ELUCIDATION OF COMBINING ABILITY AND FODDER POTENTIAL OF SORGHUM HYBRIDS

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SUMMARY

Combining ability is widely adopted and handy tool for comparing performances of parental lines in hybrid combinations in plant breeding experiments. It helps in understanding the nature of gene action for yield and its related traits. The present study was conducted to study the combining ability effects and estimation of economic heterosis for morpho-physiological traits related to fodder production, quality traits and antinutritional factors in sorghum which had a deep impact on fodder quality and in turn animal health. The material for the present investigation comprised of twenty-five hybrids developed using ten parents in line × testers mating design and two standard checks (SSG 59-3 and CSH 24MF). Observations were recorded for twelve morphological, four quality and 2 anti-nutritional parameters. Economic heterosis was estimated for all the characters. Six hybrids 31A × SSG 59-3 (139.1%), 126A × IS 2205 (131.15%), 14A × SSG 59-3 (109.24%), 94031A × SSG 59-3 (108.52%), 126A × HJ 541 (98.64%) and 14A × IS 2205 (76.09%) exhibited high significant positive economic heterosis for Green fodder yield in 1st cut. Female parent 14A was the best combiner for leaf length, GFY and DFY in 1st cut, protein content and HCN content. Whereas, the male parent 94031A was the best combiner for stem diameter, leaf: stem ratio, GFY and DFY in 2nd cut, phenol content and IVDMD. The IS 18551 was the best combiner for leaf length and HCN content. The correlation analysis revealed that GFY 1st cut had significant positive correlation with PH, DFY 1st cut at both genotypic and phenotypic level; and had significant negative correlation with stem diameter and IVDMD at both genotypic level and phenotypic level, respectively.

Key words : Combining ability, forage sorghum, heterosis, forage quality, sorghum hybrids

Sorghum bicolor (L.) Moench "camel" among crops is the fifth most important crop of semi-arid tropics in Asia and Africa having use as food, feed, fodder, fuel and fertilizer. Besides this, it is also a moderately salt tolerant crop (Devi *et al.,* 2018). It originated in Africa and belongs to the family Poaceae, subfamily Panicoideae, tribe Andropogoneae and genus *Sorghum.* India is the 2nd largest producer of sorghum after USA and other sorghum producing countries are Nigeria, China, Mexico, Sudan and Argentina. Sorghum is the most important fodder crop in the northern and central parts of India during summer and *Kharif* season, which is the lean period for green fodder availability.

For any agriculture-based country fodder crops are as much important as grain crops. Livestock sector being sub-sector of Indian agriculture contributes about 9 per cent to GDP and employs around 8 per cent of the labour force. In such context crops with multiple uses fetches more area as compared to others because crop residues used as animal feed and fodder (Tonapi *et al.,* 2011). India is contemplating for white revolution, which is possible only with an adequate supply of nutritious feeds and fodders. The livestock population in India is nearly 512.05 million in 2019 and they produced about 165.4 million tonnes milk annually (Anonymous, 2017-18). For the success of the white revolution, there is need for a continuous and steady supply of quality green fodder to enhance milk production potential of livestock.

Among various cereal fodder crops sorghum is important for those areas which are too dry for maize. High productivity fast-growing habit and better water use efficiency under drought make it a vital forage crop of semi-arid tropics. It is highly palatable

and more digestible than maize and pearl millet and uses approximately 40-50 per cent less water than corn to produce the same dry matter. As far as forage quality is concerned, it is defined as an expression of characteristics that affect consumption and is assessed by digestibility and palatability and most rapid method of improving forage sorghum quality is to improve IVDMD (Amigot *et al*. 2005). The utilization of sorghum fodder is limited due to HCN as an anti-quality factor. The permissible/safe threshold limit for HCN in sorghum fodder is 200mg/kg on fresh weight basis. Increased palatability and digestibility has moved forage sorghum into a prominent production role in water-short agricultural production areas.

