Plant Archives
Journal home page: www.plantarchives.org

PARENTAL SELECTIONS IN SORGHUM (*SORGHUM BICOLOR* L.) ON THE BASIS OF HETEROSIS AND COMBINING ABILITY IN ASSOCIATION WITH SSR DIVERSITY IN SUB-TROPICAL PLAINS OF UTTARAKHAND, INDIA

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ABSTRACT

Selection of genetically diverse and complementary parents for important key traits is most difficult task in any hybrid breeding programme. The objective of this study was to estimate heterosis and relative combining abilities with associated SSR diversity for identification of unique *sorghum* genotypes. A total of forty crosses and thirteen parental lines including five cytoplasmic male sterile (CMS) lines and eight pollinator lines with two standard check varieties were phenotyped using six agro-morphological traits and genetic diversity was estimated by using five polymorphic SSR markers. *Sorghum* genotypes were crossed with CMS lines using a line × tester mating design and 40 hybrids, 13 parents and two check varieties were field-evaluated using alpha lattice design with three replications. General combining ability (GCA), specific combining ability (SCA) and heterosis for grain yield and other associated attributes were determined. SSR diversity estimates were ranged from 0.54 to 0.90. Among CMS lines, 11A2 and MR750A2 and among pollinators, UPC2 and M35-1 were reported as best general combiners. A2 cytoplasm was found to be more efficient to produce more heterotic combination with experimental lines. Cross, 11A2 x UPC2 gave best results of heterosis for most of the characters. MR750 A2 x UPC2, 11A2 x UPC2, ICSA467 x UPC2, ICSA467 x CS3541, ICSA 467 x RS29, ICSA 467 x M35-1 and 11A2 x M35-1 revealed significant and positive values of heterosis, SCA and GCA. However, no direct correlation was detected with heterosis and molecular diversity for most of the characters. These results may be used for the exploitation of hybrid vigor in *sorghum* breeding programmes.

Keywords: GCA, heterosis, phenotypic traits, SCA, *sorghum bicolor*, SSR markers

INTRODUCTION

For arid and semi-arid areas, *sorghum* is very important cereal crop with multiple uses and ranks fifth after wheat, rice, maize and pearl millet among cereals worldwide. In India and other countries, it is generally grown as fodder crop. Today there is a great deficit between demand and supply of this crop due to increase in population at multiple rates. Stephens and Holland (1954) and Doggett (1969) discovered cytoplasmic male sterility in *sorghum* which boosted up the yield by using hybrid potential at genetic level. Male sterility is used for the production vigorous hybrids by exploiting combining abilities of various parental combinations results an increase in various phenotypic characters like days to flowering, plant height, test weight, etc. and finally yield. Analysis of combining abilities (GCA and SCA) helps in estimating *heterosis*, selection of vigorous parents and important yield contributing attributes for a particular crop, also for *sorghum.*

Selection of good parents the most important step for any plant breeding programme. In conventional plant breeding, selection is done on the basis of various morphological markers based on their phenotypic performance. These markers are highly influenced by environment, so selection based on them is always challenged till the estimation of *heterosis*. However as per present need, more specific selection techniques are needed for the further enhancement of genetic gain. The use of molecular markers like SSRs has been proposed as a more efficient method of selecting parental inbred lines and superior hybrid combinations, which can reduce the number of multi-location trials of potential hybrids (Menkir *et al*., 2004; Barata and Carena, 2006). So, the present investigation has been done for the estimation of combining abilities in relation to *heterosis* and also the correlation of SSR diversity with experimental findings for thirteen *sorghum* genotypes and their respective crosses.

MATERIAL AND METHODS

The experimental studies were conducted at the Instructional Dairy Farm of the G.B. Pant University of Agriculture and Technology, Pantnagar (U.S. Nagar) India, during *Kharif* season in 2013-14 and 2014-2015 and at the Maize laboratory, Department of Genetics and Plant Breeding, G. B. Pant University of Agriculture and Technology, Pantnagar (U.S. Nagar). The experimental materials for the present study consist of forty F_1 crosses developed through line × tester mating design involving five diverse CMS lines (female), eight pollinator (male) lines and two check varieties. The details of parental lines (lines and testers) and their F_1s

Table 1: Parentage, origin/source and important characteristic features of parental lines used for the study

Name of the Parental line	Parentage	Origin/Source	Tillering/ Non-Tillering
ICSA 467	-	ICRISAT	Non-tillering
ICSA 469	[(ICSB 37 x ICSV 702) x PS 19349B]3-3-4-2	ICRISAT	Non-tillering
ICSA 276	(ICSB 101 x TRL 74/C 57) x PM17467B]2-5-1-3-3	ICRISAT	Non-tillering
11A2	Non-milo	DSR, Hyderabad	Non-tillering
MR 750A2	Non-milo	DSR, Hyderabad	Non-tillering
Pant Chari 5	CS 3541 x IS 6953	Pantnagar	Non-tillering
UPC 2	VIDISHA 60-1x ISC 953	Pantnagar	Non-tillering
CSV15	SPV 475 x SPV 462	DSR, Hyderabad	Non-tillering
CS3541	IS 3675 x IS3541	DSR, Hyderabad	Non-tillering
RS 29	IS 108 x SPV 126	DSR, Hyderabad	Non-tillering
M 35-1	Selection from Maldandi landraces	Mahol	Non-tillering
JJ1041	-	Indore	Non-tillering
SPV1616	-	DSR, Hyderabad	Non-tillering
CSH-20MF (National)	2219A x UPMC-503	Pantnagar	Tillering
CSH-24MF (National)	ICSA 467 X PC6	Pantnagar	Tillering

Table 2: Range of SSR loci scored, number and size of exclusive loci amplified in the *sorghum* genotypes

SSR primers	Sequence	Chromo-some location	Allele size (bp)	Total no. of alleles	No. Of polymorphic alleles	% Polymorphi-sm	PIC
Drenshsbm- 95	F GTGGTTTGTTCCAGCCTTTG R GGGGGAGATGTGTTTCTACG	1	30	2	2	100	0.50
Xcup05	F GGAAGGTTTGCAAGAACAGG R CCAGCCCAACAAGTGCTATC	1	60	7	4	57	0.77
Xtxp250	F GCACATCCTCTAAAACTACTTAGT R GAACAGGACGATGTGATAGAT	1	140	4	2	50	0.78
TS304T	F ACATAAAAGCCCCTCTTC R CTTTCACACCCTTTATTCA	1	115	5	3	60	0.87
TS050	F TCGTGGATTTGCATTCCTTGAA R GAATGTGCCTTGTTTCTGTGCG	1	70	4	4	100	0.72
	Mean			4.4	3	73.4	0.73

