



Combining Ability Analysis for Grain Yield and Yield Components using Potential Restorers in Pearl Millet

Bharath Kumara K.*, B.K. Athoni and C.D. Soregaon

University of Agricultural Sciences, Dharwad 580 005, India

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Abstract: Three A₁ CMS sources (ICMB 94555, ICMB 98222 and ICMB 96666) were crossed with fifteen potential restorer lines in line × tester fashion to elucidate the information on the combining ability for seed yield and its component traits. A total of forty five crosses were evaluated for eleven different quantitative traits. Among the three lines used in the study, ICMB 96666 and ICMB 98222 exhibited significant general combining ability (GCA) effects for most of the characters studied and were found to be the good combiners. Likewise, among testers PRLN 117 and PRLN 109 were found to be good general combiners for most of the traits under observation. The estimates of variance components revealed predominance of non-additive gene action for most of the characters studied.

Key words: Pearl millet, A₁ CMS source, combining ability, Line × tester analysis, gene action.

Pearl millet [*Pennisetum glaucum* (L.) R. BR] is an important cereal crop of India but its average productivity is quite low. Development of pearl millet hybrids with improved yield potential is thus prerequisite to increase its productivity. Therefore, the choice of parents through careful and critical evaluation is of very important in order to improve productivity and total production. The seed yield and yield attributing characters in pearl millet show polygenic inheritance and are thus susceptible to environmental fluctuations. Therefore, selection of parents for hybridization is a complex problem.

The concept of combining ability was formulated by Sprague and Tatum (1942). General combining ability (GCA) is the average performance of a strain in a series of cross combinations, estimated from the performance of F₁ from the crosses, whereas specific combining ability (SCA) is used to designate those cases in which certain combinations do relatively better or worse than would be expected on the basis of average performance of lines involved. General combining ability and specific combining ability display additive and non-additive gene actions, respectively. This helps the breeders to assess the parents for adoption in heterosis breeding program. Therefore, it is essential to study combining ability to select superior combination of parents to attain maximum success in the breeding program.

The choice of the parents is governed by *per se* performance of the parents and behavior of the parents in respective hybrid

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Praveen Kumar
R.N. Kumawat
R.K. Solanki
N.K. Jat

*Correspondence

Bharath Kumara K.
knbharath920@gmail.com

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Table 1. Analysis of variance (Mean sum of squares) for morpho-phenological characters in pearl millet

Source	Df	DF	DM	PH	NP	RCF
Replication	2	0.422	3.162	440.452	0.092	0.509
Crosses/Hybrids	44	21.460**	15.470**	354.886**	0.083**	44.453**
Line	2	27.444**	36.111**	1436.333**	0.671**	1.991
Tester	14	15.342**	12.848**	330.355**	0.126**	11.083
L × T	28	24.157**	15.953**	250.196**	0.096**	30.839**
Error	88	2.861	1.572	71.720	0.029	2.372
Contribution of line %		2.711	0.028	18.399	13.787	24.090
Contribution of tester %		25.656	34.342	36.737	12.477	31.762
Contribution of L × T %		71.632	65.630	44.863	73.735	44.148
GCA variance		0.337	0.280	24.923**	0.001	4.042**
SCA variance		7.291**	4.818**	59.965**	0.021**	8.850**
GCA/SCA		0.046	0.058	0.415	0.080	0.457

