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## Combining ability analysis for grain yield and its contributing traits in sorghum (*Sorghum bicolor* (L.) Moench)

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### Abstract

An experiment was conducted to assess the potential parental lines and crosses for grain yield and its contributing traits in sorghum (*Sorghum bicolor* (L.) Moench) using line x tester mating design. Thirty hybrids derived from mating five testers with six lines in L x T design along with their parents and two checks viz., CSH 15 R and CSV 22 R were evaluated in Randomized Block Design with three replications. Observations were recorded on randomly selected 5 five plants in each replication for grain yield and its contributing characters. Results evidenced the higher estimates of sca variances than the corresponding gca variances for the characters plant height, panicle length, panicle breadth, number of primaries per panicle, grain yield, fodder yield and harvest index. For general combining ability effects, Parbhani Moti and CSV 29R among the lines and PBMR 3, PBMR 5 among tester exhibited higher mean values and desired gca effects for grain yield and its contributing traits plant height, panicle breadth, number of primary branches, 100 grain weight and harvest index. CSV 29 R x PBMR 3 identified as best hybrid for grain yield as it exhibited significantly desirable sca effect followed by Parbhani Moti x PBMR 4, Phule Anuradha x PBMR 3, Parbhani Moti x PBMR 1, MS 104B x PBMR 3 and Parbhani Moti x PBMR 5. In addition to grain yield per plant these crosses also performed better for panicle breadth, number of primary branches per panicle, 100 seed weight and harvest index. Most of the crosses were derived from the parents with high x high or high x low gca effects indicating scope for selection of superior segregants with desirable genes in early segregating generations of bi-parental crosses or heterosis breeding to exploit non additive gene effects will be useful.

**Keywords:** Brown midrib sorghum, general combining ability, fodder quality parameters

### 1. Introduction

Lentil (*Lens culinaris* Medik) is a member of Leguminaceae family and it is commonly known Sorghum [*Sorghum bicolor* (L.) Moench] is the fifth major cereal crop of world following wheat, rice, maize and barley in terms of production and utilization. In India it is grown as dual purpose crop that serves both food and fodder requirement of rural population and cattle. Due to assured grain and fodder yields even under low input and receding moisture regimes than the other cereal crops, sorghum ensures certain degree of stability and sustainability to agriculture production of rain fed farming. Keeping in view the importance of sorghum as dual purpose crop under rainfed situation there is necessity to improve varieties and hybrids for grain and fodder yield. The knowledge of gene effects for different traits in governing grain, fodder yield and quality in sorghum is of prime importance before starting a precise breeding programme for their improvement.

Combining ability provides information on general and specific combining ability of parents for various polygenic traits. Both GCA and SCA components play an important role in selecting superior parents for hybrid combinations [5, 12] and represent a powerful method to measure the nature of gene action involved in quantitative traits [1]. GCA effects represent the fixable component of genetic variance, and are important to develop superior genotypes, while SCA represents the non- fixable component of genetic variation, it is important to provide information on hybrid performances. Therefore the present investigation was initiated to identify potential parents and the crosses for grain yield and its contributing traits and to elucidates the nature and magnitude of various types of gene actions involved in the expression of quantitative traits [4, 16].

### 2. Materials and Methods

Six lines viz., MS 104B, PMS 71B, ICSR 196, Parbhani Moti, CSV 29R and Phule Anuradha and five testers viz., PBMR 1, PBMR 2, PBMR 3, PBMR 4 and PBMR 5 belonging to the

different height, midrib colour and yield traits representing a fairly wide range of genetic diversity were crossed in a line x tester mating design for the development of experimental material to estimate combining ability. 30 F1s along with 12 parents and two checks *viz.*, CSH 15 R and CSV 22 R were evaluated at Sorghum Research Station, VNMKV, Parbhani during rabi 2018-19 in randomized block design with three replications. Both parents and F1 were raised each in two rows of 3 m length with a spacing of 45 cm x 15 cm. All the recommended practices were followed to raise good crop of *kharif* sorghum. The biometrical observations on grain yield and other related components *viz.*, days to 50 per cent flowering, plant height, panicle length, number of primaries per panicle, were recorded on randomly selected 5 five plants in each replication for grain yield, fodder yield and yield contributing traits. Data was analyzed by the methods outlined by [11] using mean values of five random plants in each replication from all treatments to find out the significance of treatment effect. The variation among the hybrids was further partitioned into genetic components attributable to general combining ability (GCA) and specific

combining ability (SCA) following the method suggested by [8].