Table 3: Correlation among various phenotypic markers during the pooled over years in *sorghum*

Character	Days to 50% Flowering	Plant Height (cm)	Panicle Length (cm)	Panicle Weight (g)	Yield/ Plant (g)	1000 Seed Weight (g)
Days to 50% Flowering	1.00	0.08	0.13	0.15	0.07	-0.35**
Plant Height (cm)	0.08	1.00	0.22**	0.11	0.15*	0.31**
Panicle Length (cm)	0.13	0.22**	1.00	0.06	-0.02	-0.09
Panicle Weight (g)	0.15	0.11	0.06	1.00	0.88**	-0.02
Yield/ Plant (g)	0.07	0.15*	-0.02	0.88**	1.00	0.16*
1000 Seed Weight (g)	-0.35**	0.31**	-0.09	-0.02	0.16*	1.00

*, ** Significant at 5 and 1% levels of probability, respectively

Table 4: Correlation among various phenotypic markers during the pooled over years in *sorghum*

Source of Variation	df	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Panicle Length (cm)	Panicle Width (cm)	Panicle Weight (g)	Seed Yield/ Plant (g)	1000 Seed Weight (g)
Replicates	2	1.67	6.53	254.12	1.84	1.73	377.31	361.91*	0.03
Environments	1	562.67**	1139.6**	6809.71**	286.99**	194.14**	68839.57**	72141.62**	0.03
Rep * Env.	2	1.02	2.95	74.10	1.23	1.27	62.02	60.78	0.41
Treatments	52	140.91**	59.63**	10601.08**	28.89**	8.34**	7916.69**	3557.82**	111.03**
Parents	12	152.08**	54.13**	13032.77**	16.46**	9.03**	4948.88**	2995.14**	158.73**
Parents(Line)	7	208.52**	46.45**	7578.97**	11.00	12.88²	5978.36**	2993.54**	199.57**
Parents(Testers)	4	28.28**	65.37**	1020.65	29.05**	4.50**	3555.61**	3084.51**	126.60**
Parents(LvsT)	1	252.17**	62.90**	99257.80**	4.32	0.21	3315.57**	2648.87**	1.39*
ParentvsCrosses	1	550.38**	454.16**	189932.47**	145.73**	0.25	23960.07**	12650.83**	1506.22**
Crosses	39	126.97**	51.21**	5254.62**	29.72**	8.33**	8418.49**	3497.80**	60.57**
Lineeffect	7	439.25**	55.47	15942.15**	92.45**	26.62**	28835.64**	8824.15**	123.90**

Testereffect	4	190.60**	234.25**	4736.54	10.92	5.33	5540.55	2934.33	127.07*
Line * Testereffect	28	39.82**	24.00**	2656.75**	16.73**	4.19**	3725.34**	2246.71**	35.24**
Env * Treat	52	11.63**	15.76**	1828.23**	11.62**	4.90**	2544.64**	1561.77**	0.48**
Env * Parents	12	28.54**	23.52**	3921.07**	27.65**	11.19**	2787.88**	1157.20**	0.94**
Env * Parents(L)	7	40.54**	24.66**	2925.78**	33.56**	8.08**	2557.54**	929.25**	0.43
Env * Parents(T)	4	12.28**	25.53**	2888.62**	11.66	19.26**	3846.60**	1625.55**	1.62**
Env * PAR(LvsT)	1	9.59	7.50	15017.97**	50.33**	0.62	165.37	879.38**	1.76*
Env * ParentvsCross	1	0.89	17.77*	493.06	64.67**	38.92**	2042.05**	1212.15**	0.10
Env * Crosses	39	6.70**	13.32**	1218.52**	5.33	2.10**	2482.68**	1695.22**	0.35
Env * Lineeffect	7	7.68	14.18	1424.93	12.73**	2.14	2790.44	1767.55	0.25
Env * Testereffect	4	21.43**	22.31	3519.01**	4.92	4.45	1188.55	3976.69*	0.67
Env * L * Teffect	28	4.35	11.82**	838.27**	3.54	1.75	2590.62**	1351.22**	0.33
Error	208	3.12	3.84	454.02	6.38	0.80	239.10	84.60	0.28
Total	317	28.86	18.54	2360.34	11.76	3.33	2092.87	1125.56	18.48

Table 5: Correlation among various phenotypic markers during the pooled over years in *sorghum*

