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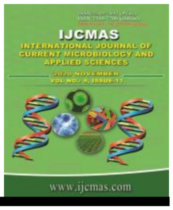

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Estimation of Combining Ability and Gene Action for Various Traits of Baby Corn in Line × Tester Analysis

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ABSTRACT

The increasing demand for baby corn intended us towards the development of single cross hybrids for baby corn speciality traits. The experiment consisted of the crossing of nine lines with three testers in line × tester mating design where the layout of the field was done under RCBD design with two replications at the University of Agricultural Sciences Dharwad during *Kharif* season 2019. The parental material consists of F_4 generation lines belonging to one heterotic group whereas the testers were derived from another heterotic group, representing sufficient genetic diversity and genetic distance between both lines and testers along with two commercial checks HM-4 (National baby corn check) and CPB 468 (Private hybrid). The line BBCP-27-1(L2) was identified as the best general combiner for various baby corn traits such as the number of ears per plant (Prolificacy), cob weight with husk (g), cob weight without husk (g) and baby corn yield without husk per plant (g). The estimates of specific combining effects indicated that the hybrid BBCP-11-1× BBCH-51-2 showed desirable *sca* effects for cob weight with husk (g), cob weight without husk (g), ear length (cm) and baby corn yield without husk per plant (g). The preponderance of both additive and non-additive gene action was observed for baby corn traits indicating the scope of operation of the selection force.

Keywords

Line × tester, Baby corn, Combining ability, *gca*, *sca*

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Introduction

Maize being a unique cereal on earth possesses speciality features at the different growth stages, one being the ‘Baby corn’. The young unfertilized corn ears harvested 2-3 days after silk emergence depending upon the developmental conditions of the plants is called baby corn. The geographical location of India paves the way towards foreign exchange with many countries belonging to Asia, Europe, Persia and many other Gulf countries. The dehusking of baby corn is mainly hand-operated that demands a huge labour force, suits developing countries like India due to the availability of low-cost labour (Ranjan *et al.,* 2013). The short duration of baby corn helps farmers to take 3-4 crops per year and fits well in different cropping systems by generating additional remuneration to the farmer’s income in peri-urban areas (Dass *et al.,* 2009). The scarcity of work done in the development of high yielding baby corn cultivars leads to their limited availability in the market. Currently, some early maturing grain maize cultivars are mainly used for baby corn purposes (Dhasarathan *et al.*, 2012). The line × tester analysis, is often, used in breeding programs of several cultivated crops, due to its efficiency in selecting parents for the development of hybrids with desired phenotypes. The estimates of general and specific combining ability of parents help breeder in the improvement of various quantitative and qualitative features of the crop and to evolve an economically sound hybrid. The elucidation of gene action also helps in the assessment of the heritability of the trait from one generation to the next generation. Hence, the current study aimed at the identification of promising lines, testers and single cross hybrids with desirable features for baby corn production through estimates of general and specific combining ability along with the type of gene action for various traits of baby corn.

Materials and Methods

The nine lines and three testers were crossed in 9 × 3 (line × tester) to produce 27 possible F_1 hybrids. Nine lines, three testers, F_1 hybrids and two commercial check hybrids i.e. HM-4 (National check), CPB 468 (Private check) were grown at the University of Agricultural Sciences Dharwad in India during the 2019 *Kharif* season. The genotypes were assigned at random to the experimental unit in each block and each row contained 10 plants. Each replication consists of 12 parents (lines and tester), 27 F_1 crosses and two check hybrids with a 3-meter long row for each genotype. The distance between rows and plants was 60 cm and 20 cm respectively. The twelve lines namely BBCP-8-2, BBCP-27-1, BBCP-37-2, BBCP-49-1, BBCP-27-2, BBCP-11-1, BBCP-41-1, BBCP-15-3, BBCP-10-1 and testers BBCH-95-2, BBCH-51-2, BBCH-120-1 were belonging to two different heterotic groups representing sufficient diversity between lines and testers. The crop was cultivated by following the recommended package of practices for cultivation. The observations were recorded on 10 plants selected by following systematic random sampling. The mean data of the following characters was used for analyzing the general combining ability (GCA), SCA (specific combining ability) and gene action using software WINDOSTAT (V 9.2) following the standard given by Kempthorne (1957). Baby corn yield and component characters are days to 50 % silking, number of baby corn per plant, husked weight of baby corn, dehusked weight of baby corn, baby corn length, baby diameter and baby corn yield without husk per plant.

