COMBINING ABILITY FOR BIOLOGICAL NITROGEN FIXATION TRAITS AND YIELD COMPONENTS IN BLACK GRAM [VIGNA MVNGO (L.) HEPPER]

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Abstract: Twenty three black gram genotypes comprising of five lines with nitrogen fixing capacity, three high yielding testers and their 15 cross combinations were evaluated in randomized block design with three replications during summer 1995-96, at the Department of Plant Breeding and Genetics, College of Agriculture, Thiruvananthapuram. The best general combiners for important biological nitrogen fixation traits were COBG 305 and Pant U 19 among lines and T 9 among testers. Pant U 19 x T 9 was the best specific cross combination for the above traits. For number of pods and grain yield per plant, WBG 13 and T 9 were the best general combiners and hybrids, LBG 17 x VBN 1 and WBG 13 x AKU 4 were the best specific combinations.

Key words: General combining ability, line, nitrogen fixation traits, specific combining ability, tester.

INTRODUCTION

Black gram, 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 nitrogen fixing capacity of legume-Rhizobium symbionts is also of immense value. 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 cultivation of legumes is beneficial to the succeeding cereal crop (Nambiar et al., 1988). Therefore, this research programme is carried out to assess the general and specific combining abilities and the gene action involved in the inheritance of biological nitrogen fixation traits and yield components in black gram, as a preliminary step for developing high yielding varieties with good nitrogen fixing capacity.

MATERIALS AND METHODS

The material consisted of eight black gram varieties as parents and their 15 hybrids. The parents comprised of five lines and three testers. Five lines having high nitrogen fixation capacity viz., LBG 17, LBG 622, WBG 13, COBG 305 and Pant U 19 were used as female parents and crossed with three high yielding testers viz., AKU 4, T 9 and VBN 1.

The selfed seeds of lines and testers were raised in pots and hybridization was done during August-November 1995. Sufficient hybrid seeds from 15 F_1 combinations were collected separately and evaluated in 6 m² plots, along with five lines and three testers adopting a randomized block design with three replica-

tions in the summer rice fallow during January-March 1996.

Seed treatment using *Rizhobium* culture KAU-BG-2 was done. The cultural and management practices were followed as per the recommendations of the Kerala Agricultural University (KAU, 1993). From each plot, a random sample of five plants was selected for recording length of primary root, number of secondary roots, weight of nodules, nitrogen content at 50 per cent flowering, number of pods, number of seeds per pod, 100 grain weight and grain yield per plant.

The line x tester analysis was done using the linear model by Arunachalam (1974) and the general and specific combining ability effects and variances were estimated.

RESULTS AND DISCUSSION

The analysis of variance for eight characters furnished in Table 1a and table 1b revealed significant differences for all the characters. There were no significant differences among lines for the traits like weight of nodules, nitrogen content at 50 per cent flowering and 100 grain weight. The analysis revealed that among testers, there were no significant differences for characters such as length of primary root, weight of nodules, nitrogen content at 50 per cent flowering, 100 grain weight and grain yield per plant.

The general combining ability effects of parents for eight characters are given in Table 2a and 2b and specific combining ability effects of hybrids for eight characters are presented in Tables 3a and 3b. Dominance variance is greater than additive variance for all the

Source	df	Length of pri- mary root	No. of secon- dary roots	Weight of nod- ules	N (at 50% flowering)
Replication	2	0.04	0.19	1499.75	0.002
Treatments	22	**32.89	29.68	**20681.47	**1.610
Parents	7	**21.78	**18.31	**24174.60	**1.010
Crosses	14	**34.50	**31.90	**9763.75	** 1.080
Parents vs Cross	1	**88.04	**78.13	**149077.60	**13.100
Lines (female parents)	4	**68.54	**20.07	9446.19	1.050
Testers (male parents)	2	44.51	** 174.39	18923.75	1.870
Lines x Testers	8	**14.98	**2.20	**7632.53	**0.910
Error	44	0.20	0.08	1462.82	0.010

Table 1a. ANOVA for nitrogen fixation traits (mean sum of squares)

** Significant at 1% level

Table 1b. ANOVA for yield attributes (mean sum of squares)

Source	df	Number of pods	No. of seeds/pod	100 grain weight	Grain yield / plant
Replication	2	0.05	0.02	0.004	0.07
Treatments	22	**520.15	**0.60	**0.17	**39.66
Parents	7	**133.30	**0.63	**0.11	**8.62
Crosses	14	**200.50	**0.55	**0.12	**21.00
Parents vs Cross	1	**7703.21	**0.91	** 1.225	**18.35
Lines (female parents)	4	**458.51	**1.09	0.08	**52.43
Testers (male parents)	2	**226.82	1.01	0.13	11.40
Lines x testers	8	"64.92	**0.17	**0.14	**7.67
Error	44	0.18	0.01	0.01	0.22

