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Combining ability effects in CGMS based pigeonpea [*Cajanus cajan* (L.) mill sp.] hybrids

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Abstract

The objective of present study is to estimate the Combining Ability effects in CGMS based parents and crosses to find out promising cross combinations for seed yield and its components. The experimental material comprised of 40 crosses along with 13 parents (5 lines and 8 testers) and a standard check BDN 716. The experiment was laid out in Randomized Block Design with two replications. The observations were recorded on eleven characters for evaluation. The analysis of variance revealed that there were significant differences among the parents and crosses for all the characters studied. The estimates of GCA effects revealed that BDN 2004-4 B, BSMR 736 B, BDNHR 1 and BDNHR 35-8 were the good general combiners for number pods per plant and grain yield per plant. The line BDN 2004-3 B and the tester BDNHR 21-1-1 and BDNHR 36-7 have registered significant negative GCA effects for days to 50 per cent flowering and for days to maturity the negative GCA effects recorded by line BDN 2004-3 B and BSMR 736 B and testers BDNHR 24-1-1-1 and BDNHR 36-7. The crosses BDN 2004-4 A x BDNHR 35-8 and BSMR 736 A x BDNHR 22-1-1 had high *per se* performance and desirable significant SCA effects for grain yield and other components.

Keywords: Pigeonpea, general combining ability, specific combining ability, CGMS

Introduction

Pigeonpea Cajanus cajan (L.) Millsp. (2n=22) member of family Leguminosae (Fabaceae) is an important legume (pulse) crop of tropical and subtropical regions of Asia and Africa. India is considered as the center of origin of pigeonpea (Van der Maesen., 1980) because of its natural genetic variability available in the local germplasm and the presence of its wild relatives in the country. In India, pigeonpea is grown in an area of 4.45 million hectares with a production of 4.18 million tonnes (Anonymous 2018). The Indian sub-continent alone contributes nearly 92 per cent of the total pigeonpea production in the world. Although India leads the world both in area and production of pigeonpea with its productivity (937 kg/ha). In India, pigeonpea is important in the states of Maharashtra (1.29 m ha), Karnataka (0.88 m ha), Madhya Pradesh (0.64 m ha), Telangana (0.33 m ha), Uttar Pradesh (0.28 m ha) and Andhra pradesh (0.27 m ha). These six states account for over 81.89 per cent of the total pigeonpea area in India. In Maharashtra, pigeonpea having largest role in area, production and productivity. In the year 2018-19, pigeonpea covered the area of 12.20 lakh ha with production of 10.56 lakh tonnes and productivity of 866 kg/ha. One of the factors responsible for the poor productivity of pigeonpea are the lack of improved cultivars. Research for genetic improvement of this crop to raise yield levels effectively has to be strengthened countering biotic stresses, through widening genetic base. In pigeonpea, heterosis for grain yield and its component have not been reported for various quality parameters in pigeonpea hybrids by using CGMS lines and diverse restorers that will be expected to stable, good combiner across the environment. However, varieties good in *per se* performance may not necessarily produce desirable progenies when used in hybridization, proper understanding of underlying inheritance of quantitative traits and also in identifying the promising crosses for further use in breeding program.

Materials and Methods

The experiment consisted of 40 crosses developed by using 5 female and 8 male parents along with BDN 716 as check. The female parents consist of BDN 2004-1 A, BDN 2004-2 A, BDN 2004-3 A, BDN 2004-4 A and BSMR 736 A and male parents consist of BDNHR 1, BDNHR 21-1-1, BDNHR 22-1-1,

BDNHR 24-1-1-1, BDNHR 35-8, BDNHR 36-1, BDNHR 36-6 and BDNHR 36-7 along with their crosses developed during 2017-18. The randomized block design was utilized for the evaluation of the material with 2 replications and spacing of 90 x 20 cm during the *Kharif* season 2018-2019 at Agricultural research station, Badnapur. The genetic analysis was carried out for line x tester mating design as suggested by Kempthorne (1957) and the treatment SS was partitioned to source attributed to parents, crosses and parent vs crosses.