For genetic improvement of forage sorghum varieties/hybrids with desirable characteristics, a piece of deep knowledge about plant breeding strategies is required. The cytoplasmic male sterlity system in sorghum was exploited 1st time in 1962 with concomitant release of various hybrids at National / State level. It is considered as one of the outstanding achievements in this crop. Estimation of heterosis and combining ability studies provide useful information regarding the selection of suitable parents for effective hybridization programs. They indicate the nature and magnitude of various types of gene action involved in the expression of quantitative characters (Bernardo, 2014). Therefore, to explore better potential combinations for developments of hybrids with desirable characteristics, the present study elucidated the heterosis and combining ability effects of the parental lines and crosses on fodder yield and quality traits. The correlation among traits for further forage sorghum quality improvement was also studied.

MATERIALS AND METHODS

Experimental Material: The experimental material comprised of 25 forage sorghum hybrids developed using 10 parents (five female parents viz., 14A, 126A, 31A, 94031A and 94012A and five males parents viz., HJ 541, IS 2205, COFS 29, SSG 59-3 and IS 18551) in Line and Tester fashion and evaluated with two standard checks (SSG 59-3 and CSH 24MF).

Experiment site and location: The present investigation was conducted in the research area of Forage Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar in *Kharif* season. It is situated in semi-arid sub-tropical region at 29.09°N latitude and 75.43°E longitude with an elevation of 215 m (705 ft) above mean sea level. All the thirty-seven genotypes were grown in a randomized block design with a two-row plot of 2.0 m length in three replications. The recommended package of practices was followed to raise a healthy crop.

Observations of Morphological traits: The observations on five randomly taken plants from each genotype in each replication were recorded on different quantitative characters viz., plant height (cm), number of tillers/plant (TP), no. of leaves/plant (LP), leaf length (cm), leaf breadth (cm), stem diameter (cm), leaf: stem ratio (LSR) at days to 50% flowering. At the time of 1st and 2nd cut green fodder yield (GFY) (kg/plot), dry fodder yield (DFY) (kg/plot) was also determined.

Analysis of quality traits: Determination of following quality characters viz. TSS content (^{0}brix) using Refractometer, protein content (%) using Micro-Kjeldhal's method, IVDMD (%) according to Tilley and Terry (1963), HCN content(μg/g) on fresh weight basis (Gilchrist *et al*. 1967), total phenol content(mg/g)on dry weight basis (Swain and Hillis,1959) and tannin content (mg/g) on dry weight basis (Burns, 1971), was carried out at the time of 1st and 2nd cut according to the above mentioned methodology, respectively.

Statistical analysis: The analysis of variance among the genotypes for various characters was calculated to test the significance. Economic heterosis was calculated as per method suggested by Turner (1953). The combing ability analysis was carried out according to the model suggested by Kempthorne (1957), which is related to design II of Comstock and Robinson (1952) in terms of covariance of half sibs and full sibs.

RESULTS

Estimation of Heterosis for Morphological traits

All genotypes were evaluated for eighteen traits including morphological and quality traits and significant variation was reported among all traits under study. Based on the standard heterosis estimated over two checks *i.e.* SSG 59-3 and CSH 24MF, the economic heterosis for TP was in the range of -8.82% to -51.33% and no cross combinations was observed with positive heterosis over check. In case of LP, the highest significant heterosis (89.23%) was shown by the cross combination 14A × HJ 541 over check CSH 24 MF and positive significant heterosis (31.92%) was shown over check SSG 59-3. 31A × COFS 29 exhibited the highest significant heterosis

(61.32%)over the second check for 'leaf breadth'.