Results and Discussion

The analysis of variance showed highly significant differences among the crosses, parents and lines for all the traits. Whereas the testers have shown significance for all the traits except cob weight with husk, ear length and ear diameter as shown in (Table 1). The significant difference of mean squares between parents and crosses for baby corn yield and yield related traits indicated their suitability for combining ability studies as observed by Tucak *et al.*, (2012) and Atif *et al.*, (2012). The significant difference between line × tester interactions for these traits indicated the presence of specific combining ability attribution in additive and dominance variance for all the baby corn traits. These results coincide with the findings of (Amiruzzaman *et al.*, 2010). The higher value of specific combining ability variance (σ^2SCA) than the general combining ability variance (σ^2GCA), the ratio of σ^2GCA/ σ^2SCA being less than one and degree of dominance being greater than one has a major role in the manifestation of non-additive gene effects (Ojo *et al.*, 2007) as presented in

(Table 2). In the current study preponderance of non-additive gene action is reported in the expression of various baby corn traits providing vital prospects for the exploitation of gene action in hybrid breeding. In the present study, all the parameters except cob weight without husk have shown higher SCA variances than GCA variances.

The contribution of line × tester interaction is greater than the contribution of testers for all the traits of baby corn except ear diameter, indicating a higher estimate of specific combining ability effects (Table 3). The close examination of parents indicated that none of the parents showed simultaneous significant GCA effects for all the traits studied (Table 4).

The estimation of variations in GCA effects was evaluated among lines and testers for all the traits for the development of promising baby corn hybrids.

Table.1 Analysis of variance for baby corn yield and related traits among F_1 hybrids and inbred lines in maize during *Kharif* 2019

Source of Variation	d.f.	Days to 50 % silking	Number of cobs per plant	Cob weight with husk (g)	Cob weight without husk (g)	Ear length (cm)	Ear diameter (cm)	Baby corn yield without husk per plant (g)
Replication	1	3.70	0.01	0.02	1.23	0.69	0.00	8.69
Parents	11	8.49**	0.83 **	53.95**	6.42**	2.37**	0.02**	78.57**
Females (Lines)	8	7.47**	0.77**	65.33**	7.66**	2.91**	0.03**	87.54**
Males (Testers)	2	10.16**	1.28**	0.93	4.10**	0.51	0.01	81.91**
Females V/s Males (Lines V/s Testers)	1	13.34**	0.39	68.93**	1.14	1.78	0.00	0.13
Crosses	26	6.89**	0.98**	54.27**	6.40**	3.80**	0.01*	150.98**
Parents V/s Crosses	1	0.92	3.18**	3036.52**	72.39**	29.38**	0.50**	1492.58**
Error	38	1.38	0. 10	2.49	0.49	0.77	0.00	10.83

* - Significant at 5 % level of significance ** - Significant at 1 % level of significance

Table.2 Estimates of GCA variance, SCA variance and predictability ratio (σ^2 GCA/ σ^2 SCA) along with prevailing gene action

SI. No.	Characters	σ^2 GCA	σ^2 SCA	σ^2 GCA/ σ^2 SCA	σ^2 A	σ^2 D	σ^2 A/ σ^2 D
1.	Days to 50 % silking	0.18	3.26	0.05	0.37	3.26	0.11
2.	Number of cobs per plant	0.10	0.32	0.31	0.20	0.32	0.62
3.	Cob weight with husk	1.70	33.38	0.05	3.41	33.38	0.10
4.	Cob weight without husk	0.42	2.64	0.15	0.85	2.64	0.32
5.	Ear length	0.38	1.36	0.27	0.76	1.36	0.55
6.	Ear diameter	0.00	0.00	0.00	0.00	0.00	0.00
7.	Baby corn yield without husk per plant	13.02	59.84	0.21	26.05	59.84	0.43

Table.3 The proportion of contribution of female, male and female × male for baby corn yield and related traits

SI. No.	Characters	Contribution of the line (%)	Contribution of the tester (%)	Contribution of line × tester (%)
1.	Days to 50 % silking	28.81	0.80	70.38
2.	Number of cobs per plant	40.21	11.05	48.73
3.	Cob weight with husk (g)	21.67	0.83	77.48
4.	Cob weight without husk (g)	38.69	4.20	57.09
5.	Ear length (cm)	40.69	9.65	49.64
6.	Ear diameter (cm)	12.97	21.03	65.99
7.	Baby corn yield without husk per plant (g)	38.01	7.78	54.20