Source	RCM	PL	PG	GY	DFY	TW
Replication	5.311	10.792	0.089	11716.910	120545.986	14.836
Crosses/Hybrids	199.007**	9.590**	0.164**	12178.471**	83795.240**	8.166**
Line	124.607**	4.964	0.937**	17203.181*	5529.643	6.457
Tester	71.194**	8.328**	0.324**	4300.226	54131.426**	7.773**
L × T	150.880**	8.547**	0.106**	11265.764**	37378.842**	9.834**
Error	2.823	2.903	0.021	3789.075	14742.447	1.859
Contribution of line %	15.605	16.773	41.470	8.706	33.840	0.634
Contribution of tester %	36.148	26.508	17.372	32.427	37.766	22.661
Contribution of L × T %	48.247	56.718	41.157	58.867	28.387	76.704
GCA variance	11.250	0.486	0.025**	244.560*	120.127**	0.235
SCA variance	48.981**	1.930**	0.0285**	2734.415**	75.692**	2.697**
GCA/SCA	0.230	0.252	0.896	0.089	1.587	0.087

Note: *Significance at 5% probability, **significance at 1% probability

DF: days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NP: No of productive tillers plant⁻¹; RCF: Relative chlorophyll content at flowering; RCM: Relative chlorophyll content at maturity; PL: Panicle length (cm); PG: Panicle girth (cm); GY: Grain yield kg ha⁻¹; DFY: Dry fodder yield kg ha⁻¹; TW: 1000 Seed weight (g)

combination. Some idea on the usefulness of parents may be obtained from their individual performance particularly in respect of yield components (Gilbert, 1958). The mode of gene action depends upon the genetic structure and extent of divergence between the parents involved. Therefore, it is necessary to estimate the genetic potentialities of parents in hybrid combinations through systematic studies with regard to general combining ability and specific combining ability. A wide range of variability and cytoplasmic male sterility sources are available in pearl millet. In present study A₁ cytoplasm based lines and potential restorers were used to generate experimental hybrids to identify the good combiners for further utilization in hybridization programs.

Many biometrical procedures have been developed to obtain information on combining ability with line × tester analysis (Kempthorne, 1957) is one among them, which is widely used

to study combining ability of the parents to be chosen for heterosis breeding. The present investigation was under taken with a view to identify the lines with good combining ability and to identify the good specific crosses for further exploitation.

Material and Methods

The present study was carried out during *kharif* 2021 at Regional Agricultural Research Station, Vijayapura (Karnataka) India, located in the northern dry zone of Karnataka at an altitude of 593 m from mean sea level. Crossing program was done in summer 2021 and evaluation of parents and F₁'s along with checks (GHB558, VPMH 7 and Kaveri Super Boss) was taken up in *kharif* 2021. All the experimental hybrids produced were sown along with their parents and three checks including one national check (GHB558), one local check (VPMH 7) and one commercial check *i.e.*, Kaveri Super Boss in a Randomized Block Design (RBD) with three

Table 2. Estimates of general combining ability (gca) effects of lines for morpho-physiological characters in pearl millet

Parents (Lines)	DF	DM	PH	NP	RCF	RCM	PL	PG	GY	DFY	TW
ICMB 94555	0.00	0.05	-4.87**	0.03	-2.31**	0.70*	-0.18	-0.16**	-23.16*	-12.17**	-0.15
ICMB 98222	-0.53**	-0.04	-1.32	-0.08**	2.27**	-4.20**	-0.78**	0.20**	0.80	0.84	0.16
ICMB 96666	0.53**	-0.01	6.19**	0.05	0.04	3.50**	0.96**	-0.04	22.36**	11.33**	-0.01
S.E (gi)	0.22	0.18	1.25	0.02	0.31	0.30	0.25	0.02	8.25	1.81	0.20
S.E (gi-gj)	0.32	0.26	1.77	0.04	0.43	0.42	0.35	0.03	11.67	2.55	0.28
C.D. at 5%	0.45	0.36	2.48	0.05	0.61	0.59	0.49	0.04	16.39	3.59	0.40
C.D. at 1%	0.60	0.48	3.30	0.07	0.81	0.78	0.65	0.05	21.72	4.75	0.51

