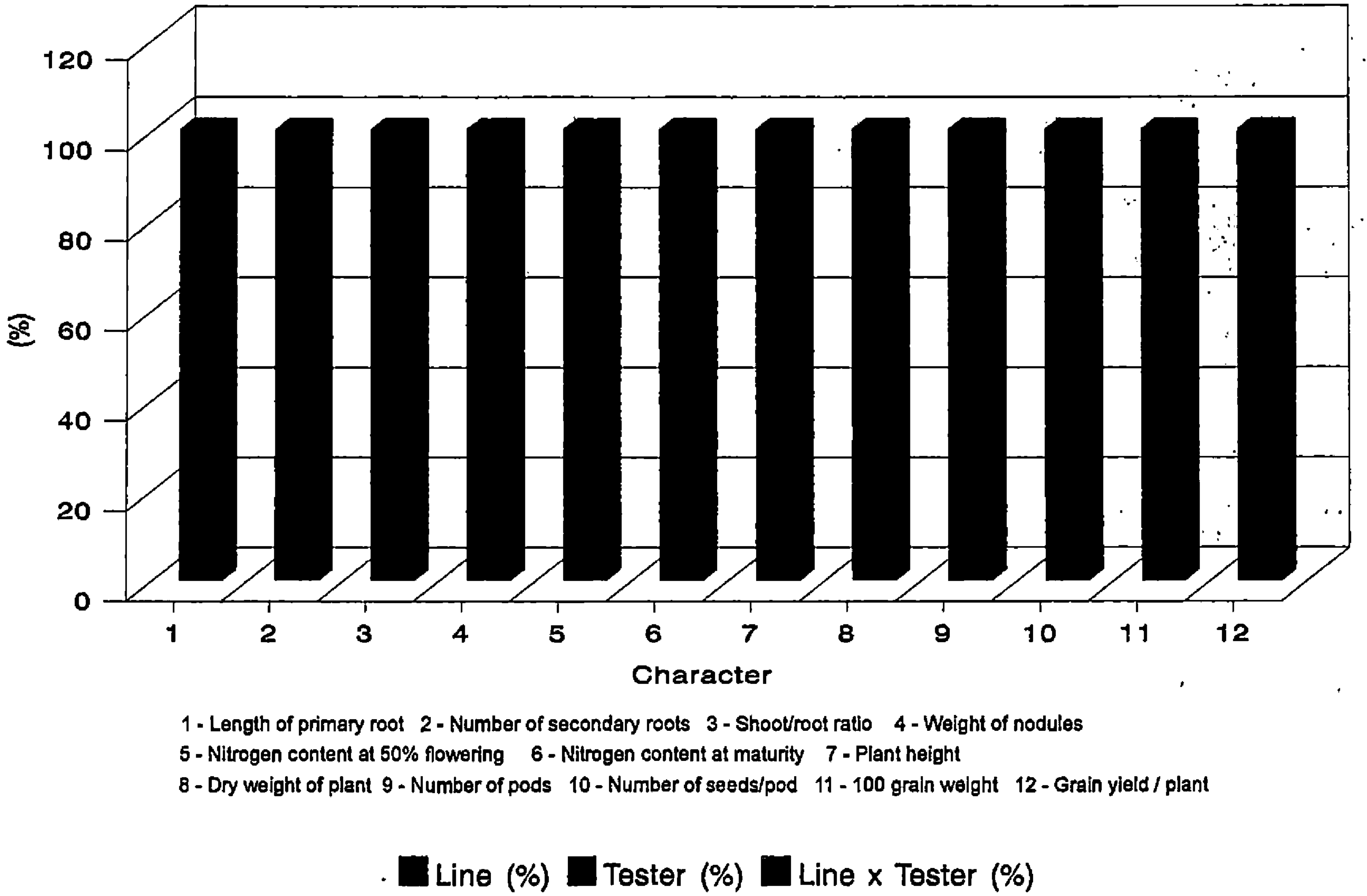

Fig. 1. Proportional contribution of lines, testers and line x testers to the total variance

4.4. Genetic components of variance

The additive variance (σ^2A) and dominance variance (σ^2D) were estimated and presented in table 9 and Fig. 2. For all the characters under study except number of secondary roots and dry weight of plants dominance variance was greater than additive variance. The additive to dominance variance ratio ranged from a minimum of 0.03 for nitrogen content at 50% flowering to a maximum of 1.49 for number of secondary roots. For nitrogen content at maturity and 100 grain weight this ratio was too small to be estimated. The ratio was low for characters such as weight of nodules (0.04) and shoot/root ratio (0.07). Medium values were observed for length of primary roots (0.14) grain yield per plant (0.19), number of pods (0.22), number of seeds per pod (0.24) and plant height (0.26). The ratio was high (1.09) for dry weight of plants.

4.5. Heterosis

From the mean values of parents and hybrids for different characters percentage of relative heterosis, heterobeltiosis and standard heterosis were estimated and the results are presented below.

4.5.1. Length of primary root

The hybrids exhibited significant heterosis for the length of primary root. Relative heterosis varied from -10.20% to 44.34%.

Table 9. Additive and dominance variances and the proportion of σ^2A to σ^2D

Sl. No.	Character	Additive variance (Lines) F = 1	Additive variance (Testers) F = 1	Additive variance (Pooled) F = 1	Dominance variance F = 1	Proportion of σ^2A to σ^2D
1.	Length of primary root	23.8	7.88	2.76	19.71	0.14
2.	Number of secondary roots	7.94	45.92	4.20	2.82	1.49
3.	Shoot/root ratio	29.57	5.35	3.09	43.95	0.07
4.	Weight of nodules	806.07	3010.99	301.38	8226.29	0.04
5.	Nitrogen content (at 50% flowering)	0.06	0.26	0.03	1.19	0.03
6.	Nitrogen content (at maturity)	n.e	n.e	n.e	0.28	n.e
7.	Plant height	214.17	63.17	24.26	93.91	0.26
8.	Dry weight of plant	26.95	125.52	11.96	10.98	1.09
9.	Number of pods	174.93	43.18	19.17	86.31	0.22
10.	Number of seeds/pod	0.41	0.22	0.05	0.21	0.24
11.	100 grain weight	n.e	n.e	n.e	0.18	n.e
12.	Grain yield/plant	19.89	0.99	1.88	9.94	0.19

F = Inbreeding coefficient n.e = not estimable

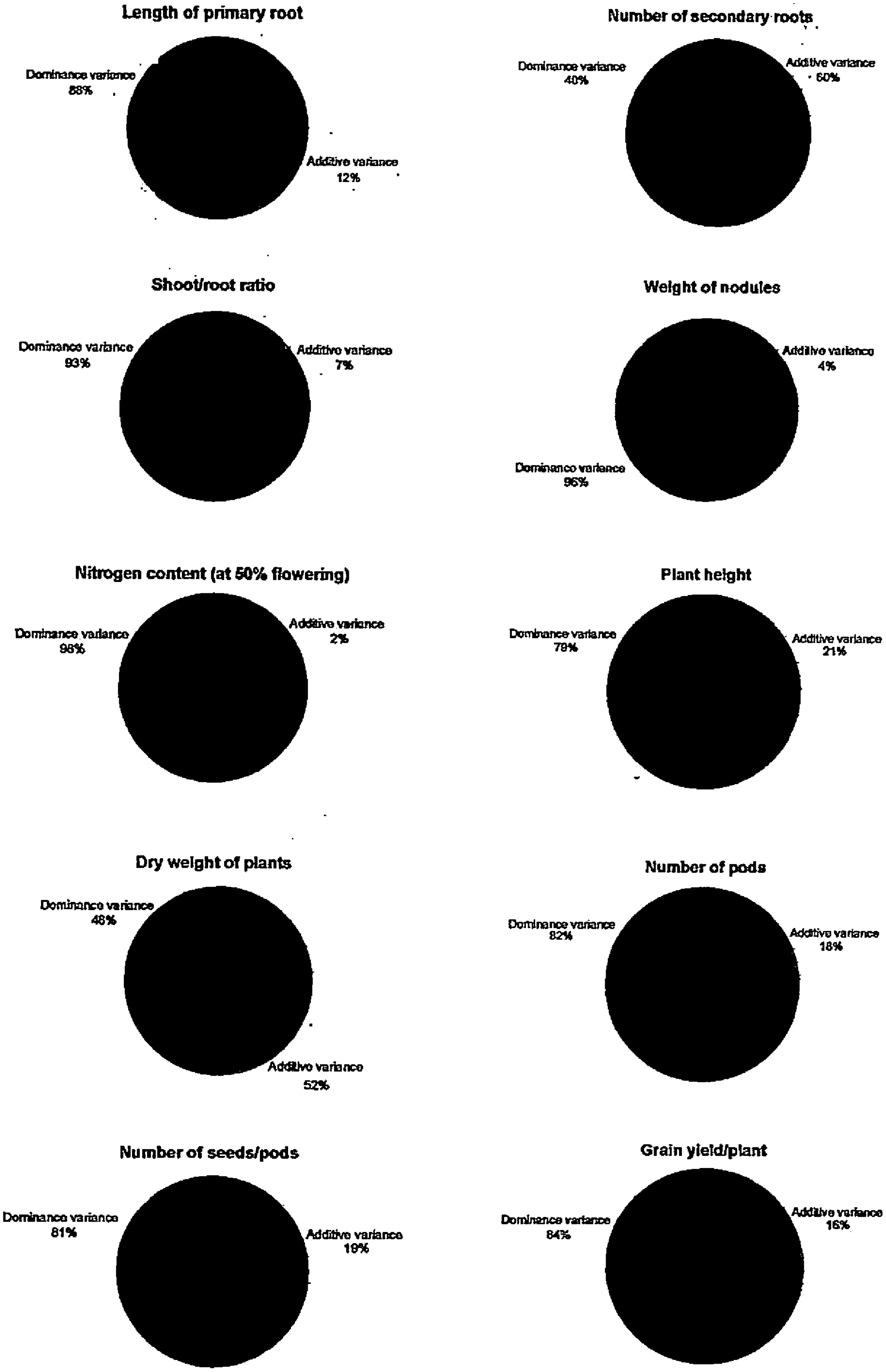

Fig. 2. Magnitude of additive and dominance variances

Except WBG13 x VBN1 all the hybrids exhibited positive heterosis and it was significant in all the cases. Among hybrid combinations with positive relative heterosis WBG13 x AKU4 had recorded highest relative heterosis of 44.34% followed by WBG13 x T9 (43.61%).

Heterobeltiosis was found to be positive and significant for all hybrid combinations except LBG622 x VBN1, WBG13 x VBN1, Pant U19 x T9 and Pant U19 x VBN1. Negative and significant heterobeltiosis was exhibited by WBG13 x VBN1 (-29.41%). Among hybrid combinations with positive heterobeltiosis WBG13 x AKU4 had recorded highest value of 23.89%.

Positive and significant standard heterosis was displayed only by two hybrids viz., WBG13 x AKU4 (23.89%) and WBG13 x T9 (21.21%). In all other hybrids standard heterosis was negative and significant (table 10 and Fig. 3).