Table.4 General combining ability (*gca*) effects of inbred lines for baby corn yield and related traits in maize

SI. No.	Inbreds	Characters						
		Days to 50 % silking	Number of cobs per plant	Cob weight with husk (g)	Cob weight without husk (g)	Ear length (cm)	Ear diameter (cm)	Baby corn yield without husk per plant (g)
Females (Lines)								
1.	BBCP-8-2	-1.88**	-0.18	0.30	1.68 **	1.11 **	0.01	3.52 *
2.	BBCP-27-1	-0.88	0.76 **	1.07 *	1.14**	0.33	0.02	9.46 **
3.	BBCP-37-2	0.44	-0.48 **	-1.44 **	0.83 *	1.02 **	0.02	-0.95
4.	BBCP-49-1	-0.55	-0.30 *	-4.77 **	-1.75 **	-1.61 **	-0.00	-6.63 **
5.	BBCP-27-2	0.11	0.70 **	3.36 **	0.66	0.56 *	0.03	7.11 **
6.	BBCP-11-1	0.11	0.08	-0.52	-1.36 **	-0.46	-0.06	-3.35 *
7.	BBCP-41-1	-0.05	-0.03	-2.11 **	-0.34	-0.04	0.01	-1.28
8.	BBCP-15-3	1.44 **	-0.51 **	2.38 **	-0.52	-1.06 **	-0.04	-5.82 **
9.	BBCP-10-1	1.27 *	-0.03	1.73 **	-0.34	0.14	0.00	-2.04
Male (Testers)								
1.	BBCH-95-2	-0.05	-0.32 **	0.05	-0.22	-0.11	0.04 *	-3.11 **
2.	BBCH-51-2	0.22	0.18 *	-0.59	-0.28	-0.44 **	-0.05 *	0.45
3.	BBCH-120-1	-0.16	0.13	0.54	0.50 *	0.56 **	0.00	2.65 **

* - Significant at 5 % level of significance ** - Significant at 1 % level of significance

Table.5 Specific combining ability (*sca)* effects of F_1 hybrids for baby corn yield and related traits

Sl. No.	**Hybrids**	**Characters**						
		Days to 50 % silking	**Number of cobs per plant**	**Cob weight with husk (g)**	**Cob weight without husk (g)**	**Ear length (cm)**	**Ear diameter (cm)**	**Baby corn yield without husk per plant (g)**
1.	BBCP-8-2 × BBCH-95-2	0.22	0.15	0.06	0.48	0.99 *	0.07	2.48
2.	BBCP-8-2 × BBCH-51-2	-0.05	-0.15	3.75 **	0.51	0.52	-0.02	0.58
3.	BBCP-8-2 × BBCH-120-2	-0.16	-0.00	-3.81 **	-0.99	-1.51**	-0.05	-3.06
4.	BBCP-27-1 × BBCH-95-2	1.72 *	-0.79 **	-6.13 **	0.42	0.06	0.02	-5.26
5.	BBCP-27-1 × BBCH-51-2	-2.05 *	1.05 **	0.18	-0.01	0.31	-0.01	8.29 **
6.	BBCP-27-1 × BBCH-120-2	0.33	-0.25	5.94 **	-0.41	-0.37	-0.01	-3.03
7.	BBCP-37-2 × BBCH-95-2	0.38	0.45	8.20 **	1.66**	0.48	0.07	7.95 **
8.	BBCP-37-2 × BBCH-51-2	1.11	0.25	-9.23 **	0.84	-0.07	0.06	4.27
9.	BBCP-37-2 × BBCH-120-2	-1.5	-0.70 **	1.02	-2.50 **	-0.40	-0.13	-12.22 **
10.	BBCP-49-1 × BBCH-95-2	0.88	-0.12	0.23	0.29	0.77	0.07	-0.36
11.	BBCP-49-2 × BBCH-51-2	-0.88	-0.93 **	2.56 **	-1.66 **	-1.94**	-0.12	-10.22 **
12.	BBCP-49-3 × BBCH-120-2	0.00	1.06 **	-2.80 **	1.37 *	1.17 **	0.05	10.59 **
13.	BBCP-27-2 × BBCH-95-2	-2.77**	-0.07	5.03 **	1.09	0.14	0.07	3.24
14.	BBCP-27-3 × BBCH-51-2	1.94 *	-0.23	-5.95 **	-0.73	15	-0.03	-4.85
15.	BBCP-27-4 × BBCH-120-2	0.83	0.31	0.91	-0.35	-0.29	-0.03	1.61
16.	BBCP-11-1 × BBCH-95-2	1.22	-0.41	-8.93 **	-2.75 **	-2.29**	-0.12	-10.28 **
17.	BBCP-11-2 × BBCH-51-2	0.44	0.38	3.92 **	2.48 **	1.35 **	0.12	10.39 **
18.	BBCP-11-3 × BBCH-120-2	-1.66	0.02	5.00 **	0.27	0.94 *	-0.00	-0.10
19.	BBCP-41-1 × BBCH-95-2	0.88	0.10	4.05 **	0.44	0.77	-0.01	1.94
20.	BBCP-41-1 × BBCH-51-2	-1.88 *	-0.4	-3.44 **	-2.18 **	-1.18**	-0.05	-10.11 **
21.	BBCP-41-1 × BBCH-120-2	1.00	0.29	-0.61	1.73 **	0.41	0.06	8.17 **
22.	BBCP-15-3 × BBCH-95-2	1.38	0.68 *	-3.23 **	-1.05	-1.49**	-0.05	1.59
23.	BBCP-15-3 × BBCH-51-2	0.11	-0.11	5.77 **	1.65 **	1.23 **	0.01	4.00
24.	BBCP-15-3 × BBCH-120-2	-1.50	-0.57 *	-2.53 **	-0.59	0.26	0.03	-5.60 *
25.	BBCP-10-1 × BBCH-95-2	-3.94**	0.00	0.71	-0.57	0.55	-0.12	-1.30
26.	BBCP-10-1 × BBCH-51-2	1.27	0.15	2.42 *	-0.89	-0.36	0.04	-2.35
27.	BBCP-10-1 × BBCH-120-2	2.66 **	-0.15	-3.13 **	1.47 *	-0.18	0.08	3.65