Note: *Significance at 5% probability, **significance at 1% probability

DF: days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NP: No of productive tillers plant⁻¹; RCF: Relative chlorophyll content at flowering; RCM: Relative chlorophyll content at maturity; PL: Panicle length (cm); PG: Panicle girth (cm); GY: Grain yield kg ha⁻¹; DFY: Dry fodder yield kg ha⁻¹; TW: 1000 Seed weight (g)

replications. Each hybrid was accommodated in 2 rows of 3 meter row length with a row spacing of 45 cm and plant to plant spacing of 15 cm

The parent materials for the present study consisted of three cytoplasm male sterile lines *viz.*, ICMB 94555, ICMB 98222 and ICMB 96666 and fifteen restorer lines *viz.*, PRLN 102, PRLN 105, PRLN 106, PRLN 109, PRLN 113, PRLN 114, PRLN 115, PRLN 116, PRLN 117, PRLN 120, PRLN 125, PRLN 129, PRLN 131, PRLN 133 and PRLN 140.

From each entry/replication, five random, competitive plants were tagged and numbered in the middle of the row to observe yield and

other quantitative characters. Mean of the plants was computed and taken for analysis. The following observations were recorded: *viz.*, days to 50% flowering, days to maturity, relative chlorophyll content at flowering and maturity stage measured by chlorophyll meter (SPAD), plant height (cm), number of productive tillers per plant, panicle length (cm), panicle girth (cm), grain yield (kg ha⁻¹), dry fodder yield (kg ha⁻¹) and thousand seed weight (g). The data were analyzed by line × tester design.

Results and Discussion

The analysis of variance for combining ability of parents and crosses for different

Table 3. Estimates of general combining ability (gca) effects of testers for morpho-phenological characters in pearl millet

Parents (Testers)	DF	DM	PH	NP	RCF	RCM	PL	PG	GY	DFY	TW
PRLN 102	-0.47	-0.46	5.21	0.02	0.32	-3.77**	-0.79	0.08	78.90**	-5.22	1.93**
PRLN 105	-0.91	-1.35*	-0.01	-0.07	-1.07	-6.52**	-0.01	-0.06	-0.11	-16.62**	-0.70
PRLN 106	-1.47*	-1.80**	-8.12*	-0.05	0.91	-4.00**	-0.99	-0.04	-13.69	-9.70*	-0.99*
PRLN 109	-0.91	-1.80**	11.66**	-0.09	-2.87**	-6.84**	0.05	0.12*	84.66**	-7.69	0.51
PRLN 113	0.64	1.32*	0.77	-0.05	-2.67**	-1.84*	-0.04	-0.13*	2.77	-4.56	0.54
PRLN 114	1.86**	1.76**	-4.45	0.09	0.63	-4.78**	0.19	0.03	-16.57	-3.90	0.09
PRLN 115	0.53	1.21*	6.43*	0.02	-2.30*	-0.51	-0.14	0.18**	-41.26*	-13.04**	-1.11*
PRLN 116	1.31	0.54	0.88	0.04	-0.87	-0.70	-0.08	-0.07	-32.21	-6.37	0.11
PRLN 117	1.53*	1.32*	6.55*	-0.05	-1.38*	3.56**	2.37**	0.08	-18.22	9.10*	1.06*
PRLN 120	-3.13**	-2.24**	3.44	0.00	1.12	7.10**	-0.08	-0.08	-10.40	18.03**	0.34
PRLN 125	-0.46	-0.68	-4.12	0.07	2.22*	6.07**	-0.54	0.02	9.36	9.14*	-0.47
PRLN 129	-0.13	-0.01	-7.34*	0.02	0.84	4.77**	-1.39*	0.12*	13.88	6.76	-0.26
PRLN 131	-0.02	1.21*	-7.67*	0.00	2.99**	7.50**	-0.48	-0.13*	-11.63	14.70**	-0.23
PRLN 133	-0.46	-0.46	7.21*	-0.07	4.6**	-3.63**	1.61*	-0.02	-2.58	-0.16	-0.15
PRLN 140	2.09**	1.43**	-10.45**	0.11	-2.47**	3.59**	0.32	-0.12*	-42.91*	9.51*	-0.67
S.E (gi)	0.50	0.41	2.80	0.06	0.70	0.66	0.55	0.05	18.45	4.04	0.44
S.E (gi-gj)	0.71	0.58	3.95	0.08	0.97	0.93	0.78	0.07	26.09	5.71	0.62
C.D. at 5%	1.00	0.81	2.48	0.12	1.37	1.31	1.10	0.10	36.66	8.02	0.87
C.D. at 1%	1.33	1.07	3.30	0.16	1.81	1.74	1.45	0.12	48.57	10.63	1.16