Genotypes	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Panicle Length (cm)	Panicle Width (cm)	Panicle Weight (g)	Seed Yield/ Plant (g)	1000 Seed Weight (g)
PC5	4.08**	-1.16**	15.53**	-1.33**	-0.28	4.54	3.12	-1.96**
UPC2	4.02**	-0.26	32.05**	3.01**	2.11**	63.34**	25.15**	-1.78**
CSV15	-2.78**	0.38	-8.83*	-0.39	-1.13**	-40.63**	-30.23**	0.98**
CS3541	-2.15**	-1.96**	-24.57**	-2.59**	-0.24	-0.32	0.77	-0.89**
RS29	-2.75**	-0.99**	-14.02**	-0.12	0.25	6.16*	10.93**	-1.96**
M35-1	5.15**	0.98**	25.88**	-0.26	-0.01	9.02**	10.84**	0.07
JJ1041	-0.82*	0.77*	-29.82**	-0.26	-0.18	-16.66**	-5.09**	3.46**
SPV1616	-4.75**	2.24**	3.78	1.95**	-0.52**	-25.45**	-15.47**	2.08**
ICSA467	0.15	-0.60*	8.49**	-0.32	0.40**	15.85**	9.75**	0.16*
ICSA 469	1.98**	0.82**	7.80*	0.70	-0.16	0.33	-0.55	-0.14*
ICSA 276	-1.17**	2.45**	-4.52	0.09	0.22	-7.01**	-6.91**	-2.25**
11A2	1.77**	0.78**	3.40	-0.55	-0.46**	3.13	5.89**	2.34**
MR750A2	-2.73**	-3.45**	-15.16**	0.09	-0.01	-12.30**	-8.18**	-0.10
CD 95% GCA(Line)	0.62	0.71	7.84	0.91	0.32	5.24	3.39	0.16
CD 95% GCA(Tester)	0.49	0.56	6.20	0.72	0.26	4.14	2.68	0.13
sl² Line HS	14.54	1.72	515.66	2.87	0.86	954.15	291.19	4.12
sl² Tester HS	3.91	4.80	88.83	0.10	0.09	111.03	59.29	2.64
sl² GCA (Average) HS.	8.00	3.61	253.00	1.16	0.39	435.31	148.48	3.21
sl² L * T (SCA)	6.14	3.35	364.04	1.74	0.56	585.71	359.69	5.84
sl² e	2.53	4.64	40.03	0.69	0.51	264.41	394.35	0.00
sl² a(F = 1)	0.31	0.69	63.50	0.43	0.09	171.96	111.93	0.00
sl² D(F = 1)	0.77	0.77	126.94	-0.06	0.15	40.73	162.01	0.02
sl² a / Var.D	0.59	0.74	102.54	0.13	0.13	91.20	142.75	0.01
Degree of Dominance	0.46	2.65	121.93	-0.92	0.32	793.17	420.89	0.04
sl² a(F = 0)	0.50	0.65	78.75	1.05	0.13	35.18	14.76	0.03
sl² D(F = 0)	16.00	7.23	505.99	2.33	0.78	870.61	296.96	6.42
sl² a / Var.D	6.14	3.35	364.04	1.74	0.56	585.71	359.69	5.84
Degree of Dominance	2.61	2.16	1.39	1.34	1.38	1.49	0.83	1.10
sl² p	0.62	0.68	0.85	0.86	0.85	0.82	1.10	0.95
Heritability (Narrow Sense) %	32.00	14.46	1011.99	4.65	1.56	1741.23	593.92	12.85
Genetic Advance 5 %	24.56	13.42	1456.18	6.95	2.26	2342.82	1438.77	23.36
Predictability Ratio	1.30	1.08	0.69	0.67	0.69	0.74	0.41	0.55

Table 6: Correlation among various phenotypic markers during the pooled over years in *sorghum*

S. No.	SSR SM	Days to 50% flowering				GCA		Plant height (cm)				GCA	
		MP	BP	SP	SCA	P1	P2	MP	BP	SP	SCA	P1	P2
ICSA 467 x PC5	0.68	-8.60**	-13.44**	9.82**	-2.81**	0.15		22.74**	-5.32	35.36**	-1.29	8.49**	
ICSA 469 x PC5	0.72	1.87	-5.50**	19.90**	1.85**	1.98**		19.97**	-5.29	35.39**	-0.52	7.80*	
ICSA 276 x PC5	0.59	-0.55	-8.35**	16.28**	2.67**	-1.17**	4.08**	-6.96	-24.59**	7.81	-50.28**	-4.52	15.53**
11A2 x PC5	0.63	2.29*	-4.28**	21.45**	3.06**	1.77**		40.19**	7.40	53.54**	44.72**	3.40	
MR750A2 x PC5	0.68	-11.61**	-19.35**	2.33	-4.77**	-2.73**		18.27**	-9.98*	28.69**	7.36	-15.60**	
ICSA 467 x UPC2	0.77	0.45	-1.53	16.28**	1.42*	0.15		22.74**	-5.32	35.36**	-1.29	8.49**	
ICSA469 x UPC2	0.63	2.39*	-1.75	16.02**	-0.58	1.98**		19.97**	-5.29	35.39**	-0.52	7.80*	
ICSA 276 x UPC2	0.68	0.11	-4.60**	12.66**	0.40	-1.17**	4.02**	-6.96	-24.59**	7.81	-50.28**	-4.52	32.05**
11A2 x UPC2	0.54	0.56	-2.63*	14.99**	-1.04	1.77**		40.19**	7.40	53.54**	44.72**	3.40	
MR750A2 x UPC2	0.68	-1.86	-7.44**	9.30**	-0.20	-2.73**		18.27**	-9.98*	28.69**	7.36	-15.60**	
ICSA 467 x CSV15	0.81	-7.42**	-10.48**	1.55	-1.28	0.15		22.74**	-5.32	35.36**	-1.29	8.49**	
ICSA 469 x CSV15	0.77	0.72	-0.48	8.01**	1.05	1.98**		19.97**	-5.29	35.39**	-0.52	7.80*	
ICSA 276 x CSV15	0.72	-4.85**	-5.31**	1.29	-0.13	-1.17**	-2.78**	-6.96	-24.59**	7.81	-50.28**	-4.52	-8.83*
11A2 x CSV15	0.77	-2.15	-4.21**	5.94**	-0.07	1.77**		40.19**	7.40	53.54**	44.72**	3.40	
MR750A2 x CSV15	0.81	-5.28**	-5.85**	-0.26	0.43	-2.73**		18.27**	-9.98*	28.69**	7.36	-15.60**	
ICSA 467 x CS3541	0.68	-6.30**	-6.83**	5.68**	0.75	0.15		22.74**	-5.32	35.36**	-1.29	8.49**	
ICSA 469 x CS3541	0.54	-6.32**	-7.83**	3.36*	-2.58**	1.98**		19.97**	-5.29	35.39**	-0.52	7.80*	
ICSBA276 x CS3541	0.59	-3.54**	-5.76**	5.68**	2.07**	-1.17**	-2.15**	-6.96	-24.59**	7.81	-50.28**	-4.52	-8.83*
11A2 x CS3541	0.63	-8.58**	-9.22**	1.81	-3.37**	1.77**		40.19**	7.40	53.54**	44.72**	3.40	
MR750A2 x CS3541	0.95	-3.22**	-6.45**	4.91**	3.13**	-2.73**		18.27**	-9.98*	28.69**	7.36	-15.60**	
ICSA 467 x RS29	0.85	-6.92**	-7.24**	5.94**	1.52*	0.15		22.74**	-5.32	35.36**	-1.29	8.49**	
ICSA 469 x RS29	0.78	-3.25**	-5.66**	7.75**	0.85	1.98**		19.97**	-5.29	35.39**	-0.52	7.80*	
ICSA 276 x RS29	0.75	-11.45**	-14.25**	-2.07	-2.33**	-1.17**	-2.75**	-6.96	-24.59**	7.81	-50.28**	-4.52	-14.02**
11A2 x RS29	0.83	-5.98**	-7.47**	5.68**	-0.27	1.77**		40.19**	7.40	53.54**	44.72**	3.40	
MR750A2 x RS29	0.75	-9.09**	-12.90**	-0.52	0.23	-2.73**		18.27**	-9.98*	28.69**	7.36	-15.60**	
ICSA 467 x M35-1	0.68	-5.35**	-10.71**	14.21**	-1.05	0.15		22.74**	-5.32	35.36**	-1.29	8.49**	
ICSA 469 x M35-1	0.63	3.61**	-4.24**	22.48**	2.45**	1.98**		19.97**	-5.29	35.39**	-0.52	7.80*	
ICSA 276 x M35-1	0.68	-3.41**	-11.31**	13.44**	-0.23	-1.17**	5.15**	-6.96	-24.59**	7.81	-50.28**	-4.52	25.88**
11A2 x M35-1	0.63	-2.49*	-9.09**	16.28**	-1.34	1.77**		40.19**	7.40	53.54**	44.72**	3.40	
MR750A2 x M35-1	0.59	-4.00**	-12.73**	11.63**	0.16	-2.73**		18.27**	-9.98*	28.69**	7.36	-15.60**	