* - Significant at 5% level of significance ** - Significant at 1 % level of significance

Table.6 Best parents identified on basis of GCA effects and *per se* performance for different baby corn traits

Characters	**Parent**	**GCA effects**	***Per se* performance**
Days to 50 % silking	BBCP-8-2	-1.88**	58.50
Number of cobs per plant	BBCP-27-1	0.76 **	3.10
	BBCP-27-2	0.70 **	3.75
	BBCH-51-2	0.18 *	2.30
Cob weight with husk (g)	BBCP-27-2	3.36 **	22.15
	BBCP-15-3	2.38 **	39.38
	BBCP-10-1	1.73 **	23.38
	BBCP-27-1	1.07 *	26.32
Cob weight without husk (g)	BBCP-8-2	1.68 **	4.16
	BBCP-27-1	1.14**	6.18
	BBCP-37-2	0.83 *	2.92
	BBCH-120-1	0.50 *	4.42
Ear length (cm)	BBCP-8-2	1.11 **	7.37
	BBCP-37-2	1.02 **	6.64
	BBCP-27-2	0.56 *	6.75
	BBCH-120-1	0.56 **	7.03
Ear diameter (cm)	BBCH-95-2	0.04 *	1.08
Baby corn yield without husk per plant (g)	BBCP-27-1	9.46 **	19.25
	BBCP-27-2	7.11 **	17.82
	BBCP-8-2	3.52 *	13.29
	BBCH-120-1	2.65 **	17.30

* - Significant at 5% level of significance ** - Significant at 1 % level of significance

Table.7 Top three single cross hybrids for baby corn yield and yield related traits on *per se* mean