Results and Discussion

Analysis of variance for line x tester analysis

The analysis of variance indicated that the differences due to crosses were significant for all of the characters except pod length. The analysis of variance due to lines were significant for all the characters except days to 50 per cent flowering and number of pods per plant. The analysis of variance due to testers were significant for the characters plant height, days to 50% flowering, days to maturity and number of seeds per pod. The analysis of variance due to line x tester were significant for all the characters except plant height, number of seeds per pod, pod length and grain yield per plant.

Combining Ability Analysis

Combining ability is the capacity of an individual to transmit superior performance to its offspring. Combining ability analysis on one hand is useful in the identification of potential parents for developing commercial hybrids while on other side it helps to select parents to develop base population for further crop improvement programmes. There were significant differences among the genotypes for characters, which led to the combining ability analysis. Thus were partitioned genetic effects between genotypes into general combining ability and specific combining ability. Regarding to the significance of g_i in two directions in traits, we can declare that parents have potential of transfer of high and low Values for each trait. Hence in cases, which increasing and decreasing the value of traits are desired, we should consider positive and negative values of gi respectively. Therefore for days to 50 per cent flowering and days to maturity negative GCA and SCA effects were desirable, while in case of other characters, positive GCA and SCA effects were desirable.

The mean squares of GCA effect were significant for all characters except pollen fertility and number of primary branches per plant. The mean square of SCA effect were significant for all the characters except plant height, number of primary branches per plant, number of seeds per pod and pod length. This indicated the presence of significant differences between males and females for these traits.

General combining ability (GCA effects)

None of the CGMS lines or pollinators was found to be a good general combiner for all the characters studied. Investigation of GCA effects revealed that the parents BDN 2004-4 B and BSMR 736 B among lines, BDNHR 1, BDNHR 35-8 among testers were the good general combiners for yield and most of the yield contributing characters. Hence these good general combiners of males and females may be extensively used in future for pigeonpea breeding programmes. The negative GCA effect was desirable in days to 50 per cent flowering and days to maturity, which was observed in BDN 2004-3 B and BSMR 736 B among lines and among testers it was observed in BDNHR 36-7 and BDNHR 24-1-1-1. Among these parents, BSMR 736 B, BDN 2004-4 B, BDNHR 1 and BDNHR 35-8 had desirable GCA

effect for grain yield per plant, number of secondary branches per plant and number of pods per plant. In general, good general combiners for grain yield also had good or average combining ability for one or more yield components. In most of the parents high GCA effects were associated with high *per se* mean for yield and yield components. It is important to mention here that the parents which showed good GCA effects for grain yield per plant also indicated significantly positive GCA effects for number of pods per plant. The results are in corroborance with the findings of Singh and Srivastava (2001), Banu *et al.* (2006) ^[3], Baskaran and Muthiah (2007), Phad *et al.* (2007), Acharya *et al.* (2009) ^[1], Singh *et al.* (2009), Shoba *et al.* (2010), Gupta *et al.* (2011) ^[5], Thiruvengadam *et al.* (2012), Mesharam *et al.* (2013), Pandey *et al.* (2015) and Mhasal *et al.* (2015).

Specific Combining Ability (SCA) effect of crosses

In crop improvement programme specific combining ability is important to pinpoint specific cross combination for commercial exploitation or varietal development. Specific combining ability effect is the index to determine usefulness of a particular combination in the exploitation of heterosis. The specific combining effects of the present investigation (table 2) are discussed below:

For the trait plant height, none of the crosses exhibited significant positive or negative SCA effects among forty crosses.

For days to 50 per cent flowering negative SCA effects are desirable. Six crosses showed significant negative SCA effects. Maximum significant negative SCA effect was shown by BDN 2004-1 A x BDNHR 22-1-1. These results are in agreement with the earlier results reported by Singh and Srivastava (2001), Banu *et al.* (2006) ^[3], Shoba *et al.* (2010), Meshram *et al.* (2013) and Yamamura *et al.* (2014).

Twenty one crosses showed significant positive SCA effect for pollen fertility. Maximum significant positive SCA effect was shown by BDN 2004-2 A x BDNHR 36-6 followed by BDN 2004-1 A x BDNHR 1.For days to maturity negative SCA effects are desirable. Six crosses showed significant negative SCA effects. Maximum significant negative SCA effect was registered by BSMR 736 A x BDNHR 22-1-1. These results are in agreement with the earlier results reported by Singh and Srivastava (2001), Banu *et al.* (2006) ^[3], Shoba *et al.* (2010), Meshram *et al.* (2013) and Yamamura *et al.* (2014).