Note: *Significance at 5% probability, **significance at 1% probability

DF: days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NP: No of productive tillers plant⁻¹; RCF: Relative chlorophyll content at flowering; RCM: Relative chlorophyll content at maturity; PL: Panicle length (cm); PG: Panicle girth (cm); GY: Grain yield kg ha⁻¹; DFY: Dry fodder yield kg ha⁻¹; TW: 1000 Seed weight (g)

Table 4. Estimates of specific combining ability (sca) effects for morpho-physiological characters in pearl millet

S. No.	Crosses	DF	DM	PH	NP	RCF	RCM	PL	PG	GY	DFY	TW
1.	ICMA 94555 × PRLN 102	-1.56	-1.94**	-3.02	-0.123	-2.35	2.64*	-0.07	-0.30**	-20.47	-11.16	-0.89
2.	ICMA 94555 × PRLN 105	0.22	1.62*	-3.46	-0.23*	-2.39*	-4.77**	-0.71	0.07	41.26	-6.68	1.23
3.	ICMA 94555 × PRLN 106	-0.89	0.06	-5.02	0.08	-0.24	5.20**	-1.53	-0.02	47.44	14.56*	1.76*
4.	ICMA 94555 × PRLN 109	-1.78*	-0.94	-11.12*	0.12	0.92	-0.25	2.02*	-0.27*	-29.93	4.52	-0.58
5.	ICMA 94555 × PRLN 113	-3.67**	3.05**	-2.57	0.14	-2.08	3.26**	1.69	0.07	48.26	-3.05	-1.77*
6.	ICMA 94555 × PRLN 114	3.11**	3.50**	0.65	0.01	2.58*	1.12	0.36	0.08	16.98	-10.26	0.31
7.	ICMA 94555 × PRLN 115	3.44**	2.06**	9.10	-0.06	-4.35**	6.02**	-2.04*	-0.30**	-31.17	8.63	0.54
8.	ICMA 94555 × PRLN 116	4.00**	0.73	1.99	-0.15	-2.75*	-7.52**	-0.31	0.12	-34.05	-1.98	-0.71
9.	ICMA 94555 × PRLN 117	1.11	0.94	11.99*	0.14	0.79	-0.82	0.84	0.16	-15.94	-2.03	0.74
10.	ICMA 94555 × PRLN 120	-1.22	0.50	1.43	-0.10	0.29	-1.69	-0.24	0.06	66.37*	-5.89	-1.54*
11.	ICMA 94555 × PRLN 125	1.44	0.94	-3.68	0.23*	1.85	0.77	-1.38	0.10	-69.44*	15.34*	1.14
12.	ICMA 94555 × PRLN 129	-0.56	0.28	8.54	0.08	3.20**	6.57**	0.53	-0.07	-45.57	7.73	-2.37**
13.	ICMA 94555 × PRLN 131	4.33**	2.06**	1.21	-0.10	6.39**	4.14**	-1.84	0.01	-118.82**	5.96	-0.47
14.	ICMA 94555 × PRLN 133	-3.22**	-3.61**	-8.68	0.10	2.38	-4.56**	1.87	0.10	70.89*	0.07	-0.35
15.	ICMA 94555 × PRLN 140	-4.78**	-3.16**	2.65	-0.15	-4.21**	-10.11**	0.82	0.20*	74.18*	-15.77*	2.94**
16.	ICMA 98222 × PRLN 102	1.31	1.14	11.43*	0.33**	-0.06	1.44	0.21	0.47**	13.61	10.03	0.66
17.	ICMA 98222 × PRLN 105	0.76	0.37	1.65	0.15	-2.23	7.77**	-0.70	-0.02	-32.10	2.04	-0.09
18.	ICMA 98222 × PRLN 106	2.64**	3.15**	9.10	0.06	-0.38	-7.73**	1.41	-0.01	1.26	-9.81	-1.32
19.	ICMA 98222 × PRLN 109	1.76*	1.82*	-5.35	-0.03	-0.09	2.26	-1.37	0.24**	23.90	-8.25	-1.03
20.	ICMA 98222 × PRLN 113	0.87	2.04**	3.21	0.06	1.54	-5.61**	-1.00	-0.09	26.78	-6.10	0.38
21.	ICMA 98222 × PRLN 114	-1.69	-2.07**	6.76	-0.14	-3.23**	-3.78**	-0.37	-0.14	16.50	-1.17	-2.01*