4.5.2. Number of secondary roots

Relative heterosis for number of secondary roots was found to be significant and positive for all the hybrid combinations except LBG17 x VBN1, LBG622 x VBN1, COBG305 x VBN1 and Pant U19 x VBN1. Among hybrids with significant positive relative heterosis highest value was observed in WBG13 x T9 (45.38% followed by LBG622 x T9 (35.65%). Negative and significant relative heterosis was displayed by LBG17 x VBN1 (-20.61%) and LBG622 x VBN1 (-5.23%).

Table 10. Estimate of heterosis for length of primary root and number of secondary roots.

Parents/Hybrids	Length of primary root					Number of secondary roots				
	Mean	MP	Heterosis %			Mean	MP	Heterosis %		
			RH	HB	SH			RH	HB	SH
L_1	12.87					12.40				
L_2	10.50					9.07				
L_3	18.70					12.97				
L_4	11.17					10.63				
L_5	10.93					8.63				
T_1	13.40					15.93				
T_2	12.87					10.10				
T_3	10.70					9.43				
L_1 x T_1	15.07	13.14	14.72*	12.44*	-19.43*	18.03	14.17	27.29*	13.18*	13.18*
L_1 x T_2	15.27	12.87	18.65*	18.65*	-18.36*	14.33	11.25	27.41*	15.59*	-10.04*
L_1 x T_3	14.50	11.79	23.06*	12.69*	-22.46*	8.67	10.92	-20.61*	-30.11*	-45.61*
L_2 x T_1	12.73	11.95	6.56*	-4.98*	-31.91*	15.80	12.50	26.40*	-0.84	-0.84
L_2 x T_2	13.38	11.69	18.40*	7.51*	-26.02*	13.00	9.59	35.65*	28.71*	-18.41*
L_2 x T_3	12.27	10.60	15.72*	14.64*	-34.40*	8.77	9.25	-5.23*	-7.07*	-44.98*
L_3 x T_1	23.17	16.05	44.34*	23.89*	23.89*	18.43	14.45	27.57*	15.69*	15.69*
L_3 x T_2	22.67	15.79	43.61*	21.21*	21.21*	16.77	11.54	45.38*	29.31*	5.23*
L_3 x T_3	13.20	14.70	-10.20*	-29.41*	-29.41*	12.23	11.20	9.23*	-5.66*	-23.22*
L_4 x T_1	15.37	12.29	25.10*	14.68*	-17.83*	15.23	13.28	14.68*	-4.39*	-4.39*
L_4 x T_2	14.93	12.02	24.27*	16.06*	-20.14*	13.7	10.37	32.15*	28.84*	-14.02*
L_4 x T_3	13.30	10.94	21.64*	19.10*	-28.88*	9.80	10.03	-2.33*	-7.84*	-38.49*
L_5 x T_1	14.13	12.17	16.16*	5.47	-24.42*	14.83	12.28	20.76*	-6.90*	-6.90*
L_5 x T_2	12.90	11.90	8.40*	0.26	-31.02*	11.97	9.37	27.76*	18.48*	-24.89*
L_5 x T_3	11.87	10.82	9.71*	8.54*	-36.54*	9.13	9.03	1.11	-3.18	-42.68*
CD (0.05)			0.64	0.74	0.74			0.41	0.47	0.47

* Significant at 1% level

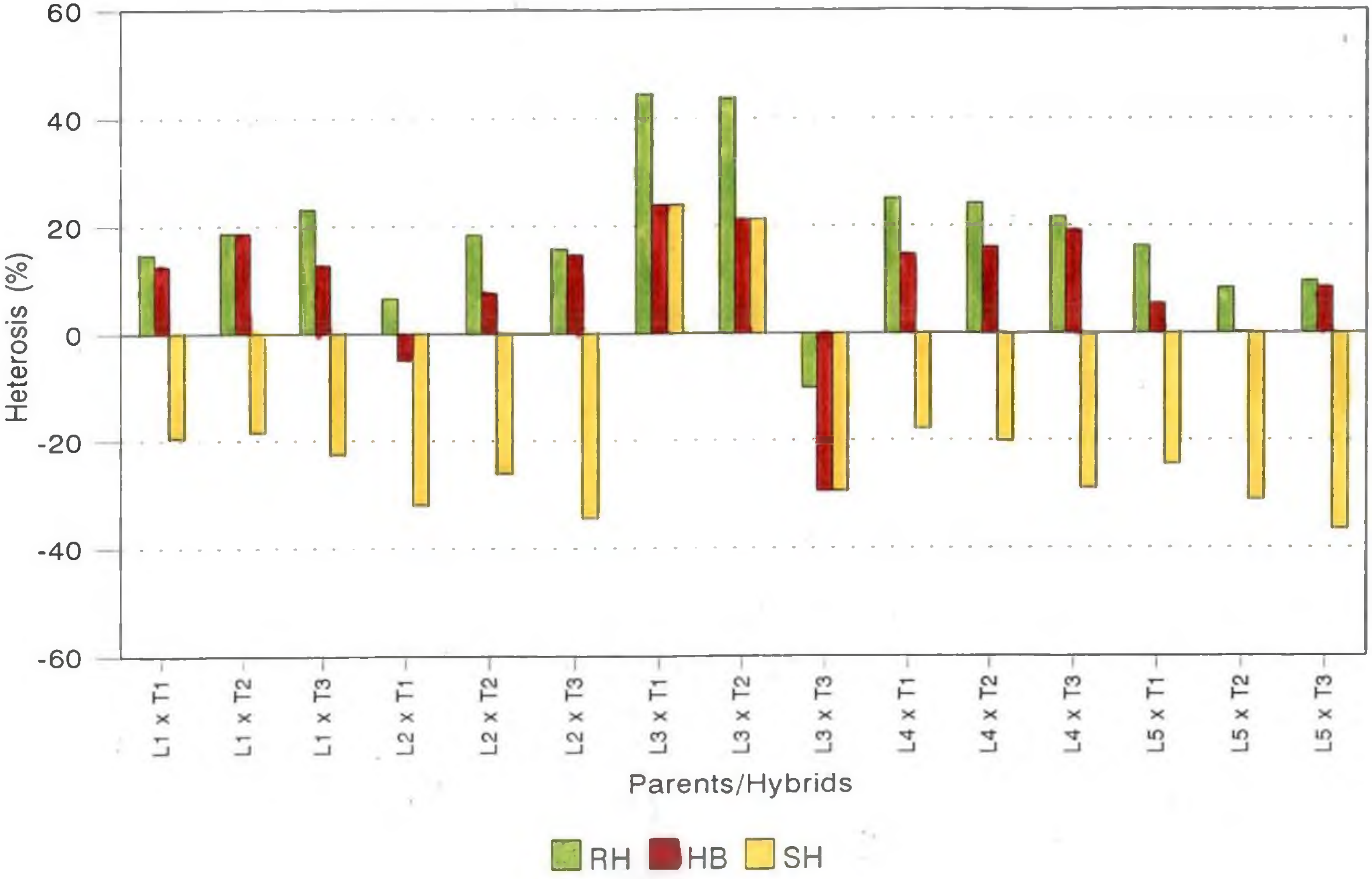

Fig. 3. Estimate of heterosis in blackgram - Length of primary root

Heterobeltiosis was found to be positive and significant for the hybrids viz., LBG17 x AKU4 (13.18%), LBG17 x T9 (15.59%), WBG13 x AKU4 (15.69%), Pant U19 x T9 (18.48%), LBG622 x T9 (28.71%), COBG305 x T9 (28.84%) and WBG13 x T9 (29.31%). Negative and highest significant heterobeltiosis was recorded by LBG17 x VBN1 (-30.11%).

Only three hybrids viz., WBG13 x T9 (5.23%), LBG17 x AKU4 (13.18%) and WBG13 x AKU4 (15.69%) expressed positive and significant standard heterosis. Significant negative standard heterosis was observed in the hybrid LBG17 x VBN1 (-45.61%) (table 10).

4.5.3. Shoot/root ratio

Significant and positive relative heterosis was recorded by the crosses viz., COBG305 x VBN1 (7.30%), Pant U19 x T9 (13.69%), COBG305 x T9 (14.14%), WBG13 x AKU4 (17.43%), Pant U19 x AKU4 (17.58%), WBG13 x VBN1 (17.90%), LBG622 x VBN1 (24.58%) and LBG17 x VBN1 (32.97%). Three hybrids such as LBG17 x T9 (-9.60%), LBG622 x T9 (-10.93%) and COBG305 x AKU4 (-12.0%) showed significant and negative heterosis.

Among the fifteen hybrids only five recorded significant and positive heterobeltiosis. They are Pant U19 x AKU4 (6.29%), Pant U19 x T9 (10.30%), WBG13 x VBN1 (17.21%), LBG622 x VBN1 (18.83%) and LBG17 x VBN1 (25.57%). Highest negative and significant value for heterobeltiosis was shown by LBG622 x T9 (-27.07%).

Only two hybrid combinations viz., Pant U19 x AKU4 (6.29%) and Pant U19 x T9 (10.30%) displayed significant and positive standard heterosis. All other hybrids expressed significant and negative standard heterosis. Highest negative standard heterosis was exhibited by WBG13 x VBN1 (-34.27%) (table 11).

4.5.4. Weight of nodules

In general relative heterosis was found to be positive and significant in all hybrids except for LBG17 x T9 (-2.20%) and Pant U19 x VBN1 (38.44%). Positive relative heterosis ranged from 38.44% to 453.62%, WBG13 x VBN1 exhibited highest relative heterosis 456.62% followed by WBG13 x AKU4 (422.10%).

Positive and significant heterobeltiosis was shown by hybrids like COBG305 x AKU4 (42.25%), COBG305 x T9 (56.1%), Pant U19 x T9 (58.93%), LBG622 x AKU4 (82.52%), WBG13 x VBN1 (266.48%) and WBG13 x AKU4 (292.68%). Only one hybrid combination ie., Pant U19 x VBN1 (-25.44%) displayed negative and significant heterobeltiosis.

Only two hybrids such as COBG305 x T9 (26.24%) and Pant U19 x T9 (58.93%) expressed positive and significant standard heterosis. COBG305 x AKU4 (3.49%) recorded positive and non-significant standard heterosis. Hybrid combinations Pant U19 x VBN1 (-25.44%) and LBG622 x VBN1 (-32.28%) recorded significant negative standard heterosis (table 11 and Fig. 4).

Table 11. Estimate of heterosis for shoot/root ratio weight of nodules.