In forage sorghum, the thin stem is preferred over the thick stem. Hence, in case of 'stem diameter', negative heterosis is more desirable. The heterosis recorded for stem diameter was ranged between -38.33 to 151.55 per cent. The cross 94031A × SSG 59-3 was recorded with the highest significant negative heterosis over second check (CSH 24MF). For 'leaf stem ratio', cross 126A × HJ 541 was recognized for the highest amount of positive significant heterosis (30.48%) over second check CSH 24MF and same cross with positive significant heterosis (27.38%) over first check SSG 59-3.

In our study material range of heterosis for 'green fodder yield in 1st cut' was 126.67to -76.74 per cent. The highest amount of significant positive heterosis was expressed by cross 31A × SSG 59-3 (139.12%) over the first check SSG 59-3. Maximum significant positive heterosis with respect to 'green fodder yield in 2nd cut' was recorded for hybrids 94012A × HJ 541 (126.67%) and 31A × HJ 541 (126.67%) over the first check SSG 59-3, and it was varied in the range of 126.67% to -76.74%. For 'dry fodder yield in 1st cut', heterosis was varied from 146.22% to -43.22%, with the highest significant positive heterosis being recorded in cross 126A × HJ 541 (146.22% and 124.08%) over the checks CSH 24MF and SSG 59-3, respectively. For 'dry fodder yield in 2nd cut', cross 94031A × SSG 59-3 (223.38%) was recognized as best hybrid over the first check SSG 59-3.

Heterosis for quality parameters

As far as heterosis for quality parameters was concerned, all quality traits had shown significant heterosis over check. Range of heterosis for TSS varied from 23.92 to -43.35 per cent and the highest significant positive heterosis over the second check CSH 24MF was recorded for 31A x COFS 29 (23.92%). Range of heterosis for protein yield was 56.57% to -12.50%. Other hybrid which revealed positive heterosis over the first check SSG 59-3 was 126A x COFS 29 (31.25%) and 14A x HJ 541 (30.13%). The highest significant economic heterosis for IVDMD% was shown by the cross 126A x HJ 541 over the first check SSG 59-3 (18.75%) and over the second check CSH 24MF (6.36%).

The heterosis for HCN content varied from 174.12 to -32.98% and cross 126A x IS 18551 (-32.98%) was identified as best hybrid for HCN as it showed the highest amount of significant negative heterosis over the second check CSH 24MF. Range of heterosis for tannin content varied in the range of

157.97 to -95.35%. Range of heterosis for phenol varied from 61.51% to -15.48%. The highest amount of significant negative heterosis was recorded for the cross 94031A × COFS 29 (-15.48%) the first check SSG 59-3.

Analysis of variance for combining ability

Analysis of variance for combining ability was calculated for all the eighteen characters and the results are presented in Table 1. All the characters except 'number of tillers per plant' were reported as highly significant indicating a prominent contribution of these characters towards combining ability except the trait 'number of tillers per plant'. The study revealed that SCA variances (σ^2 SCA) were higher than GCA variance (σ^2 GCA) for all the characters under study (Table 1). The 'ratio of σ^2 GCA/σ^2 SCA' was less than unity for thirteen characters indicating preponderance of non-additive gene action (dominance and epistasis).

GCA effects of parents

Estimation of variation due to GCA was partitioned into male and female parents for seeking out potential parents for further breeding program. The results of the GCA estimates are presented in **Table2**. The study revealed that no GCA effect was observed for plant height and number of tillers/plant. The 14A (3.99) had positive significant GCA effect for leaves/plant. Among testers IS 18551 (7.76) exhibited positive significant value for leaf length. For stem diameter, 126A (-0.19) and 94031A (-0.32) lines exhibited negative GCA effect. For leaf stem ratio, only 94031A (0.11) exhibited positive significant GCA effect.