Out of forty crosses, none of the crosses exhibited significant negative or positive SCA effect for number of primary branches per plant.

For the trait number of secondary branches per plant, three crosses showed significant positive SCA effect the cross BDN 2004-4 A x BDNHR 35-8 showed maximum significant positive SCA effect. These findings were in perfect agreement with Phad *et al.* (2007), Thiruvengadam *et al.* (2012) and Pandey *et al.* (2015)

For the trait number of pods per plant three crosses exhibited significant positive SCA effects. Maximum significant positive SCA effect was registered by BDN 2004-2 A x BDNHR 24-1-1-1 followed by BSMR 736 A x BDNHR 22-1-1 and BDN 2004-1 x BDNHR 1. Present observations are in close agreement with the earlier reports of Pandey *et al.* (2015) and Yamamura *et al.* (2014).

For the trait number of seeds per pod and pod length none of the crosses, exhibited significant positive SCA effect.

Eight crosses showed significant positive SCA effect for 100 Seed weight. Maximum significant positive SCA effect was registered by the cross BDN 2004-2 A x BDNHR 36-7 followed by BDN 2004-2 A x BDNHR 35-8. These results are in agreement with the earlier results reported by Ghodke *et al.* (1993), Shoba *et al.* (2010), Meshram *et al.* (2013) and Yamamura *et al.* (2014).

Three crosses exhibited significant positive SCA effect for grain yield among which BSMR 736 A x BDNHR 22-1-1

manifested maximum positive SCA effect followed by BDN 2004-4 A x BDNHR 35-8 and BDN 2004-2A x BDNHR 24-1-1-1. These results are in agreement with the findings of Khapre *et al.* (1993), Phad *et al.* (2007), Sarode *et al.* (2009), Gupta *et al.* (2011)^[5], Arbad *et al.* (2013)^[2] and Yamamura *et al.* (2014) for grain yield per plant.

Sources of			Mean sum of squares												
Variation	d. f.	Plant height (cm)	Days to 50% flowering	Pollen fertility (%)	Days to maturity	No. of primary branches per plant	No. of secondary branches per plant	No. of pods per plant	No. of seeds per pod	Pod length (cm)	100 seed weight (g)	Grain yield per plant (g)			
Replications	1	380.89	12.01	7.65	1.51	2.59	1.68	1035.36	0.03	0.19	0.31	133.54			
Crosses	39	235.47*	44.78**	1029.33**	158.99**	3.26**	15.71**	3984.89*	1.03**	0.17	6.86**	285.52**			
Parents (Line)	4	1023.12**	30.20	2941.87*	510.45**	15.25**	54.85**	24653.48	9.36**	0.64**	55.56**	1454.39**			
Parents (Tester)	7	361.97**	118.01*	916.11	382.01**	2.24	22.20	1551.99	0.17*	0.20	1.39	264.94			
Line x Tester	28	91.33	28.55**	784.42**	53.03**	1.80*	8.50*	1640.45**	0.063	0.09	1.28**	123.68			
Error	39	111.45	5.52	6.74	10.71	0.98	4.43	459.20	0.063	0.16	0.12	72.80			

* -Significant at 5% level of significance

** -Significant at 1% level of significance

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Sources of Variation						Mean	sum of squares					
	d. f.	Plant height (cm)	Days to 50 per cent flowering	Pollen fertility (%)	Days to maturity	No. of primary branches per plant	No. of secondary branches per plant	No. of pods per plant	No. of seeds per pod	Pod length (cm)	100 seed weight (g)	Grain yield per plant (g)
GCA	12	281.07*	108.33**	3.84	108.37**	1.67	11.35**	3724.45**	0.39**	1.33**	4.41**	254.31**
SCA	28	91.33	28.55**	784.42**	53.03**	1.80*	8.50*	1640.45**	0.063	0.09	1.28**	123.68**
Error	52	139.62	5.16	5.31	9.57	1.21	4.18	361.86	0.067	0.16	0.10	56.45