Parents/Hybrids	Shoot / root ratio					Weight of nodules				
	Mean	MP	Heterosis %			Mean	MP	Heterosis %		
			RH	HB	SH			RH	HB	SH
L_1	19.17					216.67				
L_2	18.77					59.17				
L_3	17.23					180.67				
L_4	22.67					248.33				
L_5	30.73					29.83				
T_1	24.83					29.83				
T_2	29.43					200.83				
T_3	17.03					19.17				
L_1 x T_1	22.5	22.0	2.27	-9.4*	-26.79*	217.5	123.25	76.47*	0.38	-12.42
L_1 x T_2	21.97	24.3	-9.60*	-25.37*	-28.52*	204.17	208.75	-2.20	-5.77	-17.79
L_1 x T_3	24.07	18.1	32.97*	25.57*	-21.69*	188.33	117.92	59.72*	-13.08	-24.16
L_2 x T_1	21.93	21.8	0.61	-11.68*	-28.63*	217.5	74.5	191.95*	82.52*	-12.42
L_2 x T_2	21.47	24.1	-10.93*	-27.07*	-30.15*	242.83	160.0	51.77*	20.91	-2.21
L_2 x T_3	22.3	17.9	24.58*	18.83*	-27.44*	168.17	69.17	143.13*	41.12	-32.28*
L_3 x T_1	24.7	21.03	17.43*	-0.54	-19.63*	232.33	44.5	422.10*	292.68*	-6.44
L_3 x T_2	23.33	23.33	0.0	-20.72*	-24.07*	186.83	130.0	43.72*	-6.97	-24.77
L_3 x T_3	20.2	17.13	17.9*	17.21*	-34.27*	216.83	39.17	453.62*	266.48*	-12.68
L_4 x T_1	20.9	13.75	-12.0*	-15.84*	-32.0*	257.0	105.25	144.18*	42.25*	3.49
L_4 x T_2	29.73	26.05	14.14*	1.02	-3.25*	313.5	190.75	64.35*	56.1*	26.24*
L_4 x T_3	21.3	19.85	7.30*	-6.03*	-30.69*	228.83	99.92	129.02*	26.66	-7.75
L_5 x T_1	32.67	27.78	17.58*	6.29*	6.29*	223.67	139.08	60.81*	-9.93	-9.93
L_5 x T_2	33.90	30.08	12.69*	10.30*	10.30*	394.67	224.58	75.73*	58.93*	58.93*
L_5 x T_3	23.80	23.88	-0.35	-22.56*	-22.56*	185.17	133.75	38.44	-25.44*	-25.44*
CD (0.05)		0.62	0.72	0.72				54.58	63.02	63.02

* Significant at 1% level

Fig. 4. Estimate of heterosis in blackgram - Weight of nodules

4.5.5. Nitrogen content at 50 per cent flowering

Significant and positive relative heterosis was observed in all hybrids except LBG622 x VBN1 (-2.70%) and WBG13 x T9 (2.72%). Highest positive and significant relative heterosis was displayed by WBG13 x VBN1 (40.61%) followed by COBG305 x VBN1 (38.14%).

All hybrids except WBG13 x T9 and LBG622 x T9 recorded positive significant heterobeltiosis. Negative and significant heterobeltiosis was shown by Pant U19 x VBN1 (-9.86%) and LBG622 x VBN1 (-18.71%). Highest positive and significant heterobeltiosis was recorded by COBG305 x T9 (36.36%) followed by LBG17 x VBN1 (31.73%) and Pant U19 x T9 (31.69%).

Standard heterosis was found to be positive and significant in hybrids like LBG622 x AKU4 (3.23%), WBG13 x VBN1 (3.84%), COBG305 x VBN1 (5.16%), Pant U19 x AKU4 (6.45%), COBG305 x AKU4 (9.68%), COBG305 x T9 (16.13%) and Pant U19 x T9 (20.65%) (table 12 and Fig. 5).

4.5.6. Nitrogen content at maturity

Relative heterosis was observed to be positive and significant for all the hybrids tested except three which had non-significant values viz., LBG622 x T9 (-3.03%), LBG622 x VBN1 (-1.05%) and WBG13 x T9 (0.54). Among hybrids highest positive relative heterosis of 27.49% was shown by LBG17 x AKU4 followed by Pant U19 x T9 (24.06%).

Table 12. Estimate of heterosis for nitrogen content at 50% flowering and maturity.

Parents/Hybrids	Nitrogen content at 50% flowering					Nitrogen content at maturity				
	Mean	MP	Heterosis %			Mean	MP	Heterosis %		
			RH	HB	SH			RH	HB	SH
L_1	3.47					2.67				
L_2	5.17					3.47				
L_3	4.17					3.13				
L_4	4.17					3.13				
L_5	4.73					3.10				
T_1	4.27					3.03				
T_2	4.4					3.13				
T_3	3.47					2.87				
L_1 x T_1	5.00	3.87	29.31*	17.19*	-3.23*	3.63	2.85	27.49*	19.78*	4.81*
L_1 x T_2	5.20	3.94	32.20*	18.18*	0.65*	3.43	2.9	18.39*	9.57*	-0.96*
L_1 x T_3	4.57	3.47	31.73*	31.73*	-11.61*	3.03	2.77	9.64*	5.81*	-12.50*
L_2 x T_1	5.33	4.72	13.07*	3.23*	3.23*	3.53	3.25	8.72*	1.92*	1.92*
L_2 x T_2	5.20	4.79	8.71*	0.65*	0.65*	3.2	3.3	-3.03*	-7.69*	-7.69*
L_2 x T_3	4.2	4.32	-2.70*	-18.71*	-18.71*	3.13	3.17	-1.05*	-9.61*	-9.62*
L_3 x T_1	5.23	4.22	24.11*	22.66*	1.29*	3.23	3.03	6.59*	6.59*	-6.73*
L_3 x T_2	4.4	4.29	2.72*	0*	-14.84*	3.1	3.08	0.54*	-1.06*	-10.58*
L_3 x T_3	5.37	3.82	40.61*	28.80*	3.87*	3.63	2.95	23.16*	19.78*	4.81*
L_4 x T_1	5.67	4.34	30.77*	28.79*	9.68*	3.63	3.08	17.84*	15.96*	4.81*
L_4 x T_2	6.0	4.4	36.36*	36.36*	16.13*	3.8	3.13	21.28*	21.28*	9.62*
L_4 x T_3	5.43	3.94	38.14*	23.48*	5.16*	3.57	3.0	18.89*	13.83*	2.88*
L_5 x T_1	5.50	4.50	22.22*	16.20*	6.45*	3.53	3.07	15.22*	13.98*	1.92*
L_5 x T_2	6.23	4.57	36.50*	31.69*	20.69*	3.87	3.12	24.06*	23.40*	11.54*
L_5 x T_3	4.27	4.10	4.07*	-9.86*	-17.42*	3.17	2.99	6.15*	2.15*	-8.65*
CD (0.05)			0.14	0.16	0.16			0.12	0.14	0.14

* Significant at 1% level

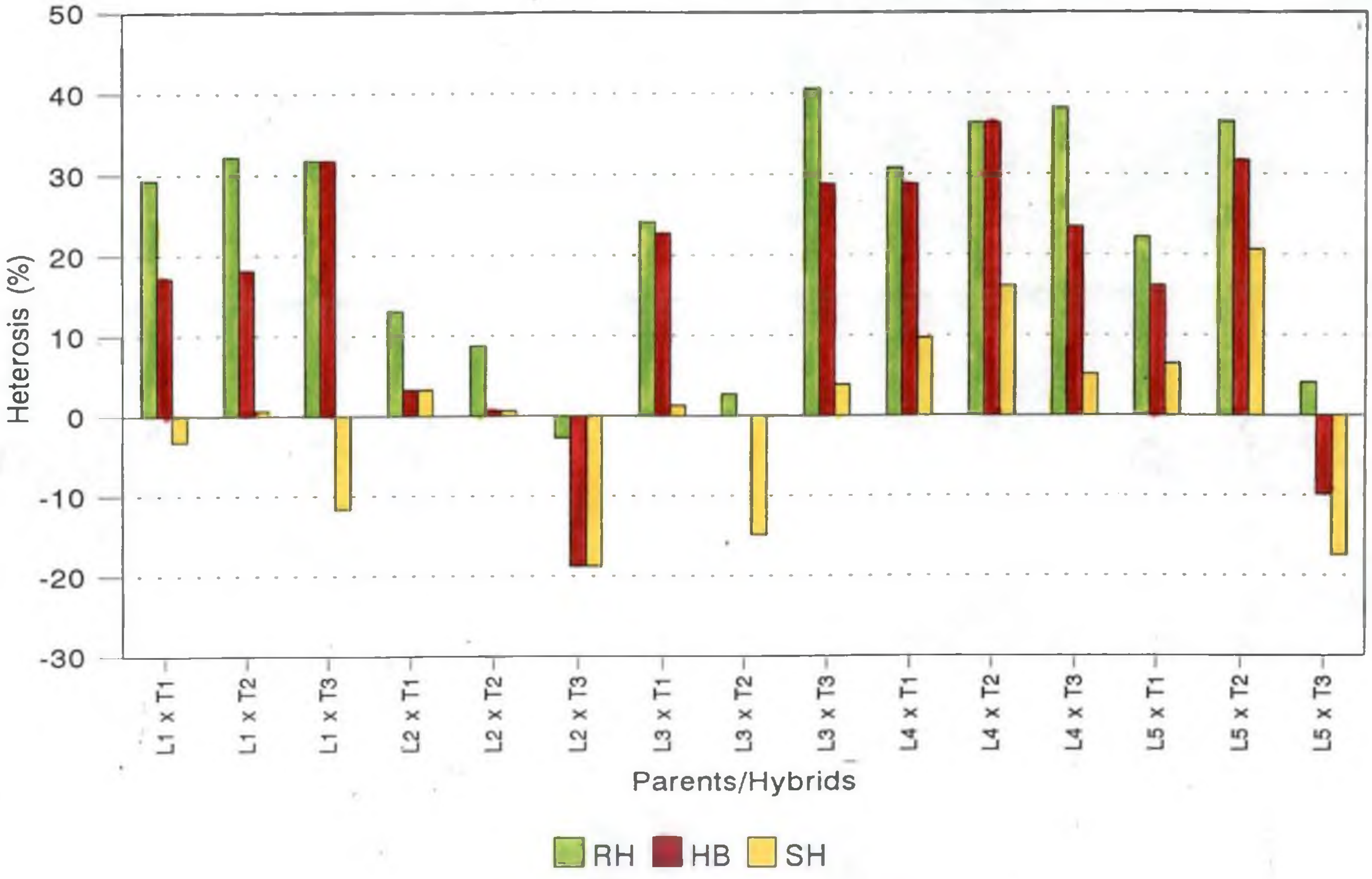

Fig. 5. Estimate of heterosis in blackgram - Nitrogen content at 50% flowering

Among hybrids with positive heterobeltiosis all others except LBG622 x AKU4 (1.92%) and Pant U19 x VBN1 (2.15%) were with significant values. Highest positive heterobeltiosis was shown by Pant U19 x T9 (23.40%) followed by COBG305 x T9 (21.28%).

Significant and positive standard heterosis was exhibited by crosses like LBG17 x AKU4 (4.81%), WBG13 x VBN1 (4.81%), COBG305 x AKU4 (4.81%), COBG305 x T9 (9.62%) and Pant U19 x T9 (11.54%). The hybrid LBG17 x VBN1 showed maximum negative and significant standard heterosis of -12.50% followed by WBG13 x T9 (-10.8%) (Table 12).