Hybrid	SSR SM	Days to 50% flowering				GCA		Plant height (cm)				GCA	
		MP	BP	SP	SCA	P1	P2	MP	BP	SP	SCA	P1	P2
ICSA 467 x JJ1041	0.77	-4.68**	-7.29**	5.17**	-0.91	0.15		22.74**	-5.32	35.36**	-1.29	8.49**	
ICSA 469 x JJ1041	0.63	-3.71**	-4.29**	3.88*	-3.58**	1.98**		19.97**	-5.29	35.39**	-0.52	7.80*	
ICSA 276 x JJ1041	0.68	-4.70**	-4.82**	2.07	-1.60*	-1.17**	-0.82**	-6.96	-24.59**	7.81	-50.28**	-4.52	-29.82**
11A2 x JJ1041	0.54	9.37**	7.71**	19.12**	6.46**	1.77**		40.19**	7.40	53.54**	44.72**	3.40	
MR750A2 x JJ1041	0.77	-4.15**	-5.30**	1.55	-0.37	-2.73**		18.27**	-9.98**	28.69**	7.36	-15.60**	
ICSA 467 x SPV1616	0.59	-4.28**	-8.20**	4.13**	2.35**	0.15		22.74**	-5.32	35.36**	-1.29	8.49**	
ICSA 469 x SPV1616	0.90	-2.07	-4.05**	4.13**	0.52	1.98**		19.97**	-5.29	35.39**	-0.52	7.80*	
ICSA 276 x SPV1616	0.68	-7.96**	-9.18**	-2.84	-0.83	-1.17**	-4.75**	-6.96	-24.59**	7.81	-50.28**	-4.52	3.78
11A2 x SPV1616	0.90	-9.03**	-11.68**	-2.33	-3.44**	1.77**		40.19**	7.40	53.54**	44.72**	3.40	
MR750A2 x SPV1616	0.68	-5.94**	-6.17**	-1.81	1.40*	-2.73**		18.27**	-9.98**	28.69**	7.36	-15.60**	
CD 95% SCA					1.39								

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S. No.	SSR SM	Days to 50% flowering				GCA		Plant height (cm)				GCA	
		MP	BP	SP	SCA	P1	P2	MP	BP	SP	SCA	P1	P2
ICSA 467 x PC5	0.68	0.12	-6.88	13.99*	1.14	-0.32		-0.06	-27.60**	-25.69**	-40.05**	15.85**	
ICSA 469 x PC5	0.72	-1.96	-4.68	6.26	-1.73	0.70		-0.26	15.82*	-1.48	6.81	0.33	
ICSA 276 x PC5	0.59	-0.45	-3.59	8.35	-0.62	0.09	-0.39	-0.26	25.10*	-20.73**	-10.78	-7.01**	15.53**
11A2 x PC5	0.63	5.42	2.76	13.95*	1.37	-0.55		-0.12	27.14**	16.74*	27.59**	3.13	
MR750A2 x PC5	0.68	9.17	4.69	10.23	-0.16	0.09		-1.33*	64.36**	-3.80	16.44**	-12.30**	
ICSA 467 x UPC2	0.77	13.54**	11.77*	36.81**	2.28*	-0.32		69.86**	43.54**	47.33**	-4.36	15.85**	
ICSA469 x UPC2	0.63	8.05	4.81	24.29**	-1.74	0.70	-0.26	-2.59**	34.44**	14.36*	-31.50**	0.33	4.54
ICSA 276 x UPC2	0.68	3.46	0.76	19.49**	-2.28*	0.09		3.01**	63.57**	15.85*	-22.23**	-7.01**	
11A2 x UPC2	0.54	11.72*	8.10	28.18**	0.44	-0.55		98.03**	75.39**	61.04**	26.12**	3.13	
MR750A2 x UPC2	0.68	24.93**	13.38**	34.45**	1.30	0.09		137.54**	116.92**	53.64**	31.97**	-12.30**	
ICSA 467 x CSV15	0.81	-9.20*	-15.01**	4.04	-2.17*	-0.32		-37.84**	-40.19**	-33.59**	-5.10	15.85**	
ICSA 469 x CSV15	0.77	7.65	5.37	17.47**	0.03	0.70		-35.20**	-42.78**	-36.46**	6.71	0.33	
ICSA 276 x CSV15	0.72	5.56	2.91	15.66*	0.20	0.09	-0.26	-38.43**	-51.65**	-46.31**	1.29	-7.01**	-16.66**
11A2 x CSV15	0.77	3.79	1.85	12.94*	0.19	-0.55		-49.22**	-53.61**	-48.49**	-11.66	3.13	
MR750A2 x CSV15	0.81	20.08**	14.41*	22.13**	1.75	0.09		-34.69**	-50.13**	-44.62**	8.77	-12.30**	
ICSA 467 x CS3541	0.68	-11.64*	-16.20**	2.57	-0.33	-0.32		56.45**	27.10**	30.46**	37.47**	15.85**	
ICSA 469 x CS3541	0.54	-2.88	-3.62	7.45	-0.18	0.70		6.52	-6.59	-20.54**	-13.01*	0.33	
ICSBA276 x CS3541	0.59	-1.08	-2.23	9.88	1.01	0.09	-0.12	57.31**	56.36**	0.28	21.27**	-7.01**	-25.45**
11A2 x CS3541	0.63	0.69	0.19	11.10	1.94	-0.55		9.61	-6.91	-14.53*	-8.03	3.13	
MR750A2 x CS3541	0.95	-7.50	-13.03*	-4.52	-2.44*	0.09		-17.48	-21.08*	-49.39**	-37.71**	-12.30**	