22.	ICMA 98222 × PRLN 115	-2.36**	-2.85**	-2.79	-0.07	3.47**	-8.88**	0.23	0.27**	37.48	-4.13	0.89
23.	ICMA 98222 × PRLN 116	-2.47**	-1.52*	-8.24	-0.09	0.01	1.41	0.50	-0.11	24.72	-12.90	-1.03
24.	ICMA 98222 × PRLN 117	-3.36**	-2.96**	-6.57	-0.14	-0.42	0.98	-1.95*	-0.10	0.85	-1.33	-2.01*
25.	ICMA 98222 × PRLN 120	-1.69	-1.41*	-0.13	0.02	-2.06	-0.86	1.23	-0.16	-14.38	4.06	0.35
26.	ICMA 98222 × PRLN 125	-1.36	-0.63	-0.57	-0.05	-0.79	-6.50**	1.23	-0.06	0.44	-2.98	1.46
27.	ICMA 98222 × PRLN 129	0.98	0.04	-5.02	-0.20	-1.45	-1.03	0.21	0.14	-15.20	-7.38	1.01
28.	ICMA 98222 × PRLN 131	-1.47	-1.52*	6.99	0.22*	-1.22	-7.89**	-1.24	0.01	111.55**	14.55*	2.91**
29.	ICMA 98222 × PRLN 133	1.64	1.82*	-12.57*	-0.05	2.53*	11.01**	-1.13	-0.16	-93.80*	5.21	1.20
30.	ICMA 98222 × PRLN 140	4.42**	2.59**	2.10	-0.09	4.38**	17.42**	2.76**	-0.26**	-101.62*	18.13*	-1.37
31.	ICMA 96666 × PRLN 102	0.24	0.79	-8.42	-0.21*	2.40*	-4.09**	-0.14	-0.16	6.86	1.14	0.23
32.	ICMA 96666 × PRLN 105	-0.98	-1.99**	1.81	0.08	4.63**	-3.00*	1.42	-0.05	-9.20	4.63	-1.14
33.	ICMA 96666 × PRLN 106	-1.76*	-3.21**	-4.08	-0.14	0.62	2.54*	0.13	0.02	-48.697	-4.75	-0.44
34.	ICMA 96666 × PRLN 109	0.02	-0.87	16.47**	-0.10	-0.83	-2.01	-0.65	0.04	6.04	3.73	1.60*
35.	ICMA 96666 × PRLN 113	2.80**	1.01	-0.64	-0.21*	0.54	2.36*	-0.68	0.01	-75.03*	9.12	1.39
36.	ICMA 96666 × PRLN 114	-1.42	-1.43*	-7.41	0.13	0.66	2.66*	0.02	0.06	-33.47	11.42	1.70*
37.	ICMA 96666 × PRLN 115	-1.09	0.79	-6.30	0.13	0.89	2.86*	1.82	0.04	-6.31	-4.50	-1.43
38.	ICMA 96666 × PRLN 116	-1.53	0.79	6.25	0.24*	2.74*	6.11**	-0.18	-0.01	9.33	14.88*	1.74*
39.	ICMA 96666 × PRLN 117	2.24*	2.02**	-5.42	-0.01	-0.36	-0.15	1.10	-0.06	15.09	3.36	1.27
40.	ICMA 96666 × PRLN 120	2.91**	0.90	-1.30	0.08	1.77	2.55*	-0.98	0.10	-51.99	1.84	1.19
41.	ICMA 96666 × PRLN 125	-0.09	-0.32	4.25	-0.19	-1.06	5.74**	0.15	-0.03	68.99**	-12.36	-2.60**
42.	ICMA 96666 × PRLN 129	-0.42	-0.32	-3.53	0.13	-1.75	-5.53**	-0.74	-0.06	60.77	-20.51*	1.36
43.	ICMA 96666 × PRLN 131	-2.87**	-0.54	-8.19	-0.12	-5.16**	3.75**	3.08**	-0.02	7.27	-5.28	-2.44**
44.	ICMA 96666 × PRLN 133	1.58	1.79*	21.25**	-0.05	-4.91**	-6.45**	-0.74	0.07	22.91	-2.36	-0.86
45.	ICMA 96666 × PRLN 140	0.36	0.57	-4.75	0.24*	-0.16	-7.31**	-3.58**	0.07	27.44	13.90	-1.57*
	S.E _(ij)	0.87	0.70	4.84	0.10	1.20	1.14	0.96	0.08	31.95	6.99	0.76
	S.E(S _{ij} -S _{id})	1.23	1.00	6.84	0.14	1.70	1.62	1.35	0.11	45.18	9.89	1.08
	C.D. at 5%	1.73	1.40	9.62	0.20	2.37	2.27	1.90	0.16	63.50	13.90	1.52
	C.D. at 1%	2.30	1.85	12.74	0.27	3.14	3.01	2.52	0.22	84.12	18.41	2.01