### 3. Results and Discussion

The mean squares due to line x tester was significant for all the characters except for days to 50 per cent flowering indicating significant contribution of line x tester interaction towards the SCA variance (Table 1). Estimates of sca variances were higher than the corresponding gca variances for the characters plant height, panicle length, panicle breadth, number of primaries per panicle, grain yield, fodder yield and harvest index among yield and growth parameters indicating the predominance of non-additive gene action controlling these traits. Heterosis breeding therefore will be more realistic for exploitation of non-additive gene effects [2, 17]. reported the similar results. However values of GCA: SCA ratio for days to 50% flowering and 100 seed weight was more than 1 indicating aforesaid traits are resulted in by the additive gene action, hence selection for this trait in advanced segregating generations would be rewarding. Preponderance of additive gene action for these traits was also reported earlier [3].

**Table 1:** Analysis of variance for combining ability for yield and yield contributing traits of sorghum genotype

Source of variation	D.F.	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle breadth (cm)	No. of Primaries /panicle	Grain yield /plant (g)	100 seed weight (g)	Fodder yield/plant (g)	Harvest Index (%)
Replicates	2	1.233	4.211	8.823	0.055	3.019	16.478	0.014	5.990	7.596
Crosses	29	38.037**	1649.51**	22.969**	1.197**	289.838**	242.804**	0.790 **	536.940**	48.291**
<b>Estimates of variance components</b>										
$\sigma^2$ Line		1.856**	123.915	2.107	0.105	35.773*	37.454**	0.195**	35.028	5.317
$\sigma^2$ Tester		10.366**	301.615**	1.840	0.144*	27.692	20.483	0.039	87.558**	2.829
$\sigma^2$ GCA		6.498**	220.842**	1.961**	0.126**	31.365**	28.197**	0.110**	63.681**	3.960
$\sigma^2$ SCA		0.985	261.377**	4.691**	0.245**	57.907**	42.262**	0.077**	103.085**	12.124
$\sigma^2$ GCA/ $\sigma^2$ SCA		6.597	0.845	0.418	0.514	0.542	0.667	1.429	0.618	0.327

### 4. General combining ability (GCA) effects

The estimates of general combining ability (GCA) effects of all the parents comprising six female and four male parents for yield and yield contributing characters is presented in Table 2. Perusal of results indicated that the line Phule Anuradha and testers; PBMR 3 and PBMR 3 exhibited significant negative GCA effects for days to 50% flowering indicating the superiority of these parents in transmitting desirable genes for early flowering. Negative gca and sca effects for day to 50 per cent flowering also reported by [13]. Parbhani Moti and CSV 29R among the lines exhibited higher mean values and desired gca effects for grain yield and its

contributing traits; plant height, panicle breadth, number of primary branches, 100 grain weight and harvest index. Among the testers, PBMR 3 and PBMR 5 were found to be good general combiner with desired *per se* performance for grain yield and most of the yield contributing traits. Both of these lines and testers, also manifested higher mean and desired gca effects for fodder yield. The results are in accordance to the earlier findings [9, 7]. Therefore there is good scope to use these lines as source of genes in future breeding programme to breed the dual purpose sorghum hybrids or varieties with higher grain and fodder yield potential.

**Table 2:** Estimates of general combining ability effects (GCA) of parents for yield and yield contributing traits.

Sr. No.	Panicle length (cm)	Days to 50% flowering	Plant height (cm)	Panicle breadth (cm)	No. of Primaries/panicle	Grain yield/plant (g)	100 seed weight (g)	Fodder yield/plant (g)	Harvest Index (%)
<b>Lines</b>									
MS 104 B	-0.206	0.267	1.744	-0.326**	-2.878 **	-4.590 **	-0.228 **	-4.566	-1.316*
PMS 71B	1.569**	0.467	-8.256 **	0.106	0.089	-2.872 **	-0.344 **	1.379	-1.502*
ICSR 196	1.330**	-1.067	-11.456 **	-0.200**	-6.411 **	-4.978 **	-0.450 **	-9.79**	-1.03
Parbhani Moti	-1.928**	1.067	11.878 **	0.580**	7.756 **	7.254 **	0.639**	5.418**	2.727**
CSV 29 R	0.910	1.667**	14.678 **	0.056	6.689 **	8.495 **	0.447**	5.166**	3.232**
Phule Anuradha	-1.674**	-2.400**	-8.589 **	-0.216**	-5.244 **	-3.308 **	-0.063	2.394*	-2.112**
SE (m)	0.465	0.604	1.621	0.065	0.764	0.714	0.045	1.023	0.085
<b>Testers</b>									
PBMR 1	0.666	-2.700 **	-25.967**	-0.280**	-2.661 **	-0.319	-0.248 **	-4.655	0.581
PBMR 2	1.488**	-0.367	-5.522**	-0.233**	-4.578**	-4.067 **	-0.097 *	-6.526**	-0.603
PBMR 3	0.432	-2.644**	13.311**	0.658**	8.061**	7.815**	0.282**	9.894**	1.879**
PBMR 4	-2.266**	0.411	-0.078	-0.152*	-3.522**	-1.599*	-0.038	-9.123**	0.789*
PBMR 5	-0.321	5.3**	18.256**	0.008	2.700**	-1.830**	0.101*	10.409**	-2.646**
SE (m)	0.425	0.551	1.480	0.059	0.698	0.652	0.041	0.934	0.078