Cross	SSR SM	MP	BP	SP	SCA	GCA P1	GCA P2	PH MP	PH BP	PH SP	PH SCA	PH GCA P1	PH GCA P2
ICSA 467 x RS29	0.85	-2.90	-5.74	15.38*	0.27	-0.32	-1.33**	33.29**	31.87**	35.35**	37.32**	15.85**	-40.63**
ICSA 469 x RS29	0.78	-4.24	-5.80	8.56	-2.38*	0.70		-18.78**	-25.00**	-24.66**	-24.82**	0.33	
ICSA 276 x RS29	0.75	6.82	5.50	21.57**	1.35	0.09		-6.50	-23.76**	-23.42**	-15.87**	-7.01**	
11A2 x RS29	0.83	2.60	0.66	16.01**	0.66	-0.55		8.10	3.46	3.93	9.38	3.13	
MR750A2 x RS29	0.75	9.82*	0.97	16.35**	0.10	0.09		0.77	-20.26**	-19.90**	-6.02	-12.30**	
ICSA 467 x M35-1	0.68	-5.81	-11.54*	8.28	-1.29	-0.32	1.95**	44.72**	1.51	4.19	-5.86	15.85**	6.16*
ICSA 469 x M35-1	0.63	10.96*	8.99	21.50**	0.86	0.70		84.21**	36.87**	16.42*	25.50**	0.33	
ICSA 276 x M35-1	0.68	7.97	5.63	18.72**	0.80	0.09		35.30**	11.79	-29.17**	-26.17**	-7.01**	
11A2 x M35-1	0.63	-1.93	-3.42	7.10	-1.34	-0.55		60.02**	16.03*	6.54	9.91	3.13	
MR750A2 x M35-1	0.59	16.91**	11.00	19.35**	0.96	0.09		68.92**	44.11**	-15.65**	-3.37	-12.30**	
ICSA 467 x JJ1041	0.77	-0.18	-7.05	13.78*	0.02	-0.32	-2.59**	-1.98	-22.46**	-20.41**	-12.02*	15.85**	63.34**
ICSA 469 x JJ1041	0.63	14.75**	11.70**	24.53**	1.58	0.70		17.03*	-0.38	-15.26**	10.17	0.33	
ICSA 276 x JJ1041	0.68	4.02	0.87	13.36*	-0.49	0.09		48.54**	44.31**	-8.56	26.17**	-7.01**	
11A2 x JJ1041	0.54	1.11	-1.32	9.43	-0.78	-0.55		-24.38**	-37.59**	-42.69**	-28.13**	3.13	
MR750A2 x JJ1041	0.77	12.73*	7.98	13.99*	-0.33	0.09		18.45	17.24	-29.94**	3.80	-12.30**	
ICSA 467 x SPV1616	0.59	10.21*	0.68	23.24**	0.09	-0.32	-2.59**	-9.33	-25.60**	-23.63**	-7.39	15.85**	9.02**
ICSA 469 x SPV1616	0.90	33.46**	27.34**	41.96**	3.55**	0.70		13.53	0.68	-14.36**	20.13**	0.33	
ICSA 276 x SPV1616	0.68	16.78**	10.99*	24.74**	0.03	0.09		31.21**	28.77**	-15.26**	26.30**	-7.01**	
11A2 x SPV1616	0.90	5.13	0.56	11.52	-2.49*	-0.55		-33.01**	-42.50**	-47.20**	-25.17**	3.13	
MR750A2 x SPV1616	0.68	20.89**	18.14**	19.62**	-1.19	0.09		-20.21*	-24.62*	-50.39**	-13.87**	-12.30**	
CD 95% SCA					2.03						11.72		

Continue...

S. No.	SSR SM	Days to 50% flowering						Plant height (cm)					
		MP	BP	SP	SCA	GCA P1	GCA P2	MP	BP	SP	SCA	GCA P1	GCA P2
ICSA 467 x PC5	0.68	-2.92**	-4.65**	6.76**	-1.98**	0.16*	0.07	-6.84	-33.72**	-25.30**	-26.17**	9.75**	10.84**
ICSA 469 x PC5	0.72	12.27**	-2.38*	5.41**	-2.02**	-0.14*		39.77**	12.64	-12.25	-4.95	-0.55	
ICSA 276 x PC5	0.59	15.28**	3.63**	11.89**	1.70**	-2.25**		54.47**	47.86**	-22.94**	-7.54	-6.91**	
11A2 x PC5	0.63	3.73**	-3.05**	20.41**	-0.79**	2.34**		60.24**	15.97**	23.53**	18.60**	5.89**	
MR750A2 x PC5	0.68	16.24**	15.59**	26.22**	3.08**	-0.10		101.18**	80.26**	8.47	20.05**	-8.18**	
ICSA 467 x UPC2	0.77	19.75**	4.83**	17.36**	0.46*	0.16*	-0.89**	54.40**	14.88**	29.46**	-2.32	9.75**	0.77
ICSA469 x UPC2	0.63	22.06**	18.97**	0.00	-3.53**	-0.14*		58.14**	34.90**	5.08	-12.45**	-0.55	
ICSA 276 x UPC2	0.68	33.55**	31.92**	13.65**	1.95**	-2.25**		90.93**	85.93**	2.27	-8.45**	-6.91**	
11A2 x UPC2	0.54	24.14**	4.08**	29.26**	1.22**	2.34**		79.36**	35.99**	44.86**	14.44**	5.89**	
MR750A2 x UPC2	0.68	18.04**	4.46**	14.05**	-0.10	-0.10		110.64**	101.59**	21.30**	8.77**	-8.18**	