Note: *Significance at 5% probability, **significance at 1% probability

DF: days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NP: No of productive tillers plant⁻¹; RCF: Relative chlorophyll content at flowering; RCM: Relative chlorophyll content at maturity; PL: Panicle length (cm); PG: Panicle girth (cm); GY: Grain yield kg ha⁻¹; DFY: Dry fodder yield kg ha⁻¹; TW: 1000 Seed weight (g)

yield component traits in line \times tester design (Table 1) indicated the significant variation for all the traits indicating the existence of genetic diversity in the parental material and varying performance of the cross combinations. The level of contribution by the lines was more for the characters such as days to 50% flowering, panicle weight, grain yield, dry fodder yield. On the other hand, testers contributed most of the characters except panicle girth. Whereas contribution of line \times tester interaction was highest for most of the traits except dry fodder yield indicating that the testers were highly divergent from lines. The SCA variance was higher than GCA variance for all the traits studied indicating predominance of non-additive type of gene action which is in agreement with the findings of Yadav and Sabharwal (2001), Vagadiya *et al.* (2010), Saini *et al.* (2018), Kumar *et al.* (2020) and Dutta *et al.* (2021).

The general combining ability effects (Table 2) indicated that ICMB 96666 was good general combiner as evident from its significant GCA effect in desirable direction for as many as five characters *viz.*, plant height, relative chlorophyll content at maturity, panicle length, grain yield and dry fodder yield. The next best general combiner was ICMB 98222 for days to 50% flowering, relative chlorophyll content at flowering and panicle girth.