4.5.7. Plant height

All hybrid combinations displayed significant positive relative heterosis for plant height. The values ranged from 6.87% to 75.80%. Maximum positive relative heterosis of 75.80% was shown by COBG305 x T9 followed by Pant U19 x VBN1 (58.66%).

Heterobeltiosis was positive and significant for all hybrids except three viz., LBG17 x AKU4 (-4.18%), Pant U19 x AKU4 (-12.70%) and COBG305 x AKU4 (-17.82%) which had significant negative heterosis. Maximum positive heterobeltiosis was recorded by COBG305 x T9 (57.93%) followed by Pant U19 x VBN1 (57.17%).

For all hybrids, except three standard heterosis was negative and significant. Significant positive heterosis was exhibited by WBG13 x VBN1 (1.89%) and WBG13 x T9 (10.68%), WBG13 x VBN1 (1.89%), WBG13 x T9 (10.68%) WBG13 x AKU4 (26.82%). Maximum negative heterosis was recorded by COBG305 x VBN1 (-34.29%) followed by Pant U19 x T9 (-32.40%) (Table 13).

4.5.8. Dry weight of plants

Among hybrids with positive relative heterosis all, except WBG13 x VBN1 had significant values. Positive relative heterosis ranged from 4.07% to 105.73%. Maximum positive relative heterosis of 105.73% was shown by LBG622 x VBN1 followed by LBG622 x AKU4 (75.52%).

Among the hybrids with positive heterobeltiosis, Pant U19 x VBN1 recorded non-significant value and others showed significant values. Significant positive heterobeltiosis ranged from 6.09% to 70.95%. LBG622 x VBN1 displayed highest positive heterobeltiosis. Maximum negative heterosis was recorded by Pant U19 x T9 (-44.28%).

Standard heterosis was negative and significant for all hybrids except three viz., LBG17 x AKU4 (6.09%), LBG622 x AKU4 (23.97%) and WBG13 x AKU4 (35.76%) which had significant positive value. Standard heterosis was maximum and negative in the case of Pant U19 x VBN1 (-71.12%) followed by Pant U19 x T9 (-70.33%) (table 13).

Table 13. Estimate of heterosis for plant height and dry weight of plants.

Parents/Hybrids	Nitrogen content at 50% flowering					Nitrogen content at maturity				
	Mean	MP	Heterosis %			Mean	MP	Heterosis %		
			RH	HB	SH			RH	HB	SH
L_1	34.13					8.97				
L_2	32.57					7.00				
L_3	47.73					10.93				
L_4	20.77					5.10				
L_5	20.77					3.07				
T_1	43.03					16.97				
T_2	26.07					9.03				
T_3	21.17					9.03				
L_1 x T_1	41.23	38.58	6.87*	-4.18*	-13.62*	18.00	12.97	38.82*	6.09*	6.09*
L_1 x T_2	44.27	30.10	47.07*	29.69*	-7.26*	10.13	9.00	12.59*	12.18*	-40.28*
L_1 x T_3	37.90	27.65	37.07*	11.04*	-20.60*	10.70	6.80	57.35*	19.33*	-36.94*
L_2 x T_1	56.20	37.80	48.68*	30.60*	17.74*	21.03	11.99	75.52*	23.97*	23.97*
L_2 x T_2	42.47	29.32	44.86*	30.40*	-11.03*	8.02	37.63	22.14*	-34.97*	*
L_2 x T_3	34.77	26.87	29.40*	6.76*	-27.16*	11.97	5.82	105.73*	70.95*	-29.47*
L_3 x T_1	60.53	45.38	33.38*	26.82*	26.82*	23.03	13.95	65.11*	35.76*	35.76*
L_3 x T_2	52.83	36.90	4318*	10.68*	10.68*	8.10	7.78	4.07*	-25.91*	-52.26*
L_3 x T_3	48.63	34.45	41.17*	1.89*	1.89*	16.17	11.04	46.53*	-4.72*	-4.72*
L_4 x T_1	35.37	31.90	10.87*	-17.82*	-25.91*	8.59	7.07	21.70*	-4.80*	-49.31*
L_4 x T_2	41.17	23.42	75.80*	57.93*	-13.76*	5.97	4.87	22.60*	16.99*	-64.83*
L_4 x T_3	31.37	20.97	49.60*	48.19*	-34.29*	5.97	4.87	22.60*	16.99*	-64.83*
L_5 x T_1	35.57	31.90	17.76*	-12.70*	-21.30*	13.63	10.02	36.11*	-19.65*	-19.65*
L_5 x T_2	32.27	23.42	37.79*	23.79*	-32.40*	5.03	6.05	-16.80*	-44.28*	-70.33*
L_5 x T_3	20.97	58.66	57.17*	-30.31*	4.9*	3.85	27.27	5.76*	-71.12*	
CD (0.05)			0.61	0.71	0.71			0.34	0.39	0.39

* Significant at 1% level

4.5.9. Number of pods

Significant and positive relative heterosis was recorded by all the fifteen hybrid combinations. The range was from 36.43% to 141.11%. Highest value was shown by LBG17 xVBN1 (141.11%) followed by WBG13 x VBN1 (137.71%).

Positive and significant heterobeltiosis was displayed by all the hybrids studied. Maximum positive heterobeltiosis was exhibited by LBG17 x VBN1 (127.36%) followed by WBG13 x VBN1 (121.35%) and WBG13 x AKU4 (104.10%).

Only one hybrid combination viz., LBG17 x AKU4 (-8.14%) showed negative and significant standard heterosis. All others exhibited significant and positive standard heterosis. Highest positive standard heterosis of 71.78% was displayed by WBG13 x T9 followed by WBG13 x AKU4 (69.70%) (table 14 and Fig. 6).

4.5.10. Number of seeds per pod

Relative heterosis was positive and significant for the hybrids viz., LBG17 x VBN1 (3.37%), Pant U19 x VBN1 (3.93%), Pant U19 x T9 (4.42%), LBG622 x T9 (5.06%), COBG305 x VBN1 (6.01%), COBG305 x AKU4 (10.76%), WBG13 x AKU4 (10.88%), LBG622 x VBN1 (12.64%) and LBG622 x AKU4 (13.50%). Significant negative relative heterosis was recorded by WBG13 x T9 (-2.90%).

Table 14. Estimate of heterosis for number of pods and seeds/pod.

Parents/Hybrids	Number of pods					Number of seeds / pod				
	Mean	MP	Heterosis %			Mean	MP	Heterosis %		
			RH	HB	SH			RH	HB	SH
L_1	18.13					6.27				
L_2	15.53					6.00				
L_3	23.73					6.77				
L_4	22.73					6.60				
L_5	16.93					5.43				
T_1	29.27					6.10				
T_2	35.20					5.87				
T_3	20.47					5.60				
$L_1 \times T_1$	32.33	23.7	36.43*	10.48*	-8.14*	6.30	6.19	1.89*	0.53*	-6.90*
$L_1 \times T_2$	46.13	26.67	73.00*	31.06*	31.06*	6.13	5.94	3.37*	-2.13*	-9.36*
$L_1 \times T_3$	46.53	19.3	141.11*	127.36*	32.20*	6.13	5.94	3.37*	-2.13*	-9.36*
$L_2 \times T_1$	36.27	22.4	61.90*	23.92*	3.03*	6.87	6.05	13.50*	12.57*	1.48*
$L_2 \times T_2$	47.87	25.37	88.70*	35.98*	35.98*	6.23	5.94	5.06*	3.89*	-7.88*
$L_2 \times T_3$	39.53	18.00	119.63*	93.16*	12.31*	6.53	5.80	12.64*	8.89*	-3.45*
$L_3 \times T_1$	59.73	26.5	125.41*	104.10*	69.70*	7.13	6.44	10.88*	5.42*	5.42*
$L_3 \times T_2$	60.47	29.47	105.20*	71.78*	71.78*	6.13	6.32	-2.90*	-9.36*	-9.36*
$L_3 \times T_3$	52.53	22.1	137.71*	121.35*	49.24*	6.27	6.19	1.35*	-7.39*	-7.39*
$L_4 \times T_1$	39.07	25.80	51.42*	33.49*	10.98*	7.03	6.35	10.76*	6.57*	3.94*
$L_4 \times T_2$	43.27	28.77	50.41*	22.92*	22.92*	6.33	6.24	1.60*	-4.04*	-6.40*
$L_4 \times T_3$	40.60	21.40	89.72*	81.79*	15.34*	6.47	6.10	6.01*	-2.02*	-4.43*
$L_5 \times T_1$	43.24	23.1	87.30*	47.84*	22.92*	5.73	5.77	-0.58*	-6.01*	-2.02*
$L_5 \times T_2$	48.93	26.07	87.72*	39.02*	39.02*	5.90	5.65	4.42*	0.57*	12.81*
$L_5 \times T_3$	36.73	18.7	96.43*	79.48*	4.36*	5.73	5.52	3.93*	2.38*	-15.27*
CD (0.05)			0.60	0.70	0.70			0.17	0.20	0.20