Cross													
ICSA 467 x CSV15	0.81	5.86**	0.16	25.68**	-0.25	0.16*		-51.06**	-51.41**	-44.44**	-8.86*	9.75**	
ICSA 469 x CSV15	0.77	34.56**	10.07**	38.11**	3.11**	-0.14*		-30.28**	-41.39**	-32.98**	11.04**	-0.55	
ICSA 276 x CSV15	0.72	0.13	-15.56**	5.95**	-2.71**	-2.25**	0.98**	-42.77**	-58.34**	-52.37**	1.16	-6.91**	-30.23**
11A2 x CSV15	0.77	4.19**	3.66**	30.07**	-1.35**	2.34**		-51.87**	-53.51**	-46.85**	-7.01	5.89**	
MR750A2 x CSV15	0.81	11.26**	4.04**	30.54**	1.20**	-0.10		-43.71**	-57.05**	-50.89**	3.67	-8.18**	
ICSA 467 x CS3541	0.68	21.73**	11.04**	24.32**	1.29**	0.16*		61.65**	23.97**	39.71**	30.65**	9.75**	
ICSA 469 x CS3541	0.54	58.38**	47.66**	36.28**	4.53**	-0.14*		24.18**	10.04	-14.28*	-4.29	-0.55	
ICSBA276 x CS3541	0.59	17.15**	13.25**	4.53**	-1.18**	-2.25**	-1.78**	66.65**	55.52**	-6.45	8.63**	-6.91**	25.15**
11A2 x CS3541	0.63	11.36**	-2.94**	20.54**	-1.82**	2.34**		15.00*	-10.03	-4.16	-2.24	5.89**	
MR750A2 x CS3541	0.95	5.84**	-2.35*	6.62**	-2.82**	-0.10		-29.11**	-29.12**	-57.35**	-32.74**	-8.18**	
ICSA 467 x RS29	0.85	7.77**	-5.37**	5.95**	-2.18**	0.16*		43.55**	34.97**	52.10**	30.87**	9.75**	
ICSA 469 x RS29	0.78	50.04**	45.73**	23.38**	2.42**	-0.14*		-20.35**	-28.91**	-29.46**	-27.17**	-0.55	
ICSA 276 x RS29	0.75	20.41**	19.37**	2.84**	-0.53**	-2.25**	-1.96**	3.47	-21.09**	-21.70**	-14.31**	-6.91**	3.12
11A2 x RS29	0.83	22.10**	2.67**	27.50**	0.96**	2.34**		18.46**	14.40*	21.86**	9.39**	5.89**	
MR750A2 x RS29	0.75	14.53**	1.67	11.01**	-0.67**	-0.10		19.61**	-3.93	-4.67	1.23	-8.18**	
ICSA 467 x M35-1	0.68	55.58**	22.93**	37.64**	3.61**	0.16*		46.71**	-2.30	10.10	-4.24	9.75**	
ICSA 469 x M35-1	0.63	53.74**	39.46**	11.28**	-2.59**	-0.14*		105.88**	52.36**	18.69**	13.26**	-0.55	
ICSA 276 x M35-1	0.68	37.44**	20.55**	3.85**	-2.31**	-2.25**	-1.96**	35.02**	15.95	-39.57**	-29.19**	-6.91**	10.93**
11A2 x M35-1	0.63	34.80**	2.67**	27.50**	-1.07**	2.34**		65.92**	12.08*	19.40**	7.42	5.89**	
MR750A2 x M35-1	0.59	50.99**	20.42**	31.49**	2.35**	-0.10		123.40**	81.12**	8.99	12.76**	-8.18**	
ICSA 467 x JJ1041	0.77	15.38**	12.72**	32.30**	-1.09**	0.16*		-0.35	-26.88**	-17.60**	-11.51**	9.75**	
ICSA 469 x JJ1041	0.63	37.22**	15.26**	35.27**	-0.07	-0.14*		50.09**	25.79**	-2.01	11.85**	-0.55	
ICSA 276 x JJ1041	0.68	24.37**	7.83**	26.55**	-0.10	-2.25**	2.08**	98.33**	97.28**	3.92	23.18**	-6.91**	-15.47**
11A2 x JJ1041	0.54	25.93**	22.47**	52.09**	1.61**	2.34**		-21.93**	-41.66**	-37.86**	-24.62**	5.89**	
MR750A2 x JJ1041	0.77	18.52**	14.39**	34.26**	-0.35	-0.10		34.78**	26.38*	-23.95**	1.10	-8.18**	
ICSA 467 x SPV1616	0.59	7.85**	-0.46	31.76**	0.15	0.16*		-21.14**	-34.60**	-26.30**	-8.42	9.75**	
ICSA 469 x SPV1616	0.90	15.41**	-7.50**	22.43**	-1.86**	-0.14*		13.90	11.21	-13.37*	12.71**	-0.55	
ICSA 276 x SPV1616	0.68	22.88**	1.43	34.26**	3.17**	-2.25**	3.46**	51.25**	28.73**	-4.46	26.54**	-6.91**	-5.09**
11A2 x SPV1616	0.90	13.04**	9.55**	45.00**	1.24**	2.34**		-33.55**	-43.62**	-39.94**	-15.99**	5.89**	
MR750A2 x SPV1616	0.68	-1.31	-9.95**	19.19**	-2.70**	-0.10		-33.57**	-39.86**	-55.36**	-14.84**	-8.18**	
CD 95% SCA					0.36						7.59		

*, ** Significant at 5 and 1% levels of probability, respectively

Priyamvada Chauhan*[1] and Pradeep Kumar Pandey[2]

have been presented in Table 1.