Sl. No.	**Characters**	**Cross**	***Per se* mean**	***sca* effect**	***gca* effect of inbreds**
1.	Days to 50 % silking	BBCP-27-2 × BBCH-95-2	53.5	-2.77**	M × M
		BBCP-27-1 × BBCH-51-2	53.5	-2.05 *	M × M
		BBCP-10-1 × BBCH-95-2	53.5	-3.94**	L × M
2.	Number of cobs per plant	BBCP-27-1 × BBCH-51-2	5.35	1.05 **	H × H
		BBCP-27-2 × BBCH-120-1	4.5	0.31	H × M
		BBCP-49-1 × BBCH-120-1	4.25	1.06 **	L × M
3.	Cob weight with husk (g)	BBCP-27-2 × BBCH-95-2	47.94	5.03 **	H × M
		BBCP-27-1 × BBCH-120-1	47.05	5.94 **	H × M
		BBCP-15-3 × BBCH-51-2	47.05	5.77 **	H × M
4.	Cob weight without husk (g)	BBCP-37-2 × BBCH-95-2	9.33	1.66**	H × M
		BBCP-8-2 × BBCH-95-2	9	0.48	H × M
		BBCP-8-2 × BBCH-51-2	8.96	0.51	H × M
5.	Ear length (cm)	BBCP-8-2 × BBCH-95-2	10.18	0.99 *	H × M
		BBCP-37-2 × BBCH-95-2	9.58	0.48	H × M
		BBCP-8-2 × BBCH-51-2	9.37	0.52	H × L
6.	Ear diameter (cm)	BBCP-27-2 × BBCH-95-2	1.38	0.07	M × H
		BBCP-37-2 × BBCH-95-2	1.37	0.07	M × H
		BBCP-8-2 × BBCH-95-2	1.37	0.07	M × H
7.	Baby corn yield without husk per plant (g)	BBCP-27-1 × BBCH-51-2	42.32	8.29 **	H × M
		BBCP-27-2 × BBCH-120-1	35.5	1.61	H × H
		BBCP-41-1 × BBCH-120-1	33.65	8.17 **	M × H

H- Significant *gca* in the desirable direction
M- Non- significant *gca*
L- Significant *gca* in an undesirable direction
* - Significant at 5 % level of significance ** - Significant at 1 % level of significance

Among the lines, BBCP-8-2, BBCP-27-1 and BBCP-27-2 had favorable genes for baby corn yield without husk per plant due to significant GCA effects. Generally, the higher *per se* performance for all the traits was associated with higher GCA effects except for days to 50 % silking. The line BBCP-8-2 has shown topmost performance for days to 50 % silking and identified as the desirable parent for early maturity. The results obtained confirm with the investigation of Ranjith *et al.*, (2014) and Kumari *et al.*, (2017).

The lines BBCP-27-1, BBCP-27-2 and BBCP-8-2 were observed to have the desired direction for maximum traits where the line BBCP-27-1 has shown significant GCA effects for the number of cobs per plant, cob weight with husk, cob weight without husk and baby corn yield without husk per plant.

Whereas, the line BBCP-27-2 has shown significant GCA effects for traits such as the number of cobs per plant, cob weight with husk, ear length and baby corn yield without husk per plant. Likewise, the line BBCP-8-2 has resulted in desirable GCA effects for days to 50 % silking, cob weight without husk, ear length and baby corn yield without husk per plant. The tester BBCH-120-1 was identified as the best combiner with high GCA effects for cob weight without husk, ear length and baby corn yield without husk per plant similar to Dhasarthan *et al.,* (2012). Whereas, the testers BBCH-51-2 and BBCH-95-2 have shown high GCA effects for the number of ears per plant and ear diameter respectively. The estimates of SCA effects indicated that none of the cross combinations exhibited desirable significant effects for all the traits studied (Table 5). Since baby corn yield is the ultimate goal of the baby corn breeding program. For this trait five hybrid combinations viz. BBCP-27-1 × BBCH-51-2, BBCP-37-2 × BBCH-95-2, BBCP-49-1 × BBCH-120-1, BBCP-11-1 × BBCP-51-2 and BBCP-41-1 × BBCH-120-1 were found good specific combinations based on high and significant SCA effects similar to the findings of Kumari *et al.*, (2017) and Izhar and Chakraborty (2013). Two cross combinations were reported to be the best combinations for various baby corn traits among which the hybrid BBCP-49-1 × BBCH-120-1 has shown good specific combining ability for the number of cobs per plant, cob weight without husk, baby corn length and baby corn yield without husk per plant. Similarly, for many other traits, a set of good specific combinations were identified based on high mean performance and SCA effects. The best hybrid combinations for various baby corn traits are represented in (Table 6). Hence (Table 7) includes the top-ranking cross combinations based on *per se* mean and SCA effects of crosses for various traits of baby corn.

In conclusion the out of 12 parental inbred lines, the line BBCP-27-1 was identified as the best general combiner for the majority of baby corn traits by exhibiting desirable GCA effects. Hence, the line can be extensively used in baby corn breeding programs. The hybrid BBCP-49-1 × BBCH-120-1 was identified as a good combiner for baby corn yield without husk per plant and the number of cobs per plant. These promising genotypes can be further utilized in advanced breeding strategies for baby corn yield and quality improvements.

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