* -Significant at 5% level of significance

** -Significant at 1% level of significance

Table 3:	General	combining	ability of	parents in	pigeonpea
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Sr. No.	Parents	Plant height (cm)	Days to 50 per cent flowering	Pollen fertility	Days to maturity	No. of primary branches per plant	No. of secondary branches plant	No. of pods per plant	No. of seeds per pod	Pod length (cm)	100 Seed weight (g)	Grain yield per plant (g)
					Femal	le parents (Lines))					
1.	BDN 2004-1 B	0.53	0.67	-5.11**	-2.47**	-0.35	-1.22*	1.02	0.54**	-0.02	-0.57**	-1.04
2.	BDN 2004-2 B	-4.99	1.23*	-21.65**	9.08**	-1.47**	-1.99**	- 49.32**	-1.30**	-0.19	3.23**	-13.20**
3.	BDN 2004-3 B	-1.31	-2.26**	8.50**	-4.97**	0.10	-0.68	- 23.29**	0.41**	0.31**	-0.20*	-2.76
4.	BDN 2004-4 B	-7.41*	-0.26	9.81**	1.71*	0.72*	2.18**	53.45**	-0.07	-0.13	-1.33**	12.74**
5.	BSMR 736 B	13.18**	0.61	8.45**	-3.35**	0.99**	1.72**	18.14**	0.41**	0.04	-1.12**	4.26*
					Male	parents (Testers)						
6.	BDNHR 1	-5.11	0.31	-7.27**	0.08	-0.36	2.23**	2.67	-0.15	-0.16	0.36**	7.42**
7.	BDNHR 21-1-1	0.66	-4.58**	-1.80*	-1.01	-0.68	-0.87	-6.15	-0.01	-0.11	0.41**	-4.64
8.	BDNHR 22-1-1	-6.86	1.31	0.78	8.58**	-0.37	-1.03	-8.76	0.04	-0.14	0.31**	0.84
9.	BDNHR 24-1-1-1	-4.50	-1.28	9.29**	-7.11**	-0.22	-0.06	12.92*	0.16	0.09	-0.14	-0.49
10.	BDNHR 35-8	-1.90	0.31	10.63**	-2.51*	0.22	-0.12	20.86**	0.10	0.04	-0.14	6.44**
11.	BDNHR 36-1	10.90**	3.71**	-10.10**	1.68	0.27	-2.25**	- 18.94**	-0.03	0.15	-0.07	-8.03**
12.	BDNHR 36-6	6.01	4.81**	-12.63**	8.28**	0.46	0.23	-0.78	-0.22*	-0.08	-0.01	-1.19
13.	BDNHR 36-7	0.80	-4.58**	11.10**	-8.01**	0.68	1.88**	-1.82	0.11	0.21	-0.72**	-0.35
	CD 5% GCA(Line)	5.97	1.14	1.16	1.56	0.55	1.03	9.61	0.13	0.20	0.16	3.79
	CD 5% GCA(Tester)	7.55	1.45	1.47	1.97	0.70	1.30	12.16	0.166	0.26	0.20	4.80

* -Significant at 5% level of significance

** -Significant at 1% level of significance

Table 4: Specific combining ability of crosses in pigeonpea

Sr No	Crosses	Plant height (cm)	Days to 50 per cent flowering	Pollen fertility	Days to maturity	No. of primary branches per plant	No. of secondary branches per plant	No. of pods per plant	No. of seeds per pod	Pod length (cm)	100 Seed weight (g)	Grain yield per plant (g)
1.	BDN 2004-1 A x BDNHR 1	5.12	2.62	21.30**	0.47	1.27	1.18	29.03*	-0.23	-0.18	0.15	7.44
2.	BDN 2004-1 A x BDNHR 21-1-1	1.89	2.52	6.60**	5.07*	-0.40	0.74	9.30	0.12	-0.24	0.35	1.99