* Significant at 1% level

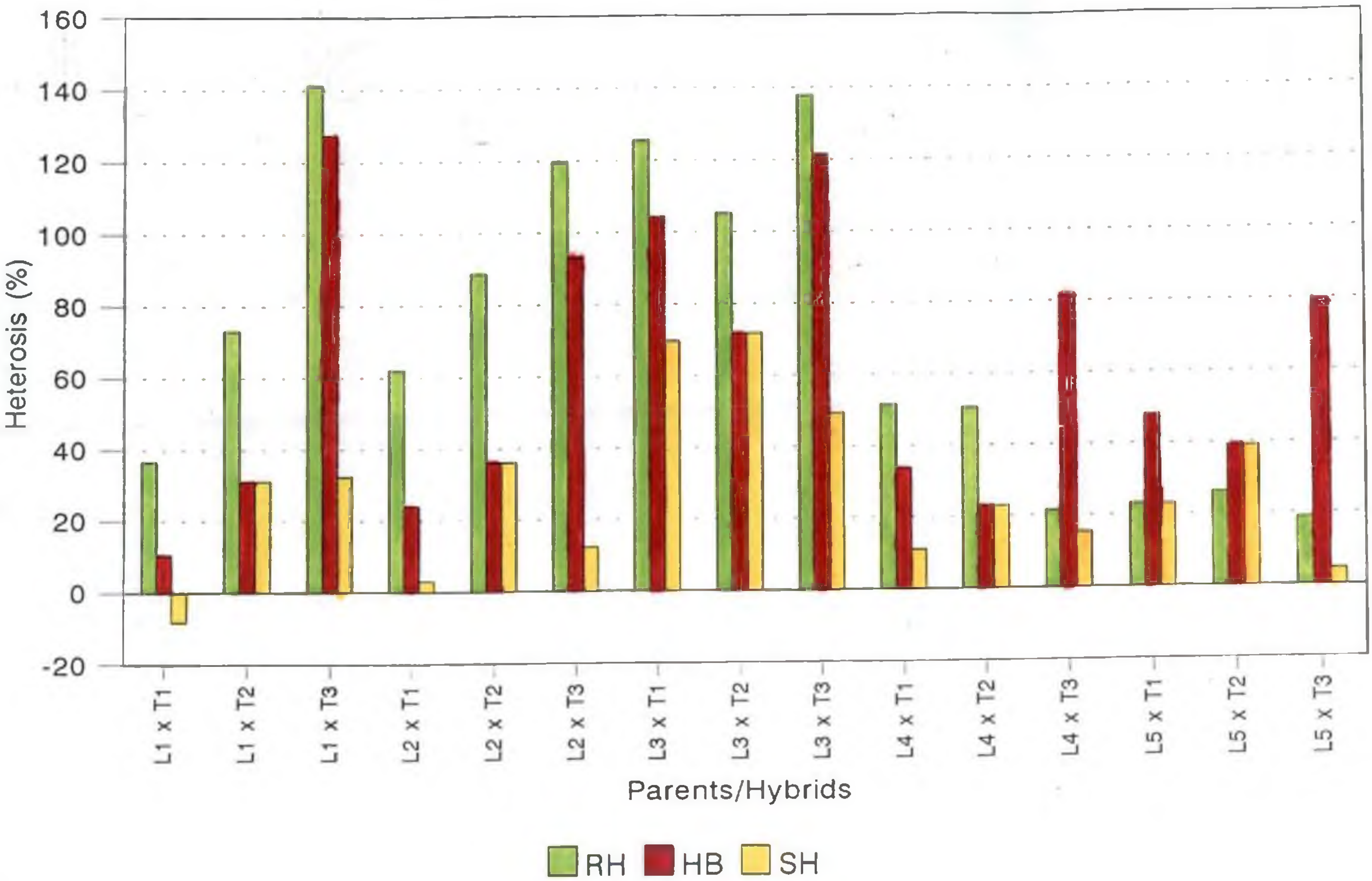

Fig. 6. Estimate of heterosis in blackgram - Number of pods

Heterobeltiosis was found to be significant and positive for hybrids like LBG622 x T9 (3.89%), WBG13 x AKU4 (5.42%), COBG305 x AKU4 (6.57%), LBG622 x VBN1 (8.89%) and LBG622 x AKU4 (12.57%). Significant negative heterobeltiosis was maximum in the hybrid WBG13 x VBN1 (-7.39%) followed by Pant U19 x T9 x AKU4 (-6.01%).

Positive and significant standard heterosis was recorded by three hybrids viz., COBG305 x AKU4 (3.94%), WBG13 x AKU4 (5.42%) and Pant U19 x T9 (12.81%). Highest significant negative standard heterosis was exhibited by Pant U19 x AKU4 (-15.27%) followed by LBG17 x T9 (-11.33%) (table 14).

4.5.11. 100 grain weight

Significant positive relative heterosis was displayed by all hybrids except LBG17 x AKU4 (-0.07%), LBG17 x T9 (0.38%), LBG622 x AKU4 (0.55%) and Pant U19 x VBN1 (2.06%). Highest positive relative heterosis was exhibited by WBG13 x AKU4 (17.05%) followed by COBG305 x VBN1 (12.70%) and LBG17 x VBN1 (11.57%).

Heterobeltiosis was found to be positive and significant in all the hybrids except four viz., LBG17 x T9 (-2.43%), LBG622 x AKU4 (-1.83%), LBG17 x AKU4 (-1.62%) and Pant U19 x VBN1 (-0.96%) which showed negative non-significant heterobeltiosis WBG13 x AKU4 expressed highest positive heterobeltiosis of 14.07% followed by COBG305 x VBN1 (11.48%).

Table 15. Estimate of heterosis for 100 grain weight and grain yield/plant.

Parents/Hybrids	100 grain weight					Grain yield / plant				
	Mean	MP	Heterosis %			Mean	MP	Heterosis %		
			RH	HB	SH			RH	HB	SH
L_1	4.52					4.88				
L_2	4.17					4.01				
L_3	4.16					6.91				
L_4	4.01					6.33				
L_5	4.17					3.92				
T_1	4.38					7.67				
T_2	4.27					8.26				
T_3	3.92					4.58				
L_1 x T_1	4.45	4.45	-0.07*	-1.62*	-1.62*	8.15	6.28	29.76*	6.17*	-1.33*
L_1 x T_2	4.41	4.40	0.38*	-2.43*	-2.43*	11.07	6.57	68.49*	34.07*	34.07*
L_1 x T_3	4.71	4.22	11.57*	4.13*	4.13*	11.41	4.73	141.13*	133.72*	38.23*
L_2 x T_1	4.30	4.28	0.55*	-1.83*	-4.86*	9.93	5.84	70.03*	29.41*	20.27*
L_2 x T_2	4.48	4.22	6.16*	5.00*	-0.88*	11.92	6.14	94.40*	44.37*	44.37*
L_2 x T_3	4.30	4.05	6.22*	2.95*	-4.94*	10.33	4.30	140.59*	125.45*	25.15*
L_3 x T_1	5.00	4.27	17.05*	14.07*	10.54*	18.32	7.29	151.35*	138.79*	121.92*
L_3 x T_2	4.46	4.22	5.81*	4.45*	-1.40*	15.95	7.59	110.33*	93.14*	93.14*
L_3 x T_3	4.36	4.04	8.00*	4.89*	-3.54*	13.17	5.75	129.18*	90.64*	59.47*
L_4 x T_1	4.60	4.20	9.73*	5.02*	1.77*	10.99	7.00	56.97*	43.27*	33.14*
L_4 x T_2	4.40	4.14	6.24*	2.97*	-2.80*	12.01	7.30	64.59*	45.42*	45.42*
L_4 x T_3	4.47	3.97	12.70*	11.48*	-1.25*	10.50	5.46	92.31*	65.74*	27.13*
L_5 x T_1	4.54	4.28	6.28*	3.65*	0.44*	9.92	5.80	71.14*	29.32*	20.19*
L_5 x T_2	4.57	4.22	8.42*	7.10*	1.11*	11.55	6.09	89.60*	39.85*	39.85*
L_5 x T_3	4.13	4.05	2.06*	-0.96*	-8.77*	8.42	4.25	97.88*	83.63*	1.94*
CD (0.05)			0.11	0.12	0.12			0.67	0.78	0.78

* Significant at 1% level

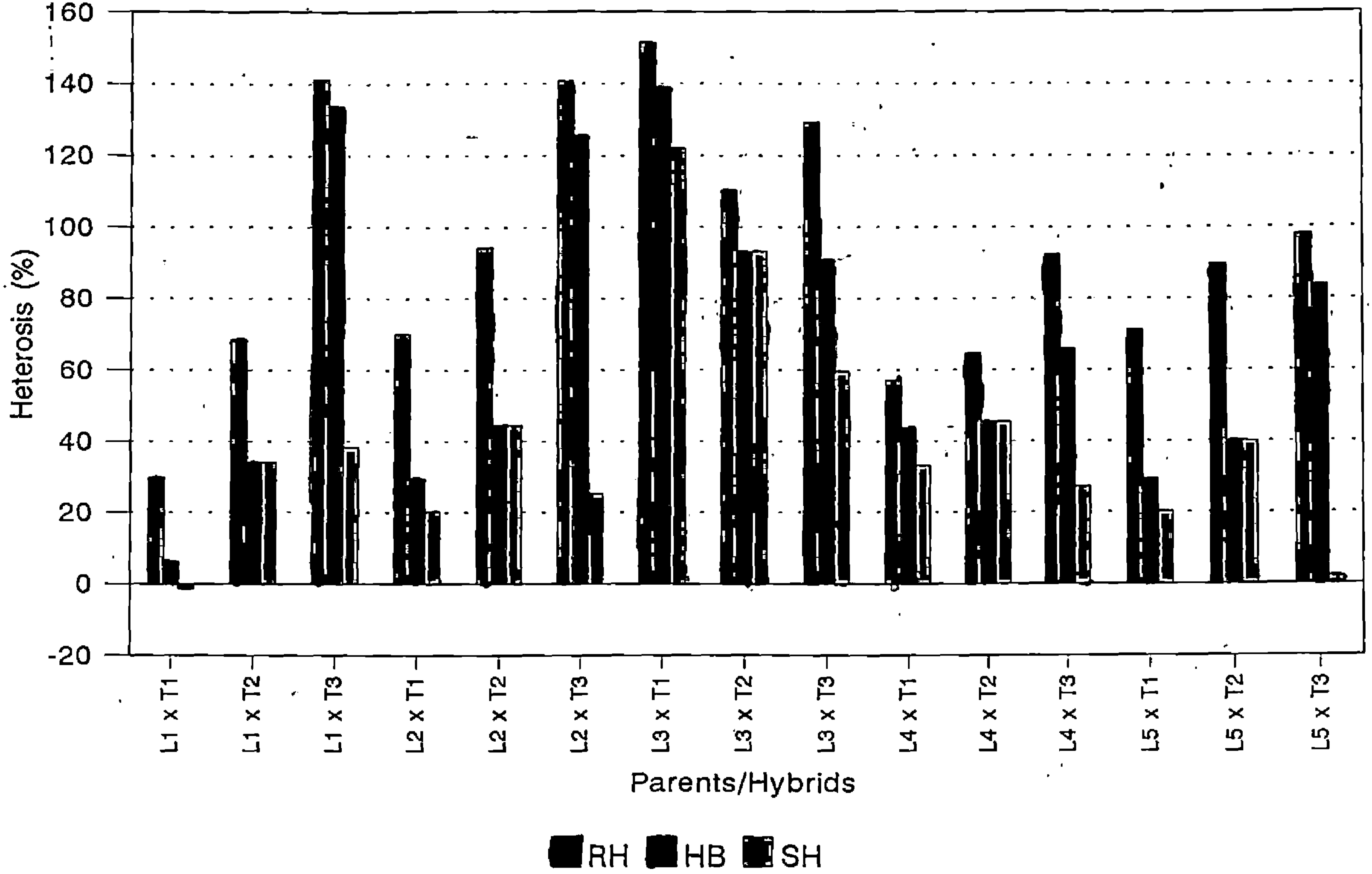

Fig. 7. Estimate of heterosis in blackgram - Grain yield per plant

Only two hybrids displayed significant positive standard heterosis. They are LBG17 x VBN1 (4.13%) and WBG13 x AKU4 (10.54%). Highest significant negative standard heterosis was shown by Pant U19 x VBN1 (-8.77%) followed by LBG622 x VBN1 (-4.94%) and LBG622 x AKU4 (-4.86%) (table 15).

4.5.12. Grain yield per plant

All the fifteen hybrids expressed significant and positive relative heterosis for this trait. Highest value of 151.35% was recorded in the case of WBG13 x AKU4 followed by LBG17 x VBN1 (141.13%) and LBG622 x VBN1 (140.59%).

Heteroboltisis was found to be positive and significant for all the hybrid combinations except one ie., LBG17 x AKU4 (6.17%). Maximum positive heterobeltiosis was exhibited by WBG13 x AKU4 (138.79%) followed by LBG17 x VBN1 (133.72%) and LBG622 x VBN1 (125.45%).