Ten competitive plants were randomly taken, from each treatment/genotype in each replication in both the years. All the selected plants were tagged and observations for all the characters were taken. The means of different characters for the purpose of statistical analysis were calculated on the basis of the individual data recorded for each character, in each replication separately, for each cross. Days to 50 % flowering were calculated by counting the number of days between planting when one half of the panicles in a plot reached the half bloom stage. The plant height was measured from ground level to the tip of the uppermost leaf of each plant. Panicle length was measured at maturity, from the bottom panicle node to the upper most floret or the tip of panicle. Panicle weight was measured at maturity. Weight of one thousand random grains from total grain yield of tagged plants was recorded in grams and mean was worked out. Average weight of grains obtained from ten random plants after threshing and sun drying was recorded in grams.

Three types of heterosis were estimated for grain yield and its components. For standard heterosis, two released hybrids of multicut forage *sorghum viz.* CSH 20 MF and CSH 24 MF as checks or standard genotypes. However, out of these checks, CSH 24 MF the released hybrid was found to be best for most of the characters. Therefore, CSH 24 MF was invariably used for estimation of standard heterosis for all the characters. Heterosis expressed as percentage increase or decrease of F_1s over better parent, mid parent and check parent was calculated as suggested by Fonseca and Petterson (1968).

For molecular analysis, five SSR primers were selected to diversify the *sorghum* genotypes (Table 2). DNA was extracted from fresh seedlings (eight days old) by the method described by Dellaporta *et al.*, (1989). For PCR amplification, a master mix without DNA template was prepared for different tubes to reduce pipetting error and redistributed in each PCR tube (18 μl each). PCR amplification was performed in a final volume of 20 μl reaction set up containing 2 μl of DNA, 1.2μl of dNTPs, 2.0 μl PCR buffer, 0.5 μl of forward primer, 0.5 μl of primer reverse primers, 0.4 μl of Taq DNA polymerase and 13.4μl of double distilled water. The reaction conditions were as follows: initial denaturation (94˚C for 5 min) followed by 35 cycles of denaturation (94˚C for 1 min), annealing at 55˚C for 2 min (temperature reduced by 1˚C for each cycle) and primer extension (72˚C for 2 min). This step was followed by final cycle of denaturation at 94˚C for 1 min, annealing at 55˚C for 1 min and extension at 72˚C for 7 min. PCR amplified DNA fragments were resolved by submerged horizontal electrophoresis in 1.5% agarose gel and visualized by staining with ethidium bromide. After completion of electrophoresis, image of the gel was viewed and saved in a gel documentation system (Alpha Imager EC). On the basis of absence and presence of SSRs band and statistical data, similarity matrix coefficient among the thirteen *sorghum* accessions were calculated by following Jaccard's similarity index (1998).

$$\text{Similarity Index (SI)} = \frac{\text{Number of matching bands in two lanes compared}}{\text{Total number of bands}}$$

All the numerical taxonomic analysis with respect to SSRs (DNA fragment analysis) was performed using the NTSYS-pc software (Rohlf, 1992).

EXPERIMENTAL RESULTS

Among all six phenotypic characters, Grain yield per plant was directly significantly associated with panicle weight (0.88), plant height (0.15) and 1000 seed weight (0.16). Plant height was found to be directly correlated with panicle length (0.22), 1000 seed weight (0.31) and grain yield (0.15). It can be seen that except days to 50 % flowering, all characters were directly or indirectly associated with grain yield (Table 3). Table 4 shows that differences among lines, testers and line x tester were significant (p < 0.01) for all characters. The interaction of lines and testers separately and also crosses with years was significant (p < 0.01) for days to 50 % flowering, plant height, panicle weight and seed yield.

For days to 50 % flowering, where negative values are good indicators, among all MR750 A$_2$ x PC5 (SM 0.68) exhibited best results for heterosis i.e. MP (-11.61%) and BP (-19.35%), also having significant value for SCA (-4.77) and good GCA for MR750 A$_2$ (-2.73). Negative and significant values were recorded in twenty eight crosses for MP and BP heterosis which were ranged from -2.49 to -11.61% and -2.63 to -14.25%, respectively. The predictability ratio for this character (1.30) shows that there is major contribution of GCA action (Table 5 and 6). For plant height which was recorded as directly associated with grain yield, most of the crosses gave positive and significant results for MP, BP and SP heterosis with estimated range from 14.08 to 56.51% (thirty six crosses), 10.91 to 42.84% (twenty two) and 13.29 to 53.54% (thirty four), respectively. UPC2 and M35-1 were found to be best general combiners having high values of GCA (32.05 and 25.88, respectively). For all the crosses involving UPC2 and M35-1, having sufficient genetic diversity among parental combinations (SSR similarity matrix ranged from 0.54 to 0.77 and 0.59 to 0.68, respectively) exhibited very good results for heterosis(Table 6).

No direct association was observed between heterosis and SSR diversity of parental combinations for panicle length. only few crosses were found to be positively and significantly heterotic i.e. ICSA 469 x SPV 1616 (SCA 3.55) having 33.46% MP, 27.34 %BP and 41.96% SP heterosis, MR750 A$_2$ x SPV 1616 having 20.89% MP, 18.14% BP and 19.62% SP heterosis, ICSA 276 x SPV 1616 with 16.78% MP, 10.99% BP and 24.74% SP heterosis, MR750 A$_2$ x UPC2 with 24.93% MP, 13.38 %BP and 34.45% SP heterosis, ICSA 467 x UPC2 (SCA 2.28) having 13.54% MP, 11.77 %BP and 36.81% SP heterosis and MR750 A$_2$ x CSV15 with 20.08% MP, 14.41% BP and 2.13% SP

heterosis. UPC 2 (GCA 3.01) and M 35-1 (GCA 1.95) were found to be best general combiner lines for this character i.e. panicle length. UPC2 (63.34) and M35-1 (9.02) were recorded as best general combiners for panicle weight, also all the crosses including these parents performed best in terms of heterosis and were well correlated with SSR diversity. Highest significant and positive values for heterosis were reported for MR750 A_2 x UPC2 (SM 0.68) i.e. 137.54% MP, 116.92% BP and 53.64% SP followed by 11A2 x UPC2 (SM 0.54) i.e. 98.03% MP, 75.39% BP and 61.04% SP. Maximum SCA (37.47) was recorded for ICSA467 x CS3541 (56.45% MP, 27.10% BP and 30.46% SP) (Table 6).