Among female parents, 14A (0.82) and among male parents, SSG 59-3 (1.87) showed positive significant GCA effects for GFY Ist cut indicating it as a good combiner. In case of GFY in 2nd cut, female parent 94031A (0.38) and male parent HJ 541 (0.97) reported positive significant GCA effect. The female parent 14A (0.17) and male parent SSG 59-3 (0.30) for DFY in Istcut showed significant positive GCA effect. The female parents, 94031A (0.07) and male parents, SSG 59-3 (0.03) showed significant positive GCA effect for dry fodder yield in 2nd cut.

Interestingly, none of the parents exhibited positive significant GCA effect for total soluble solids indicating their poor combining ability for this character. The genotype 14A (0.88) as female parent and COFS 29 (0.92) as male parent showed significant positive GCA effect for *protein yield* indicating its good general combining ability. Furthermore, two

TABLE 1

Analysis of variance for combining ability and genetic variance for different morphological and quality parameters

Sources of Variation	D.F.	PH	TP	LP	LL	LB	SD	LSR	GFY 1st	GFY 2nd	DFY 1st	DFY 2nd	TSS	CP	HCN	Ph	Tan	IVDMD
Replication	2	1283.16	6.23	23.91	62.93	4.07	0.10	0.01	10.00	0.04	0.15	0.01	11.69	0.13	70.19	1.31	0.002	9.43
Hybrids	24	26400.47**	11.41	1622.28**	4526.58**	96.75**	11.49**	0.93**	291.42**	51.93**	5.78**	0.046**	13.14**	60.71**	2643.05**	41.51**	775.35**	1145.41**
Lines	4	6436.17**	3.84*	312.67**	511.54	27.57**	5.92**	0.45**	21.97**	6.23**	0.76**	0.03**	5.73**	15.93**	4393.52**	20.63**	317.04**	429.16**
Testers	4	4953.30*	0.77	91.04	1537.14**	7.59**	1.78**	0.14**	128.80**	22.79**	2.87**	0.12**	0.85	17.46**	3397.49**	4.07**	261.65**	90.21**
Lines X Testers	16	15010.99**	6.79	1218.56**	2477.89*	61.58**	3.78**	0.33**	140.64**	22.90**	2.14**	0.02**	6.55**	27.31**	2016.82**	16.79**	196.64**	626.03**
Error	48	17896.54	19.88	659.75	33.81	24.81	2.34	0.24	40.28	7.53	1.82	0.003	6.48	7.77	32.12	8.20	7.35	96.31
Genetic variance for different morphological, quality and anti-nutritional parameters																		
σ^2 GCA-		32.36	-1.71	6.74	0.03	0.04	0.004	0.67	0.14	0.02	0.004	0.02	0.16	125.24	0.13	4.00	1.72	
σ^2 SCA-		2019.69	170.11	322.78	10.36	1.04	0.083	30.55	5.28	0.50	0.111	1.10	6.28	7206.54	3.99	76.44	128.55	
σ^2 GCA/σ^2 SCA-		0.01	-0.01	0.02	0.002	0.03	0.04	0.02	0.02	0.04	0.03	0.01	0.02	0.01	0.03	0.05	0.01	

D.F. = Degree of freedom
* Significant at 5% level
**significant at 1% level: σ^2 GCA = GCA variance
σ^2 SCA = SCA variance

TABLE 2

General combining ability effects of parents in different morphological and quality parameters