Standard heterosis was observed as positive and significant in all the hybrids except LBG17 x AKU4 (-1.33%) and Pant U19 x VBN1 (1.94%). WBG13 x AKU4 (121.92%) showed maximum positive standard heterosis followed by WBG13 x T9 (93.14%) (table 15 and Fig. 7).

DISCUSSION

DISCUSSION

The research programme was carried out as a preliminary step for developing high yielding blackgram varieties with good biological nitrogen fixation capacity along with reasonable yield. Apart from the mean performance of various genotypes, knowledge on the combining ability of different parents and crosses is a must for such an attempt. Estimate of heterosis percentage will gives reliable information on the best performing hybrid combinations that can be selected for further utilization.

5.1. Mean performance

Earlier, plant breeders used to select the parents for hybridisation on the basis of their mean performance alone. Now, the ability of a genotype to transmit desirable performance to its progeny is given importance. However, based on the mean performance, potential and desirable genotypes can be selected for crop improvement.

Among lines WBG13 and among testers AKU4 were identified as best varieties for length of primary root and number of secondary roots. The best performing hybrid for the above two traits was WBG13 x AKU4.

Pant U19 among lines and T9 among testers were the best genotypes for shoot/root ratio and weight of nodules. Pant U19 x T9 was observed as the best hybrid for the above characters.

Nitrogen content at 50 per cent flowering and at maturity was highest for LBG622 among lines and T9 among testers. Out of the fifteen hybrid combinations Pant U19 x T9 was the best one for nitrogen content.

Considering plant height and the dry weight of plants the best variety was WBG13 among lines and AKU4 among testers. WBG13 x AKU4 was the best hybrid for the above two traits.

For number of pods the best genotypes were WBG13 among lines and T9 among testers. Among hybrids the best one was WBG13 x T9.

In the case of number of seeds per pod WBG13 among lines and AKU4 among testers were the best ones. Among hybrids WBG13 x AKU4 displayed the best performance.

LBG17 among lines and AKU4 among testers were the best varieties for 100 grain weight. WBG13 x AKU4 was the best hybrid.

Grain yield per plant was highest for WBG13 among lines and T9 among testers. Among F_1's WBG13 x AKU4 recorded maximum grain yield.

Considering weight of nodules and nitrogen content at 50% flowering, the best genotypes were Pant U19 and LBG622 among lines, T9 among testers and Pant U19 x T9 among hybrids. Therefore, these can be selected for biological nitrogen fixation traits and can be utilized in the crop improvement. Main yield contributing traits like number of seeds per pod, 100 grain weight and grain yield per plant were highèst for WBG13 and LBG17 among lines, AKU4 and T9 among testers and WBG13 x AKU4 among hybrids. These can be selected and utilized as potential genotypes for high yield and yield contributing traits.

Mean performance and general combining ability effect can indicate the superiority of a genotype. In judging the genetic potentiality of a genotype that can be selected as parents for breeding programmes, combining ability assumes importance Evaluation based on the mean performance and gca effect separately may result in the identification of different genotypes. Hence evaluating the parents using both the criteria would be more relevant.

5.2. Combining ability

The concept of combining ability was introduced by sprague and Tatum (1942). According to them, combining ability is the relative ability of a biotype to transmit desirable performance to its crosses. 'General combining ability' refers to the average performance of a strain in a series of crosses, where as 'specific combining ability' indicates those cases in which certain combinations do relatively better or worse than would be expected on the basis of average performance of the lines involved. The combining ability studies reveal the nature of gene action governing the trait which determines the breeding programme. The line x tester analysis can be employed to screen a large number of genotypes for their combining ability. This is useful in deciding the relative ability of a number of females and males to produce desirable hybrid combinations. This mating design also provides information regarding the usefulness of lines and testers as parents for hybridization to generate segregating population from which promising selections can be made. The line x tester analysis has some advantages over diallel analysis. It avoids the interactions among male and female parents. Also from comparatively lower number of cross combinations reliable informations can be obtained.

5.2.1. Length of primary root

Length of primary root had significant mean sum of squares due to lines and line x tester where as that due to testers was not significant. This indicates the significance of GCA and SCA variances and the involvement of additive and non - additive gene actions for the expression of this traits. However, the ratio of σ^2A to σ^2D was less than unity indicating the predominant role of non - additive gene action. No literature was found to support or to contradict this result.

Among the lines, WBG13 had significant positive gca effect where as among testers AKU4 and T9 had significant positive gca effects. Tester VBN1 showed significant negative gca. Among hybrid combinations, LBG17 x VBN1, LBG622 x VBN1, WBG13 x AKU4, WBG13 x T9, COBG305 x VBN1 and Pant U19 x VBN1 recorded significant and positive sca effects. Both the parents involved in the crosses LBG17 x VBN1, LBG622 x VBN1, COBG305 x VBN1 and Pant U19 x VBN1 were with negative general combining ability. The hybrids viz. WBG13 x AKU4 and WBG13 x T9 had positive general combiners as both parents. Since the character is predominantly under the control of non-additive gene action combination breeding will be helpful for the improvement, as heterosis breeding is not a viable proposition.

5.2.2. Number of secondary roots

Number of secondary roots recorded significant mean sum of squares due to lines, testers and line x tester. Significant GCA and SCA variances were observed for this character indicating that additive and non-additive genetic components were important for the expression of this trait. The ratio of σ^2A to σ^2D was more than unity indicating that this character was under the control of additive gene action. No related literature was available in agreement or against this finding.

The estimate of combining ability revealed that the lines WBG13 and LBG17 and the testers AKU4 and T9 had significant positive gca effects. Significant negative gca effects were recorded by lines LBG622, COBG305 and Pant U19 and the tester VBN1. The hybrids LBG17 x AKU4, WBG13 x T9, COBG305 x VBN1 and Pant U19 x VBN1 recorded significant positive sca effects. Both the parents involved in the crosses of LBG17 x AKU4 and WBG13 x T9 were positive general combiners. COBG305 x VBN1 and Pant U19 x VBN1 involved negative x negative general combiners. Since this characters is under the control of additive gene action, selection will be helpful for the improvement.

5.2.3. Shoot/root ratio

A significant mean sum of squares due to lines and line x tester were recorded for shoot/root ratio while that due to testers was not significant. This indicates the significance of GCA and SCA variances and the involvement of additive and non-additive genetic components in the expression of this character. The ratio of σ^2A to σ^2D was less than unity which implies the predominance of non-additive gene action. This is in agreement with the findings of Sreekumar (1993) in green gram.

Among lines Pant U19 exhibited significant positive gca effect where as among testers gca effect was significant for T9. Out of all hybrids,positive and significant sca effects were shown by six viz., LBG17 x VBN1 and LBG622 x VBN1, the hybrids of negative x negative general combiners and WBG13 x AKU4, COBG305 x T9, Pant U19 x AKU4 and Pant U19 x T9 which are the hybrids of positive x positive general combiners. Since shoot/root ratio is under the control of non-additive gene action it can be utilized through combination breeding.

5.2.4. Weight of nodules

Mean sum of squares due to lines, testers and line x tester were non-significant for weight of nodules. This indicates the non-significance of GCA and SCA variances and thereby additive and non-additive gene actions for the expression of this trait. But the ratio σ^2A to σ^2D was less than unity suggesting the non-additive gene action which is in agreement with the result reported earlier by Sreekumar (1995) in cowpea. Contrary to the present result Miller *et al.* (1986) in cowpea found highly significant SCA variance for nodule weight. However Singh and Murty (1988) reported in greengram the significance of both GCA and SCA variance for nodule weight.

Among lines COBG305 and Pant U19 and among testers T9 had significant positive gca effects. Out of 15 hybrid combinations, only one viz., Pant U19 x T9 recorded significant and positive sca effect. Positive x positive general combiners contribute to the positive sca effect. Since this character is under the control of non-additive gene action, there is no scope for applying selection pressure in the early stages and combination breeding will help in the improvement.

5.2.5. Nitrogen content at 50 per cent flowering

The lines, testers and line x tester showed non-significant mean sum of squares for nitrogen content at 50 per cent flowering, indicating the non-significance of GCA and SCA variances and additive and non-additive genetic components in the expression of this trait. This finding is contrary to the observations of Sreekumar (1995) in cowpea indicating the significance of GCA and SCA variances. The ratio of σ^2A and σ^2D was less than unity indicating the predominant role of non-additive gene action which is in agreement with the report of Sreekumar (1995) in cowpea. Hely (1972) in *Trifolium ambiguum*, Tan (1981) in alfalfa, Smith *et al.* (1982) in crimson clover and Singh and Murthy (1988) in greengram reported the role of additive and non-additive genetic components in the expression of nitrogen content in plant. Contrary to the present finding additive gene action was reported by Pinchbeck *et al.* (1980) in spanish clover.

Among lines COBG305 and Pant U19 and among testers AKU4 and T9 showed significant positive gca effects. Negative and significant gca effects were displayed by LBG17, LBG622 and WBG13 among lines and VBN1 among testers. Significant positive sca effects were expressed by four hybrids. Out of these hybrids LBG622 x AKU4 involved negative x positive general combiners, WBG13 x VBN1 involved negative x negative general combiners, COBG305 x VBN1 involved positive x negative general combiners and Pant U19 x T9 involved positive x positive general combiners. Since, this trait is under the control of non-additive gene-action for improvement combination breeding can be adopted.

5.2.6. Nitrogen content at maturity

A non-significant mean sum of squares due to lines, testers and line x tester was recorded for nitrogen content at maturity. This indicates the non-significance of GCA and SCA variances and additive and non-additive gene actions. The ratio of σ^2A to σ^2D was too small to be estimated. No literature was obtained to support or contradict the results.

Analysis of combining ability effects revealed that COBG 305 and Pant U19 among lines and AKU4 and T9 among testers expressed significant positive gca effects. Negative and significant gca effects were shown by LBG17, LBG622 and WBG13 among lines and VBN1 among testers. Four hybrids showed significant positive sca effects. LBG17 x AKU4 and LBG622 x AKU4 involved negative x positive general combiners. WBG13 x VBN1 was the hybrid with negative x negative general combiners. Pant U19 x T9 had general combining parents with positive effect.

5.2.7. Plant height

Plant height had significant mean sum of squares due to lines, testers and line x tester. Significant GCA and SCA variances was found for this trait indicating that additive and non-additive genetic components were important for the expression of this trait. But the ratio of σ^2A to σ^2D is less than unity suggesting predominant role of non-additive gene action.

Similar results were obtained by Pillai (1980) and Rajarathinam and Rathnaswamy (1990) in blackgram and Jayarani (1993) in cowpea. On the other hand Sagar and Chandra (1977) in blackgram reported the predominance of additive gene action for this character.