**Table 3:** Estimates of specific combining ability effects (SCA) of crosses for yield and yield contributing traits in sorghum

Sr. No.	Crosses	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle breadth (cm)	No. of Primaries/panicle	Grain yield/plant (g)	100 seed weight (g)	Fodder yield/plant (g)	Harvest Index (%)
1	MS 104B x PBMR 1	1.233	5.033	-1.018	-0.39**	-7.706 **	-9.737**	-0.102	-6.438**	-5.187 **
2	MS 104B x PBMR 2	2.233	9.589*	1.34	0.426**	10.878**	10.178**	0.097	13.15**	5.807**
3	MS 104 B x PBMR 3	-0.156	2.422	-1.398	0.079	2.906	5.215**	0.398**	6.624**	0.238
4	MS 104B x PBMR 4	-2.211	-12.189**	-0.713	-0.438**	-1.011	0.573	-0.074	-12.17**	2.828**
5	MS 104B x PBMR 5	-1.1	-4.856	1.789	0.322*	-5.067**	-6.23**	-0.32**	-1.165	-3.687**
6	PMS 71 B x PBMR 1	0.033	-1.3	1.933	0.007	8.661**	7.788**	0.367**	-6.923**	5.452**
7	PMS 71 B x PBMR 2	-0.633	-10.744**	-2.055	-0.276	-1.422	1.04	-0.041	-9.862**	1.787
8	PMS 71B x PBMR 3	-0.022	22.422**	-4.453**	0.17	-3.228	-4.803**	-0.520 **	4.572	-2.632**
9	PMS 71 B x PBMR 4	-0.411	-23.522**	3.025**	-0.23	-0.978	-6.425**	0.194	5.369*	-4.879**
10	PMS 71 B x PBMR 5	1.033	13.144**	1.55	0.330*	-3.033	2.399	-0.001	6.843**	0.273
11	ICSR 196 x PBMR 1	0.567	-1.767	2.843**	-0.307*	7.994**	5.402**	0.394**	18.903**	-0.116
12	ICSR 196 x PBMR 2	1.233	-26.211**	-0.566	0.816**	-6.589**	-8.763 **	-0.151	-6.356**	-5.455**
13	ICSR 196 x PBMR 3	-1.489	6.956	1.7	-0.434**	2.106	0.514	-0.05	6.375**	-0.157
14	ICSR 196 x PBMR 4	0.789	25.344**	-2.166*	0.472**	-5.978**	2.432	-0.366 **	-4.338	2.85**
15	ICSR 196 x PBMR 5	-1.1	-4.322	-1.811	-0.548**	2.467	0.416	0.172	-14.584**	2.878**
16	Parbhani Moti x PBMR 1	0.142	10.567**	-1.423	0.307*	9.994**	2.503	-0.136	4.221	0.5
17	Parbhani Moti x PBMR 2	-0.9	3.456	0.442	-0.543**	-10.089**	-1.832	0.033	-2.864	-0.552
18	Parbhani Moti x PBMR 3	0.044	-22.378**	2.79**	0.09	-9.394 **	-11.218**	0.034	-17.284**	-2.134*
19	Parbhani Moti x PBMR 4	0.656	6.344	1.085	-0.527**	9.856**	7.533**	0.155	9.066**	1.839*
20	Parbhani Moti x PBMR 5	0.1	2.011	-2.893 **	0.548**	-0.367	3.014	-0.087	6.861**	0.347
21	CSV 29 R x PBMR 1	-1.167	15.1**	-3.447 **	0.367*	-8.272 **	-9.302**	0.13	-2.699	-3.832 **
22	CSV 29 R x PBMR 2	-3.167 *	12.989**	2.531*	-0.62**	5.644**	1.87	-0.181	-5.842*	2.086*
23	CSV 29 R x PBMR 3	3.444*	-9.178*	1.843	-0.35*	-0.994	5.287**	0.07	-2.508	2.304*
24	CSV 29 R x PBMR 4	-0.611	-2.789	-1.279	0.486**	-3.744*	0.458	-0.026	9.616**	-1.266
25	CSV 29 R x PBMR 5	1.543	-16.122**	0.353	0.116	7.367**	1.686	0.008	1.433	0.709
26	Phule Anuradha x PBMR 1	-0.767	-27.633**	-0.483	-0.057	-10.67 **	3.345*	-0.654 **	-7.064**	3.183**
27	Phule Anuradha x PBMR 2	1.233	10.922**	-1.692	0.196	1.578	-2.493	0.242*	11.774**	-3.673**
28	Phule Anuradha x PBMR 3	-1.822	-0.244	1.113	0.446**	8.606**	5.004**	0.066	2.221	2.382*
29	Phule Anuradha x PBMR4	1.789	6.811	0.048	0.236	1.856	-4.572**	0.117	-7.542**	-1.372
30	Phule Anuradha x PBMR 5	-0.433	10.144**	1.013	-0.821**	-1.367	-1.284	0.228*	0.612	-0.52
	SE (m)	1.9086	5.126	1.4712	0.2056	2.4167	2.2580	0.1410	3.2338	1.2741
	C.D. @ 5%	3.8204	10.262	2.9449	0.4116	4.8376	4.5198	0.2822	6.4731	2.5504
	C.D. @ 1%	5.0831	13.654	3.9182	0.5476	6.4365	6.0137	0.3755	8.6125	3.3933