3.	BDN 2004-1 A x BDNHR 22-1-1	-8.12	-7.37**	-13.91**	-7.02**	-1.46	0.35	-34.98*	-0.07	-0.15	-0.28	-11.80*
4.	BDN 2004-1 A x BDNHR 24-1-1-1	-15.14	1.72	11.04**	2.67	-0.06	-0.81	19.18	0.15	0.41	-0.82**	4.78
5.	BDN 2004-1 A x BDNHR 35-8	5.81	1.62	8.58**	-3.92	0.39	0.24	-2.30	-0.08	0.12	0.13	0.33
6.	BDN 2004-1 A x BDNHR 36-1	-0.14	-0.27	13.23**	0.87	1.29	0.57	-35.25*	0.24	-0.21	0.31	-1.13
7.	BDN 2004-1 A x BDNHR 36-6	12.79	-1.87	-54.70**	4.27	-0.24	-1.71	-0.11	-0.16	-0.02	0.45	-6.72
8.	BDN 2004-1 A x BDNHR 36-7	-2.21	1.02	7.85**	-2.42	-0.76	-0.56	15.12	0.009	0.27	-0.31	5.10
9.	BDN 2004-2 A x BDNHR 1	3.05	-2.93	-45.31**	0.41	-0.85	-2.89	-54.11**	0.21	0.19	-0.02	-10.95*
10.	BDN 2004-2 A x BDNHR 21-1-1	0.30	2.46	10.46**	-3.98	0.41	3.61*	14.25	-0.12	-0.14	-0.59*	7.86
11.	BDN 2004-2 A x BDNHR 22-1-1	6.91	8.56**	19.00**	-1.58	0.75	0.52	-1.53	-0.07	-0.16	-1.002**	-0.18
12.	BDN 2004-2 A x BDNHR 24-1-1-1	3.48	-3.33*	11.97**	1.61	0.55	3.55*	50.68**	0.10	-0.03	0.61*	12.38*
13.	BDN 2004-2 A x BDNHR 35-8	0.34	-5.93**	11.91**	1.01	-1.13	-1.38	16.69	0.16	-0.10	1.39**	-2.55
14.	BDN 2004-2 A x BDNHR 36-1	-4.46	2.16	-41.64**	0.31	-0.93	-0.60	-8.30	-0.40*	0.08	-0.41	-3.30
15.	BDN 2004-2 A x BDNHR 36-6	-6.47	0.06	21.85**	-1.78	-0.02	-0.44	16.68	0.18	0.24	-1.61**	-0.15
16.	BDN 2004-2 A x BDNHR 36-7	-3.16	-1.03	11.75**	4.01	1.25	-2.39	-34.37*	-0.04	-0.08	1.62**	-3.10
17.	BDN 2004-3 A x BDNHR 1	-9.32	3.56*	11.28**	-4.02	-0.83	-1.00	23.70	0.14	0.36	-0.09	3.86
18.	BDN 2004-3 A x BDNHR 21-1-1	-1.51	-1.03	-5.35**	-1.92	-0.11	-2.99*	-34.42*	-0.04	0.06	0.42	-2.95
19.	BDN 2004-3 A x BDNHR 22-1-1	-0.37	-0.43	2.89	9.47**	0.77	-0.03	23.83	-0.09	0.07	0.59*	2.05
20.	BDN 2004-3 A x BDNHR 24-1-1-1	5.15	1.66	-8.46**	1.17	-0.37	-1.30	-31.34*	-0.21	-0.11	0.27	-8.47
21.	BDN 2004-3 A x BDNHR 35-8	-2.53	-3.93*	-5.80**	-5.42*	0.48	-0.79	-5.08	0.04	0.13	-0.82**	0.10
22.	BDN 2004-3 A x BDNHR 36-1	7.09	0.66	4.34*	4.37	-1.11	1.13	23.61	0.07	-0.24	-0.78**	6.43
23.	BDN 2004-3 A x BDNHR 36-6	-2.35	0.56	6.68**	-2.72	0.39	2.34	-9.14	0.06	-0.23	0.82**	-0.85
24.	BDN 2004-3 A x BDNHR 36-7	3.85	-1.03	-5.58**	-0.92	0.77	2.64	8.84	0.03	-0.04	-0.40	-0.16
25.	BDN 2004-4 A x BDNHR 1	-3.32	-3.93*	7.42**	-1.71	-0.15	1.27	-7.09	-0.11	-0.17	0.36	-6.23
26.	BDN 2004-4 A x BDNHR 21-1-1	-6.37	-1.03	-2.48	6.38**	0.11	-0.71	2.72	-0.05	0.28	0.40	-5.77
27.	BDN 2004-4 A x BDNHR 22-1-1	4.64	5.56**	-10.39**	6.78**	-1.24	-2.35	-37.86**	0.24	0.09	0.39	-5.48
28.	BDN 2004-4 A x BDNHR 24-1-1-1	5.48	-0.83	-5.70**	-7.51**	0.65	0.77	-13.29	-0.12	-0.05	-0.72**	-2.09
29.	BDN 2004-4 A x BDNHR 35-8	-0.79	3.06	-5.16**	-1.61	1.31	3.93**	25.91	0.13	0.03	0.30	14.52**
30.	BDN 2004-4 A x BDNHR 36-1	-7.94	-1.83	8.07**	-0.31	0.61	-1.63	15.71	-0.13	0.10	0.20	-5.73
31.	BDN 2004-4 A x BDNHR 36-6	6.27	0.56	17.98**	1.08	0.12	-1.42	3.40	-0.04	-0.14	-0.42	6.76
32.	BDN 2004-4 A x BDNHR 36-7	2.02	-1.53	-9.73**	-3.11	-1.39	0.17	10.49	0.12	-0.15	-0.52*	4.03
33.	BSMR 736 A x BDNHR 1	4.47	0.68	5.29**	4.85*	0.57	1.44	8.46	-0.006	-0.20	-0.39	5.88
34.	BSMR 736 A x BDNHR 21-1-1	5.69	-2.91	-9.22**	-5.55*	-0.001	-0.65	8.13	0.10	0.04	-0.59*	-1.13
35.	BSMR 736 A x BDNHR 22-1-1	-3.06	-6.31**	2.41	-7.65**	1.18	1.51	50.54**	0.004	0.14	0.30	15.42**
36.	BSMR 736 A x BDNHR 24-1-1-1	1.02	0.78	-8.85**	2.05	-0.76	-2.21	-25.23	0.08	-0.20	0.65**	-6.60
37.	BSMR 736 A x BDNHR 35-8	-2.83	5.18**	-9.52**	9.95**	-1.05	-2.00	-35.22*	-0.25	-0.19	-1.01**	-12.40*
38.	BSMR 736 A x BDNHR 36-1	5.45	-0.71	15.99**	-5.25*	0.14	0.53	4.22	0.22	0.26	0.67**	3.74
39.	BSMR 736 A x BDNHR 36-6	-10.24	0.68	8.18**	-0.85	-0.24	1.24	-10.83	-0.03	0.15	0.74**	0.96
40.	BSMR 736 A x BDNHR 36-7	-0.50	2.58	-4.29*	2.45	0.13	0.14	-0.09	-0.11	0.00	-0.37	-5.87
	CD 95% SCA	16.90	3.25	3.29	4.42	1.57	2.92	27.20	0.37	0.58	0.46	10.74