The estimates of combining ability revealed that all lines showed significant gca effect. The lines LBG622 and WBG13 had positive and significant gca. LBG17, COBG305 and Pant U19 showed significant negative gca. Among testers AKU4 and T9 had positive and significant gca. VBN1 displayed negative and significant gca. Out of the six hybrids with significant positive sca effect, LBG17 x T9 and COBG305 x T9 had negative x positive general combiners, LBG17 x VBN1 and Pant U19 x VBN1 had negative x negative general combiners and LBG622 x AKU4 and WBG13 x AKU4 had positive x positive general combiners. Since non-additive gene action controls plant height predominantly, for the improvement of this, combination breeding is suggested.

5.2.8. Dry weight of plants

Dry weight of plants recorded significant mean sum of squares due to lines, testers and line x tester. Significant GCA and SCA variances were observed for this character indicating that additive and non-additive genetic components were important for the expression of this trait. This finding is in agreement with the results of Singh and Murthy (1988) in greengram and Sreekumar (1995) in cowpea. Here the ratio of σ^2A to σ^2D is greater than unity suggesting the predominant role of additive gene action. This is in line with the report of Pinchbeck *et al.* (1980) in spanish clover. Non-additive gene action for dry weight was reported by Miller *et al.* (1986) and Sreekumar (1995) in cowpea.

Three lines such as LBG17, LBG622 and WBG13 exhibited positive and significant gca effects. AKU4 is the only one tester that had positive and significant gca effects. Among lines Pant U19 and COBG305 and among testers T9 and VBN1 had significant negative gca effects. Among hybrids with significant positive sca effect, LBG17 x VBN1 and LBG622 x VBN1 involved positive x negative general combiners, WBG13 x AKU4 involved positive x positive general combiners, COBG305 x T9 and Pant U19 x VBN1 involved negative x negative general combiners. Since this trait is under the control of additive gene action, selection will be helpful for the improvement.

5.2.9. Number of pods

Number of pods had significant mean sum of squares due to lines, testers and line x tester. Significant GCA and SCA variances were observed for this character indicating that additive and non-additive genetic components were important for the expression of this trait. However, the ratio of σ^2A to σ^2D is less than unity suggesting a predominant role of non-additive gene action. In agreement to this, significance of GCA and SCA variances and importance of non-additive gene action for number of pods was reported by Sagar and Chandra (1977), Pillai (1980), Dasgupta and Das (1987), Singh *et al.* (1987) and Rajarathinam and Rangaswamy (1990) in blackgram. Similar findings were reported by Deshmukh and Manjare (1980) and Sreekumar (1993) in greengram, Thiyagarajan *et al.* (1990), Anilkumar (1992), Jayarani (1993) and Sreekumar (1995) in cowpea. Contrary to this preponderance of additive gene action was reported by Chauhan and Joshi (1981) in cowpea. Dubey and Lal (1983) in pea, Wilson *et al.* (1985) and Saxena and Sharma (1989) in greengram. Significant SCA variance for the trait was observed by Kalia *et al.* (1991) in blackgram.

Among lines WBG13 and among testers T9 exhibited positive and significant gca effect. LBG17, LBG622, COBG305 and Pant U19 among lines and AKU4 and VBN1 among testers showed negative and significant gca effect. Significant and positive sca effects were displayed by the crosses LBG17 x VBN1 , COBG305 x AKU4, COBG305 x VBN1 and Pant U19 x AKU4 with parents which are negative x negative general combiners, LBG622 x T9 and Pant U19 x T9 both with parents which are negative x positive general combiners and WBG13 x AKU4 with positive x negative general combiners as parents. Number of pods is found to be under the control of non-additive gene action and therefore improvement is possible through combination breeding.

5.2.10. Number of seeds per pod

Mean sum of squares due to lines, testers and line x tester were significant for number of seeds per pod indicating that both GCA and SCA were important for this character. This suggests the involvement of both additive and non-additive gene action for the expression of this trait. The ratio of σ^2A to σ^2D was found to be less than unity indicating the predominant role of non-additive gene action. Singh and Singh (1971) reported that additive and non-additive components of variance were significantly high for this trait, in blackgram. In agreement to the present findings and Deshmukh and Manjare (1980) and Sreekumar (1993) in greengram and Jayarani (1993) and Sreekumar (1995) in cowpea reported the importance of non-additive gene action in controlling the number of seeds per pod. Contrary to this additive gene action was reported by Malhotra (1983) in blackgram, Wilson *et al.* (1985) and Saxena and Sharma (1989) in greengram and Chauhan and Joshi (1981), Thiyagarajan *et al.* (1990) and Anilkumar (1992) in cowpea. Pillai (1980) in blackgram observed that variances due to GCA and SCA were not significant for this character. Kalia (1991) in blackgram foudn significant SCA variance for number of seeds per pod.

Estimate of combining ability revealed that the lines LBG622, WBG13 and COBG305 and the tester AKU4 had significant positive gca effect. Among lines T9 and VBN1 expressed significant negative gca effect. Out of the fifteen hybrids only two had significant and positive sca effect. They were, WBG13 x AKU4 which involved positive x positive general combiners and Pant U19 x T9 which involved negative X negative general combiners. Since the character is predominantly under the control of non-additive gene action further utilization can be done through combination breeding.

5.2.11. 100 Grain weight

For 100 grain weight, the lines, testers and line x tester exhibited non-significant mean sum of squares indicating the non-significance of GCA and SCA variances and hence that of additive and non-additive gene actions. Contrary to this Pillai (1980) in blackgram reported highly significant GCA and SCA variances for 100 grain weight indicating the importance of both additive and non-additive gene actions. Singh and Jain (1972) and Sawant (1995) in cowpea also found importance of both GCA and SCA variances in the inheritance of this character. Significance of SCA variance alone was reported by Sreekumar (1993) in greengram indicating non-additive gene action. In the present study, because of high environmental variances the ratio of σ^2A to σ^2D was too low to be estimated. But, Pillai (1980) in blackgram observed a preponderance of additive gene action over non-additive. Malhotra (1983) in blackgram, Thiyagarajan *et al.* (1990), Jayarani (1993) and Sreekumar (1995) in cowpea observed the predominance of non-additive gene action for 100 grain weight.

Among lines only one viz., WBG13 and among testers AKU4 alone had positive and significant gca effect LBG622 and Pant U19 among lines and VBN1 among testers showed negative and significant gca effect. Four hybrids like LBG17 x VBN1, LBG622 x T9, WBG13 x AKU4 and Pant U19 x T9 displayed positive and significant sca effect. The parents of LBG17 x VBN1 were positive x negative general combiners and that of LBG622 x T9 and Pant U19 x T9 were negative x negative general combiners where as WBG13 x AKU4 had parents with positive gca effect.

5.2.12. Grain yield per plant

Grain yield per plant had significant mean sum of squares due to lines and line x tester. This indicated the significant of GCA and SCA variances and the involvement of additive and non-additive gene actions for the expression of this character. The ratio of σ^2A to σ^2D was less than unity which suggests the predominance of non-additive gene action. Similar observations were made by several workers in blackgram (Singh and Dhaliwal, 1972; Sagar and Chandra, 1977; PIllai, 1980; Dasgupta and Das, 1987; Singh *et al.*, 1987 Rajarathenam and Rathnaswamy, 1990), greengram (Deshmukh and Manjare, 1980 and Sreekumar 1993) and in cowpea (Thiyagarajan *et al.*, 1990; Anilkumar, 1992 and Sreekumar, 1995). However, additive gene action contradicting the present result was reported by Malhotra (1983) in blackgram, Saxena and Sharma (1989) in green gram, and Chauhan and Joshi (1981) in cowpea. Kalia *et al.* (1991) observed significant SCA variance for the trait, in blackgram.

Combining ability analysis revealed that among lines only one viz., WBG-13 and among testers T9 had significant and positive gca effect. Among lines LBG17, LBG622, COBG305 and pant U19 and among testers AKU4 and VBN1 expressed negative and significant gca effect. The two hybrids that had significant positive sca effect were LBG17 x VBN1 which involved negative general combiners and WBG13 x AKU4 which involved positive x negative general combiners. For the improvement of grain yield per plant combination breeding is suggested due to the preponderance of non-additive gene action.

For important nitrogen fixing traits like nodule weight and nitrogen content the best general combiners were COBG305 and Pant U19 among lines and T9 among testers. The hybrid Pant U19 x T9 was the best specific combiner for these characters. Considering the number of pods and grain yield per plant, among lines WBG13 and among testers T9 were the best general combiners. The best specific combinations were LBG17 x VBN1 and WBG13 x AKU4. These genotypes were identified as potential ones for further utilization in crop improvement programmes.

On the whole, based on mean performance and gca effects, for biological nitrogen fixation, Pant U19 among lines and T9 among testers were the best genotypes. For nitrogen fixing traits, these parents can be used in the breeding programmes. Based on mean performance and sca effects the best specific combiner for nitrogen fixing capacity was Pant U19 x T9 this can be exploited further to develop stable hybrid derivatives through pedigree selection. For yield and component traits, considering both mean performance and gca effects, WBG13 among lines&T9 among testers were the best general combiners. These can be advantageously used as parents for producing high yielding varieties. The hybrid WBG13 x AKU4 was the best one based on mean performance and sca effects. This can be improved further for obtaining stable high yielding varieties.

The results of present research programme reveal that WBG13 x AKU4 is the best combiner for biological nitrogen fixation traits and yield components and utilizing this superior blackgram varieties with these attributes can be developed.

5.3. Heterosis

To exploit the phenomenon of hybrid vigour, knowledge on the magnitude and direction of heterosis is of paramount importance. Heterosis is the superiority of an F_1 hybrid over both its parents. It may be positive or negative. Common measures of heterosis are relative heterosis, heterobeltiosis and standard heterosis. The parent expressing maximum value for a trait is considered as standard parent for that trait For hybrid vigour exploitation, the mean performance, sca effect and heterosis per cent have to be taken in to account. The high sca effect may not be the appropriate criteria for heterosis because the hybrids with low mean value may some times posses high sca effect if the gca effect of the parents are very low. Similarly mere heterosis value also is misleading since the heterosis of hybrids tend to be high when the parental means are low and the heterosis would tend to be low when the parental means are already high. Mean performance and standard heterosis are considered for identification of desirable combination for commercial exploitation.

In the present study, manifestation of heterosis was observed in some cross combinations, for all the characters. Positive heterosis is desirable for all the traits studied, for commercial utilization.

For length of primary root highest of positive relative heterosis of 44.34 per cent was recorded by the hybrid combination WBG13 x AKU4. Highest positive heterobeltiosis and standard heterosis were also exhibited by this hybrid.

Maximum positive relative heterosis and and heterobeltiosis for number of secondary roots was displayed by WBG13 x T9. Standard heterosis for this trait was maximum for WBG13 x AKU4.

The hybrid, LBG17 x VBN1 exhibited highest positive relative heterosis and heterobeltiosis for shoot/root ratio, while positive standard heterosis was maximum for the cross Pant U19 x T9.

In the case of weight of nodules, highest positive relative heterosis of 453.62 per cent was shown by WBG13 x VBN1. Positive heterobeltiosis was maximum for WBG13 x AKU4 (292.68 per cent). Highest positive and significant standard heterosis was displayed by the cross Pant U19 x T9 (58.93

per cent) Positive heterosis for this trait, which determines the nitrogen fixation efficiency was reported earlier by Sreekumar (1995) in cowpea in conformity to the result of the study.