Molecular diversity was not found directly associated with 1000 seed weight. Almost all F1 crosses gave positive and significant results for heterosis. Mid parent heterosis was ranged from 3.73 to 58.38% (over thirty seven characters), batter parent heterosis was ranged from 2.67 to 47.66% (over twenty seven crosses) and standard heterosis was recorded in range of 2.84 to 52.09% (over thirty nine crosses). JJ1041 (3.46), SPV1616 (2.08) and CSV15 (0.98) among lines and ICSA467 (0.16) and 11A2 (2.34) among testers were found to be good general combiners for this trait. Positive and significant values for SCA were recorded for fifteen crosses. For grain yield, UPC2 (25.15), RS29 (10.93) and M35-1 (10.84) for lines and ICSA467 (9.75) and 11A2 (5.89) for testers were recorded as good general combiners. Lines PC5, UPC2 and M35-1 exhibited significant, positive and maximum values of heterosis with all the testers. MR750 A_2 x UPC2 was found to be best (110.64% MP, 101.59% BP and 21.30% SP) followed by MR750 A_2 x M35-1 (123.40% MP, 81.12% BP) and MR750 A_2 x PC5 (101.58% MP, 80.26% BP). Mid parent, better parent and Standard parent heterosis were ranged from 15.00 to 123.10% (over twenty five crosses), 12.08 to 101.59% (over eighteen crosses) and 19.40 to 44.86% (over eight parents), respectively. Positive and significant heterosis was recorded for fourteen crosses maximum in ICSA467 x CS3541 (39.71) (Table 6).

DISCUSSION AND CONCLUSION

A positive and significant association between plant height, panicle length, panicle weight 100 grain weight, and grain yield per plant indicates the utility of per se performance in the selection of the crosses as explained earlier by Premalatha *et al.,* (2006) in *sorghum*. In present investigation, UPC2 and M35-1 were found to be good general combiners for almost all the characters and also the crosses based on them exhibited good heterotic values in terms of yield. The low GCA value either positive or negative indicates that the parental mean in crossing with the other parent does not vary far from the general mean of the crosses. While, a high GCA value shows that the parental mean is superior or inferior to the general mean and indicates a desirable gene flow from parents to offspring at high intensities and informs about the aggregation of additive genes for a particular trait. A high GCA value also

indicates the higher heritability and less environmental effects on such trait which result in effective selection of parents (Day *et al.*, 2014). Highest heterobeltiosis (101.59) for grain yield was recorded in MR750 A_2 (GCA, -8.18) x UPC2 (GCA, 25.15). However, it is not always necessary that a parent having good GCA will produce heterotic F1 in hybridization and it is also indicated that one parent having low GCA can make the best combination if the other parent is selected carefully (Bao *et al.,* 2009).

If the selection is based on GCA only, it will accounted only for additive genetic variance while the non-additive genetic variance or specific combining ability (SCA) will be ignored. Therefore, selection of the parental lines should be based on both GCA and SCA. Crosses 11A_2 x UPC2 and ICSA 467 x RS29 for grain yield, 11A_2 x JJ1041 and 11A_2 x SPV1616 for 1000 grain weight and ICSA469 x RS29 for panicle weight exhibited significant and positive estimates of mid parent, better parent and standard parent heterosis with good SCA and GCA values for both the parents. The contributions of GCA and SCA to crosses are very useful to make important decisions about parental selection in plant breeding. When GCA variances are higher than SCA variances, early generation testing of genotypes becomes more effective and good hybrids can be selected on the basis of their GCA effects (Melchinger *et al.*, 1998). In present investigation also, the predictability ratio is higher than one for days to 50% flowering, while lower than one for all other characters shows the dominance of SCA as major contributing phenomenon for heterosis in various crosses in *sorghum*.

Parental selection on the basis of SCA effect only, has very less value in breeding programs. So, favourable SCA effect should be used accordingly with a high performance of hybrid having at least one parent with high significant GCA values (Makanda *et al.*, 2010). The performances of F1 crosses on the basis of SCA can be used for the interpretation of relative gene action of parents involved. High SCA due to the parents having good GCA i.e., good GCA × good GCA may also be supposed to have additive × additive gene action in a particular cross. In contrast, high SCA values derived from crosses including good × poor general combiners may be due to interaction of favourable additive gene effects of good general combiner with epistatic effects of poor general combiner. While high SCA by low GCA × low GCA crosses may be due to dominance × dominance type of non-allelic gene interaction producing over dominance which is non-fixable in behaviour (Dey *et al.*, 2014). In this context, crosses, MR750 A_2 x UPC2, 11A_2 x UPC2, ICSA467 x UPC2, ICSA467 x CS3541, ICSA 467 x RS29, ICSA 467 x M35-1 and 11A_2 x M35-1 exhibited high significant and positive values of heterosis and SCA having at least one parent with significant and positive estimates of GCA.

In present study, no direct association was observed between grain yield and SSR diversity. However, for 1000 seed weight and panicle weight which were directly

correlated with grain yield, showed some association with molecular diversity. Several previous reports also concluded that the prediction of heterosis on the basis of molecular diversity could not be possible due to lack of direct relationship between genetic variability and heterosis (Shukla and Singh, 2006). Rajendrakumar *et al.*, (2013) predicted a correlation between hybrid yield and SSR diversity in *sorghum* and reported no significant relationship between molecular and hybrid performance. Also, in some other studies, non-significant relationships between whole genome-based genetic distance and hybrid vigor were reported in rice (Hua *et al.*, 2002) and grain *sorghum* (Jordan *et al.*, 2003).

Many crosses in current investigation exhibited good values of mid-parent, better parent and even standard heterosis having high SCA and GCA effects. UPC2 and M35-1, among lines and $11A_2$ and $MR750A_2$ among testers were found to be best general combiners for grain yield. So, the parental selection based on these findings may be useful for improved breeding of *sorghum*. However, no significant relationship was detected between heterosis and SSR diversity, but these results may be helpful in further studies if more number of SSR markers is used for more precise QTL targeting of heterosis for yield. Among all F1 crosses, $11A_2$ x UPC2 gave best results of heterosis for most of the characters and can be recommended for further research in *sorghum* hybrid development program for this region.

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