Female parents	Plant height	Tillers/ plant	Leaves/ plant	Leaf length	Leaf breadth	Stem diameter	Leaf : Stem ratio	GFY 1st cut	GFY 2nd cut	DFY 1st cut	DFY 2nd cut	TSS	CP	HCN	Ph	Tan	IVDMD
14A	8.9	0.226	3.99**	-0.49	-0.36	-0.14	0.02	0.82*	-0.49**	0.17*	-0.05**	0.21	0.88**	-24.28**	0.81**	4.11**	-4.30**
126A	0.796	0.249	-0.49	-2.34	-0.72**	-0.19*	0.02	0.41	0.08	0.04	0.01	0.13	-0.36*	0.55	0.09	-0.66**	-0.54
31A	6.24	0.04	-0.87	3.41	1.01**	0.31**	-0.06**	-0.16	-0.07**	-0.07	-0.36*	0.002	0.009	-8.19**	-0.13	-1.32**	1.54**
94012A	1.59	-0.3	-0.84	2.59	0.3	0.35**	-0.10**	-0.47	0.09	-0.09	0.001	-0.53**	-0.31*	14.46**	0.05	-1.64**	0.66
94031A	-17.53*	-0.218	-1.78	-3.16	-23	-0.32**	0.11**	-0.6	0.38**	-0.04	0.07**	0.18	-0.21	17.46**	-0.82**	-0.37**	2.63**
SE (d)	7.05	0.23	1.35	3.05	0.26	0.08	0.02	0.33	0.14	0.07	0.01	0.13	0.14	2.06	0.15	0.14	0.51
Male Parents																	
SSG 59 3	9.17	-0.12	-1.09	1.03	-0.1	-0.12	-0.02	1.87**	0.11	0.30**	0.03*	-0.08	-0.35*	-3.61	0.21	-0.61**	-0.07
HJ 541	-3.18	0.04	2.06	-1.31	-0.35	-0.19*	-0.08**	0.28	0.97**	0.09	0.14	-0.06	0	-5.40*	-0.2	-1.53**	1.31*
IS 2205	0.86	0.18	-0.53	-6.12	-0.27	0.08	-0.03	0.59	-0.33	-0.02	-0.03*	-0.1	-0.18	15.13**	0.21	-1.21**	0.51
COFS 29	-13.71	-0.04	-0.56	-1.36	0.27	-0.19	0	-2.01**	-0.47**	-0.29**	-0.07**	0.13	0.92**	14.49**	-0.34**	3.63**	0.23
IS 18551	6.86	-0.17	0.13	7.76*	0.46	0.24**	-0.02	-0.73*	-0.58**	-0.06	-0.07**	0.12	-0.38**	-20.60**	0.11	-0.27	-1.98**
SE (d)	7.05	0.23	1.35	3.05	0.26	0.08	0.02	0.33	0.14	0.07	0.01	0.13	0.14	2.06	0.15	0.14	0.51

Table 3
Specific combining ability effects of hybrids for different morphological and quality parameters