For nitrogen content at 50% flowering highest relative heterosis was displayed by the hybrid WBG13 x VBN1 (40.61 per cent).. Maximum positive heterobeltiosis was exhibited by COBG305 x T9 (36.36 per cent). Highest positive standard heterosis of 20.65 present was found in the case of Pant U19 x T9. In agreement to the pre cent findings (Sreekumar, 1995) in cowpea also observed positive heterosis for nitrogen content in plant at 50 per cent flowering content in an important trait governing biological nitrogen fixation.

The hybrid combination, LBG17 x AKU4 expressed highest positive relative heterosis of 27.49 per cent, for nitrogen content at maturity. Heterobeltiosis and standard heterosis were maximum for Pant U19 x T9.

Among the hybrids tested, COBG305 x T9 displayed highest positive relative heterosis and heterobeltiosis of 75.80 per cent and 57.93 per cent respectively for plant height. Highest standard heterosis was shown by WBG13 x AKU4 (26.82 per cent). Sagar and Chandra (1977) and Pillai (1980) in blackgram also reported heterosis for plant height in conformity to the results in this study. In green gram, heterosis for this trait was reported by Sing and Jain (1970) over mid-parent and better parent. Sawant *et al.* (1995)

in cowpea observed greatest positive heterosis over mid parent for plant height.

In the case of dry weight of plants highest positive relative heterosis of 105.73 per cent and heterobeltiosis of 70.95 per cent were displayed by LBG622 x VBN1. Maximum value of standard heterosis i.e., 35.76 per cent was displayed by WBG13 x AKU4. Positive heterosis for dry weight was reported by Sreekumar (1995) in cowpea, in consonance with the present findings.

While studying the character, number of pods, it was revealed that highest relative heterosis of 141.11 per cent and heterobeltiosis of 127.36 per cent were exhibited by the hybrid LBG17 x VBN1. Highest positive standard heterosis of 71.78 per cent was exhibited by WBG13 x T9.

Sagar and Chandra (1977) in blackgram reported significant heterosis for number of pods per plant over better parent. Pillai (1980) also observed heterosis for pod number over mid parent, better parent and standard parent in the same crop. In greengram, high heterosis over better parent was observed by Patil *et al.* (1992) for this trait.

For number of seeds per pod positive relative heterosis (13.50 per cent) and heterobeltiosis (12.57 per cent) were maximum for LBG622 x AKU4. Highest positive standard heterosis of 12.81 per cent was shown by Pant U19 x T9.

The hybrid WBG13 x AKU4 exhibited highest positive relative heterosis, heterobeltiosis and standard heterosis of 17.05 per cent, 14.07 per cent and 10.54 per cent respectively, for 100 grain weight. Pillai (1980) in black gram found heterosis for this yield component over mid-parent better parent and standard parent. In greengram, Singh and Singh (1993) observed heterosis over better parent or mid parent for 100 seed weight.

For grain yield per plant highest positive relative heterosis (151.35 per cent), heterobeltiosis (138.79 per cent) and standard heterosis (121.92 per cent) were displayed by the cross WBG13 x AKU4. Sagar and Chandra (1977) reported in black gram a high degree of heterosis for this character over mid-parent and better parent. In green gram heterosis for grain yield over better parent was observed by Natarajan (1989) and Patil (1992). Sawant *et al.* (1995) and Sreekumar (1995) in cowpea also found heterosis for grain yield per plant.

Considering the biological nitrogen fixation traits like nodule weight and nitrogen content the best cross at 50% flowering, the best cross that expressed maximum standard heterosis was Pant U19 x T9. Therefore this cross may be selected and utilized for developing black gram varieties with improved nitrogen fixing capacity. Based on the yield attributes like 100 grain weight and grain yield per plant the best hybrid was WBG13 x AKU4 and this can be exploited further for yield improvement.

SUMMARY

SUMMARY

Grain legumes are the major and readily available reserve of dietary protein. The nitrogen fixing capacity of legume -*Rhizobium* symbionts is also very well known. Since the application of nitrogenous fertilizers is very expensive, exploitation of nitrogen fixing potential of leguminous crops has much practical significance for increasing crop production. The present research programme was undertaken with the objective of assessing the general and specific combining abilities and gene action involved in the inheritance of biological nitrogen fixation traits and yield components in blackgram, as a preliminary step for developing high yielding varieties with good nitrogen fixation capacity.

The research programme was carried out at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, Thiruvananthapuram, during 1995-96. The experimental material consisted of five lines, three testers and their 15 hybrids. The varieties with high nitrogen fixation capacity were used as lines and the high yielding varieties were used as testers. The lines, testers and L x T combinations were evaluated in randomized block design with three replications. Data on the following traits viz., length of primary root, number of secondary roots, shoot/root ratio, weight of nodules, nitrogen content at 50 per cent flowering, nitrogen content

at maturity, plant height, dry weight of plants, number of pods, number of seeds per pod, 100 grain weight and grain yield per plant were collected from the field experiment and utilized for estimating the combining ability.

For length of primary root WBG13 among lines and AKU4 and T9 among testers had significant positive gca effects. Among hybrids, LBG17 x VBN1, LBG622 x VBN1, WBG13 x AKU4, WBG13 x T9, COBG305 x VBN1 and Pant U19 x VBN1 recorded significant positive sca effects.

The lines WBG13 and LBG17 and the testers AKU4 and T9 had significant positive gca effects for number of secondary roots. The hybrids LBG17 x AKU4, WBG13 x T9, COBG305 x VBN1 and Pant U19 x VBN1 recorded significant positive sca effects

Among lines, Pant U19 and among testers T9 exhibited significant and positive gca effect for shoot/root ratio. Significant positive sca effects were shown by hybrids such as LBG17 x VBN 1, LBG622 x VBN1, WBG13 x AKU4, COBG305 x T9, Pant U19 x AKU4 and Pant U19 x T9.

Considering, weight of nodules COBG305 and Pant U19 among lines and T9 among testers had significant positive gca effects. Only one hybrid viz. Pant U19 x T9 recorded significant and positive sca effect.

Significant and positive gca effects were observed for nitrogen content at 50 per cent flowering and at maturity in the case of COBG305 and Pant

U19 among lines and AKU4 and T9 among testers. Hybrids like LBG622 x AKU4, WBG13 x VBN1 and Pant U19 x T9 showed significant positive sca effects for nitrogen content.

For plant height; LBG622 and WBG13 among lines and AKU4 and T9 among testers expressed significant positive gca effects. Among hybrids, LBG17 x T9, COBG305 x T9, LBG17 x VBN1, Pant U19 x VBN1, LBG622 x AKU4 and WBG13 x AKU4 displayed significant positive sca effect

Lines such as LBG17, LBG622 and WBG13 and the tester AKU4 exhibited positive and significant gca effects for dry weight of plants. The hybrid combinations like LBG17 x VBN1, LBG622 x VBN1, WBG13 x AKU4, COBG305 x T9 and Pant U19 x VBN1 recorded significant positive sca effects.

Among lines WBG13 and among tester T9 displayed significant positive gca effects for number of pods. The crosses LBG17 x VBN1, COBG305 x AKU4, COBG305 x VBN1 and Pant U19 x AKU4 exhibited significant positive sca effect.

In the case of number of seeds per pod, the lines LBG622, WBG13 and COBG305 and the tester AKU4 had significant positive gca effects. WBG13 x AKU4 and Pant U19 x T9 showed significant positive sca effects for this yield component.

Positive and significant gca effect for hundred grain weight were exhibited by WBG13 among lines and AKU-4 among testers. Four hybrids viz., LBG17 x VBN1, LBG622 x T9, WBG13 x AKU4 and Pant U19 x T9 expressed significant positive sca effects for this trait.

For grain yield per plant, WBG13 among lines and T9 among testers recorded significant positive gca effects. The hybrids LBG17 x VBN1 and WBG13 x AKU4 displayed significant positive sca effects.

Among the twelve characters studied, the ratio of σ^2A to σ^2D was more than unity. for dry weight of plants and number of secondary roots suggesting the predominance of additive gene action and the possibility of improvement of these traits by selection. In the case of nitrogen content at maturity and hundred grain weight it was too small to be estimated, due to high environmental variance. For other eight traits, this ratio was less than unity indicating the preponderance of non-additive gene action and the possibility of improvement of these traits through combination breeding.

Considering the mean performance and gca effect for biological nitrogen fixation traits, Pant U19 among lines and T9 among testers were the best general combiners and Pant U19 x T9 was the best specific combination based on mean and sca effect. For yield and component traits, WBG-13 among lines and T9 among testers were the superior ones, on the basis of mean and gca effect. The best hybrid was WBG13 x AKU4, based on mean and sca effect. This had reasonable nitrogen fixing capacity also.

Knowledge on the mean performance, sca effect and heterosis per cent are essential for hybrid vigour exploitation. Varying degrees of heterosis was exhibited by various cross combinations for different characters. Considering the nitrogen fixation traits like nodule weight and nitrogen content at 50 per cent flowering, maximum standard heterosis was exhibited by the hybrid, Pant U19 x T9. For yield attributes, WBG13 x AKU4 was found to be the best hybrid. These superior hybrid combinations can be exploited further, for developing superior blackgram varieties.

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COMBINING ABILITY FOR BIOLOGICAL NITROGEN FIXATION TRAITS AND YIELD COMPONENTS IN BLACKGRAM (*Vigna mungo* (L.) Hepper)

BY

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ABSTRACT OF A THESIS
SUBMITTED IN PARTIAL FULFILMENT OF
THE REQUIREMENT FOR THE DEGREE
MASTER OF SCIENCE IN AGRICULTURE
FACULTY OF AGRICULTURE
KERALA AGRICULTURAL UNIVERSITY

DEPARTMENT OF PLANT BREEDING AND GENETICS
COLLEGE OF AGRICULTURE
VELLAYANI, THIRUVANANTHAPURAM

1996

ABSTRACT

The research programme was carried out at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 1995-96. The objective was to assess the general and specific combining abilities and gene action involved in the inheritance of biological nitrogen fixation traits and yield components in blackgram, as a preliminary step for developing high yielding varieties with good biological nitrogen fixation capacity. The five lines, three testers and their 15 combinations were evaluated in a replicated field experiment and data on twelve characters were collected and subjected to line x tester analysis.

The best general combiners for important biological nitrogen fixation traits were COBG305 and Pant U19 among lines and T9 among testers. The hybrid combination Pant U19 x T9 was the best specific combiner for these characters. In the case of number of pods and grain yield per plant, among lines WBG-13 and among testers T9 were the best general combiners. The hybrids, LBG17 x VBN1 and WBG13 x AKU4 were the best specific combinations for these traits.

Considering the mean performance, sca effect and standard heterosis percentage Pant U19 x T9 was identified as the best hybrid combination for nodule weight and nitrogen content at 50 per cent flowering. Regarding yield, the best hybrid was WBG13 x AKU4. These superior combinations can be utilized further for developing improved blackgram varieties.