* -Significant at 5% level of significance

** -Significant at 1% level of significance

Conclusion

The analysis of variance indicated that the differences due to crosses were significant for all of the characters except pod length. The analysis of variance due to lines were significant for all the characters except days to 50 per cent flowering and number of pods per plant. The analysis of variance due to testers were significant for the characters plant height, days to 50 per cent flowering, days to maturity and number of seeds per pod. The analysis of variance due to line x tester were significant for all the characters except plant height, number of seeds per pod, pod length and grain yield per plant.

High magnitude of variances due to lines and testers against line x tester interaction for the characters indicated the presence of variability.

The mean squares of GCA effect were significant for all characters except pollen fertility and number of primary branches per plant. The mean square of SCA effect were significant for all the characters except plant height, number primary branches per plant, number of seeds per pod and pod length. This indicated the presence of significant differences between males and females for these traits.

The estimates of GCA effects revealed that BSMR 736 B, BDN 2004-4 B, BDNHR 1 and BDNHR 35-8 were the good general combiners for grain yield per plant and most of the yield contributing characters. The lines BDN 2004-3 B and tester BDNHR 21-1-1 and BDNHR 36-7 have registered significant negative GCA effects for days to 50 per cent flowering and days to maturity.

In general, good general combiners for grain yield also had good or average combining ability for one or more yield components. In most of the parents high GCA effects were associated with high *per se* mean for yield and yield components. High GCA due to additive gene effects of parents helps for further selection of parents.

The relative ranking of hybrids on the basis of *per se* performance and SCA effects were different for some crosses. However, the crosses BSMR 736 A x BDNHR 22-1-1, BDN 2004-4 A x BDNHR 35-8 and BDN 2004-2 A x BDNHR 24-1-1-1 had high *per se* performance and desirable significant SCA effects for grain yield and other components.

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