** Significant at 1% level

Table 2a. gca effects of lines and testers for nitrogen fixation traits

Source	Length of primary root	No. of secondary roots	Weight of nodules	N at 50% flowering
		Lines		
LBG 17	-0.07	*0.30	*-28.49	*-0.25
LBG 622	*-2.07	*-0.86	*-22.32	*-0.26
WBG 13	*4.66	*2.43	-19.82	*-0.17
COBG 305	*-0.48	*-0.47	*34.62	*0.53
Pant U19	*-2.05	*-1.40	*36.01	*0.16
SE	0.15	0.10	12.75	0.03
		Testers		
AKU 4	*1.08	*3.09	-2.22	*0.17
Т9	*0.91	*0.57	*36.58	*0.05
VBN 1	*-1.99	*-3.66	*-34.36	*-0.41
SE	0.12	0.07	9.88	0.02

* Significant at 5% level

characters under study except number of secondary roots. The additive to dominance variance ratio presented in Table 4 ranged from a minimum of 0.03 nitrogen content at 50% flowering to a maximum of 1.49 for number of secondary roots. For nitrogen content at

Source	No. of pods	No. of seeds/ pod	100 grain weight	Grain yield/ plant
		Lines	**	
LBG 17	*-3.22	*-0.18	0.04	*-1.37
LBG 622	*-3.66	*0.22	*-0.12	*-0.85
WBG 13	* 12.69	*0.19	*0.13	*4.24
COBG 305	*-3.91	*0.29	0.01	*-0.41
Pant U19	*-1.91	*-0.53	-0.07	*-1.61
SE	0.14	0.04	0.02	0.16
		Testers		
AKU 4	*-2.75	*0.29	*0.10	*-0.11
Т9	*4.45	*-0.20	-0.01	*0.92
VBN 1	*-1.70	*-0.09	*-0.09	*-0.81
SE	0.11	0.03	0.02	0.12

Table 2b. Gca effects of lines and testers for yield attrib	outes
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* Significant at 5% level

Table 3a.	Sca effects	of hybrids	for nitrogen	fixation	traits
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Crosses	Length of primary root	No of secondary roots	Weight of nodules	N at 50% flowering
LBG 17 x AKU 4	*-0.96	*1.27	16.39	-0.10
LBG 17 x T9	*-0.59	0.08	-35.74	0.04
LBG 17 x VBN1	*1.54	*-1.35	19.36	0.05
LBG 622 x AKU 4	*-1.29	0.19	10.22	*0.25
LBG 622 x T9	-0.02	-0.10	-3.24	0.06
LBG 622 x VBN1	*1.31	-0.10	-6.98	*-0.30
WBG 13 x AKU 4	*2.41	*-0.46	22.56	0.06
WBG 13 x T9	*2.08	*0.38	*-61.74	*-0.83
WBG 13 x VBN1	*-4.49	0.08	39.19	*0.77
COBG 305 x AKU 4	-0.25	*-0.76	-7.22	*-0.21
COBG 305 x T9	-0.51	0.22	10.48	0.07
COBG 305 x VBN1	*0.75	*0.55	-3.26	*0.14
Pant U 19 x AKU 4	0.09	-0.23	-41.94	-0.01
Pant U19 x T9	*-0.97	*-0.58	*90.26	*0.67
Pant U19XVBN1	*0.89	*0.82	*-48.31	*-0.66
SE	0.26	0.17	22.08	0.06

* Significant at 5% level

maturity and 100 grain weight, this ratio was too small to be estimated. Among the various characters studied, nodule weight, nitrogen content at 50% flowering, number of pods and grain yield were considered as important.