Among the testers, out of fifteen testers, eighteen of them were found in the high category *viz.*, PRLN 102, PRLN 109, PRLN 116, PRLN 117, PRLN 120, PRLN 125, PRLN 129, PRLN 131 and PRLN 133. PRLN 117 had better general combining ability for plant height, relative chlorophyll content at maturity, panicle length, dry fodder yield and thousand seed weight. Whereas PRLN 109 had better general combining ability for plant height, panicle girth and grain yield per hectare (Table 3).

Similar observations have been made by several earlier workers (Vagadiya *et al.*, 2010; Saini *et al.*, 2018; Kumar *et al.*, 2020 and Dutta *et al.*, 2021). The lines and testers exhibiting highly significant positive GCA effect for grain yield ha^{-1} and other yield components can be further used in crossing program to develop superior hybrids or to derive superior recombinants which could be used to develop parental lines.

The SCA effects (Table 4) showed that, three of the hybrids recorded higher SCA effects for

all the traits. The cross, ICMA 98222 \times PRLN 131 registered maximum SCA effect for grain yield ha^{-1} . The other crosses *viz.*, ICMA 94555 \times PRLN 140 and ICMA 94555 \times PRLN 133 also exhibited highly substantial SCA effect for grain yield ha^{-1} .

The crosses *viz.*, ICMA 98222 \times PRLN 140, ICMA 94555 \times PRLN 125 and ICMA 96666 \times PRLN 116 exhibited highly substantial SCA effect for dry fodder yield ha^{-1} .

Five hybrids recorded higher significant positive SCA effects for grain yield. The hybrids which were considered superior for this trait were, ICMA 98222 \times PRLN 131 (111.55), ICMA 94555 \times PRLN 140 (74.18) and ICMA 94555 \times PRLN 133 (70.89).

The extent of SCA effects for dry fodder yield was positive and significant for seven hybrids. The superior crosses exhibiting high sca effect for this trait were; ICMA 98222 \times PRLN 140 (18.13^{*}), ICMA 94555 \times PRLN 125 (15.34^{*}) and ICMA 96666 \times PRLN 116 (14.88^{*}).

The crosses with significant SCA for grain yield ha^{-1} also exhibited high specific combining ability for other yield components indicating that improvement in grain yield ha^{-1} could be achieved by improving other yield components like panicle length, panicle girth, number of productive tillers plant^{-1} and thousand seed weight. It was also observed that, crosses which showed significant sca effect for grain yield per hectare, also exhibited significant heterosis.

The present study and earlier reports of Vagadiya *et al.* (2010), Saini *et al.* (2018), kumar *et al.* (2020) and Dutta *et al.* (2021) clearly indicated that the grain yield ha^{-1} is predominantly under the control of non-additive gene action.

The crosses showing both significantly high heterosis and sca effect for grain yield ha^{-1} were observed in the present study. It indicates that the crosses with high SCA effect are generally heterotic in nature. The information on combining ability and heterosis considered together would be more meaningful. If the heterotic hybrids involve parents with high GCA effect, it implies that the parental contribution to heterosis is mainly through additive gene effect. The present study indicates that highly heterotic hybrids could be obtained from parents with any combination of GCA *i.e.*, High \times High, High \times Low, Low \times High

and Low \times Low which further substantiate the operation of non-additive gene action for the characters studied. However, the frequency of heterotic hybrids was comparatively more in High \times Low or Low \times High type of crosses. Therefore, it can be concluded in the present investigation that almost all the characters studied were governed by non-additive gene action. Therefore, large number of parents with wide genetic divergence should be involved in future studies to identify high grain yielding hybrids coupled with high dry fodder yield.

Conclusion

The results of current study indicated the preponderance of non-additive type of gene effects along with high heterosis and existence of superior crosses with high SCA effects. The material used in current study may be best exploited through hybrid breeding program. Highly diverse parental lines can be exploited to develop bi-parental mapping population to identify the QTL responsible for mineral accumulation in grains.

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