\*and \*\* Significant at 5% and 1% level respectively

### 5. Specific combining ability (SCA) effects

Regarding to the SCA effects, cross CSV 29 R x PBMR 2 showed significant and negative estimates for days to 50% flowering. Moreover crosses; Phule Anuradha x PBMR 3, Phule Anuradha x PBMR 1 and ICSR 196 x PBMR 3 exhibiting non-significant but negative sca effects. All these were derived from high x high cross combinations of GCA effects. High x high gca parents reflect additive x additive type of gene interaction [15] and therefore may be used as base population to select transgressive segregants for desirable accumulated genes for earliness. With the involvement of one parent with high GCA, the cross combination MS 104B x PBMR 3, Parbhani Moti x PBMR 4 and Phule Anuradha x PBMR 3 proven significant sca effects in desirable positive direction for grain yield per plant indicating prevalence of dominance genes in these crosses in inheritance of grain yield. The hybrids with high sca effects involving, high x low or low x high parental combinations may be due to accumulation of favourable genes and partly due to dominance and recessive reaction [7]. Whereas, crosses viz., MS 104 B x PBMR 2, PMS 71 B x PBMR 1 and ICSR 196 x PBMR 1 displayed significant and positive SCA effects with the involvement of low x low GCA parents displaying the importance of non-additive gene effects. While, cross CSV 29R x PBMR 3 derived from high x high parental combination in terms of gca effect indicated additive gene action influencing yield potential. [12, 6] obtained similar results for the grain yield in sorghum. Among the crosses with significant desirable effects for grain yield; ICSR 196 x PBMR 1, MS 104B x PBMR 2,

ICSR 196 x PBMR 3, Phule Anuradha x PBMR 3 and Parbhani Moti x PBMR 4 also exhibited significant positive sca effects for fodder yield per plant. Amongst these first three crosses were derived from low x low, while other two were derived from high x high and high x low gca combinations respectively [14, 3], summarized the similar results for fodder yield. In addition to grain yield per plant the crosses also performed significant sca effects in desirable direction for one or more yield contributing traits like crosses MS 104B x PBMR 2 and Phule Anuradha x PBMR 3 for panicle breadth, number of primary branches per panicle and 100 seed weight harvest index, Parbhani Moti x PBMR 4 and PMS 71 B x PBMR 1 for number of primaries, 100 seed weight and harvest index. Moreover crosses; MS 104B x PBMR 2, ICSR 196 x PBMR 3 and Phule Anuradha x PBMR 3 also exhibited significant negative sca effects for days to 50 per cent flowering indicating early flowering behavior of the crosses. There is good scope to isolate the dual purpose high yielding and early duration segregants in segregating generations from aforesaid crosses. Both additive and non-additive gene effects can be exploited in sorghum for attaining improvement in yield and yield contributing traits.

### 6. Conclusion

Parents Parbhani Moti, CSV 22 R, PBMR 3 and PBMR 5 may be utilized as a source of potential genes in future breeding programme to exploit additive gene effects. Whereas, on the basis of significant desirable sca effects F<sub>1</sub> hybrids viz., MS 104B x Bmr 7-4-1, PMS 71 B x Bmr 7-4-1,

Parbhani Moti x Bmr 7-2-2, Phule Anuradha x Bmr 7-4-1 and ICSR 196 x Bmr 7-4-1 identified as potential crosses for grain yield, fodder yield may be advanced applying recurrent selection for simultaneous exploitation of both additive and non-additive gene action to develop the high yielding sorghum genotypes.

### 7. Conflict of interest

The authors confirm that there are no known conflicts of interest associated with publication of this paper.

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