The mean sum of squares due to lines, testers and line x tester were non-significant for weight of nodules and nitrogen content at 50%flowering indicating the non-significance of GCA and SCA variances. This revealed the fact that the additive and non-additive gene actions were not important in the expression of these traits. Contrary to this, in cowpea, significance of GCA and SCA variances for nitrogen content was observed by Sreekumar (1995). However, the ratio of $\sigma^2 A$ to $\sigma^2 D$ was less than unity suggesting the predominant role of non-additive gene action for the nitrogen fixation characters, in agreement with the

Crosses	Numberofpods	Number of seeds/pod	100 grain weight	Grain yield/ plant
LBG 17 x AKU 4	*-6.58	-0.14	*-0.17	*-1.95
LBG 17 x T9	0.02	0.06	*-0.10	*-0.06
LBG 17 x VBN1	*6.56	0.08	*0.27	*2.01
LBG 622 x AKU 4	*-2.20	0.03	*-0.16	*-0.69
LBG 622 x T9	*2.20	-0.11	*0.14	0.27
LBG 622 x VBN1	0.01	0.08	0.02	0.42
WBG 13 x AKU 4	*4.91	*0.33	*0.29	*2.62
WBG 13 x T9	*-1.56	*-0.18	*-0.13	*-0.79
WBG 13 x VBN1	*-3.35	*-0.15	*-0.16	*1.84
COBG 305 x AKU 4	*0.84	0.13	0.01	-0.06
COBG 305 x T9	*-2.16	-0.08	-0.08	-0.08
COBG 305 x VBN1	*1.32	-0.05	0.06	0.14
Pant U 19 x AKU 4	*3.04	*-0.35	0.03	0.07
Pant U19 x T9	*1.51	*0.31	*0.17	0.66
Pant U19 X VBN1	*-4.55	-0.04	*-0.20	*-0.74
SE	0.24	0.07	0.04	0.27

Table 3b. Sca effects of hybrids for yield attributes

* Significant at 5% level

Table 4. Additive and dominance variances and the proportion of $\sigma^2 A$ to $\sigma^2 D$

Character	Additive variance (F=1)			Dominance vari-	Proportion of	
Character	(Lines)	(Testers)	(Pooled)	ance (F=1)	crA to $\sigma^2 D$	
Length of primary root	23.80	7.88	2.76	19.71	0.14	
No. of secondary roots	7.94	45.92	4.20	2.82	1.49	
Weight of nodules	806.07	3010.99	301.38	8226.29	0.04	
Nitrogen (at 50% flowering)	0.06	0.26	0.03	1.19	0.03	
Number of pods	174.93	43.18	19.17	86.31	0.22	
Number of seeds/ pod	0.41	0.22	0.05	0.21	0.24	
100 grain weight	n.e	n.e	n.e	0.18	n.e	
Grain yield/ plant	19.89	0.99	1.88	9.94	0.19	

F =Iinbreeding coefficient: n.e = not estimable

results reported earlier in cowpea. Since the traits are 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. Among lines, COBG 305 and Pant U 19, and among testers, T 9 had significant and positive gca effects. Out of 15 hybrids, only one viz., Pant U 19 x T 9 recorded significant and positive sca effects for nodule weight. In the case of nitrogen content, significant positive sca effects were displayed by LBG 622 x AKU 4, WBG 13 x VBN 1, COBG 305 x VBN 1 and Pant U 19 x T 9.

These hybrid combinations can be advantageously used in the breeding experiments for producing black gram varieties with good biological nitrogen fixing capacity. Number of pods and grain yield per plant had significant GCA and SCA variances indicating the involvement of both additive and non-additive gene actions in the expression of these traits. The ratio of crA to crD is less than unity suggesting a predominant role of non-additive gene action. Here also, improvement is possible through combination breeding due to the preponderance of non-additive gene action. Similar findings were reported by Rajarathinam and Rathnaswamy (1990) in black gram, Sreekumar (1993) in green gram and Sreekumar (1995) in cowpea. Among lines, WBG 13 and among testers, T 9 exhibited significant and positive gca effects for these characters. For number of pods, significant and positive sca effects were displayed by the crosses LBG 17 x VBN 1, COBG 305 x AKU 4, COBG 305 x VBN 1 and Pant U 19 x AKU 4. The cross combinations LBG 17 x VBN 1 and WBG 13 x AKU 4 had significant and positive sca effect for grain yield per plant and hence can be further utilized for evolving high yielding varieties.

On the whole, for important nitrogen fixing traits, the best general combiners were COBG 305 and Pant U 19 among lines and T 9 among testers. The hybrid Pant U 19 x T.9 was the best specific combiner. Considering yield and yield components, among lines WBG 13, and among testers, T 9 were the general combiners. The best specific combinations were LBG 17 x VBN 1 and WBG 13 x AKU 4. These genotypes were identified as potential ones for further utilization in crop • improvement programme. The results of present research programme reveal that WBG 13 x AKU 4 is the best combiner for biological nitrogen fixation traits and yield components and utilizing this, superior black gram varieties with these attributes can be developed.

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