Hybrids	PH	TP	LP	LL	LB	SD	LSR	GFY 1st	GFY 2nd	DFY 1st	DFY 2nd	TSS	CP	HCN	Ph	Tan	IVDMD
14A x SSG 59-3	-7.61	0.04	-7.26*	-0.48	-0.72	0.15	0.02	0.31	-0.23	0.05	-0.01	0.005	-0.51	-35.31**	-0.73*	-1.87**	4.73**
14A x HJ 541	-10.39	-0.53	0.33	-0.52	1.72**	0.11	0.01	-2.64**	-0.56	-0.28	-0.09*	0.25	-0.21	1.37	0.89**	-1.01**	-1.29
14A x IS 2205	3.71	0.66	0.94	3.94	-1.47*	-0.24	0.003	2.55**	-0.05	0.28	-0.02	0.03	-0.08	4.59	0.23	2.32**	-4.98**
14A x COFS 29	-14.3	-0.42	-0.52	-13.34*	-0.31	0.17	-0.01	-1.93*	-0.17	-0.18	-0.008	-0.47	0.54	13.83**	0.03	1.07**	1.76
14A x IS 18551	28.6	0.26	6.51*	10.4	0.78	-0.19	-0.01	-1.71*	1.03**	0.12	0.13**	0.18	0.26	15.50**	-0.42	-0.5	-0.21
126A x SSG 59-3	0.62	0.01	13.13**	3.43	-0.6	-0.01	-0.03	-0.99	-0.74*	-0.19	-0.10*	0.24	0.48	-15.46**	0.08	0.43	-3.59**
126A x HJ 541	-5.15	-0.11	-0.93	3.6	1.6	0.07	-0.006	1.88*	-0.29	0.49**	0.01*	-0.25	-0.37	29.53**	-0.53	-0.67*	4.17**
126A x IS 2205	17.18	-0.02	-4.21	-4.03	0.63**	0.02	0.09	-0.82	0.83*	-0.2	0.08*	-0.002	0.18	-30.82**	-0.24	-0.54	-2.11
126A x COFS 29	2.49	-0.22	-2.68	0.56	-1.12	-0.11	-0.02	0.64	0.66*	0.25	0.06	-0.18	0.22	20.92**	0.44	1.98**	1.76
126A x IS 18551	-15.15	0.35	-5.3	-3.56	-0.5	0.01	0.07	-0.72	-0.47	-0.11	-0.06	0.2	-0.51	-4.17	0.24	-1.19**	-0.23
31A x SSG 59-3	9.25	-0.16	-2.37	2.34	0.64	-0.14	0.007	0.21	0.26	0.15	0.04	0.36	-0.74**	24.21**	-0.13	-0.99**	-1.85
31A x HJ 541	-7.75	0.15	2.22	-12.59	-1.09	-0.29	-0.06	2.93**	-0.41	0.09	-0.12**	0.44	-0.31	14.19**	0.16	0.38	-1.61
31A x IS 2205	-18.41	-0.09	-1.28	2.32	0.25	-0.02	0.06	-0.42	-0.5	-0.02	-0.05	-0.48	0.94**	-4.25	-0.17	1.04*	2.29
31A x COFS 29	32.66	-0.07	4.13	12.25	0.54	0.37	-0.05	-0.64	0.17	-0.05	0.01	0	0.07	-26.23**	0.61	0.27	1.17
31A x IS 18551	-15.75	0.17	-2.7	-4.32	-0.35	0.09	0.04	-2.07**	0.48	-0.17	0.11**	-0.31	0.03	-7.91	-0.47	-0.71*	0
94012A x SSG 59-3	-9.72	0.17	1.2	-3.41	-0.17	0.42*	-0.02	0.53	0.5	0.001	0.07	-0.61*	1.45**	-3.01	0.01	4.36**	3.07**
94012A x HJ 541	23.27	0.37	-1.41	9.43	-1.98**	0.04	-0.14**	-0.86	1.07**	-0.16	0.12**	-0.17	0.88**	9.64	-0.44	1.04**	-0.34**
94012A x IS 2205	-13.73	-0.31	2.51	-4.32	0.4	-0.21	0.11*	-0.97	-0.61	-0.06	-0.05	0.45	-1.25**	18.88**	0.57	-2.40**	1.57
94012A x COFS 29	-0.08	0.37	-1.06	-0.28	0.86	-0.09	0.03	0.48	0.01	-0.78	0.001	0.21	-1.01**	-9.27	-0.11	-2.66**	1.61
94012A x IS 18551	0.27	-0.6	-1.24	-1.41	0.89	-0.16	0.02	0.82	-0.97**	0.14	-0.14**	0.12	-0.07	-16.23**	-0.03	-0.34	-2.92**
94031A x SSG 59-3	7.47	-0.07	-4.7	-1.88	0.86	-0.42*	-0.009	-0.07	0.21	-0.015	-0.004	0.01	-0.67*	29.57**	0.76*	-1.92**	-2.35*
94031A x HJ 541	0.02	0.13	-0.21	0.07	-0.25	-0.05	0.14**	-1.3	0.18	-0.14	0.07	-0.26	0.01	-54.75**	-0.09	0.25	2.08
94031A x IS 2205	11.24	-0.22	2.04	2.09	0.18	0.45*	-0.08	-0.32	0.34	0.01	0.05	0	0.2	11.60*	-0.38	-0.41	3.22**
94031A x COFS 29	-20.77	0.35	0.13	0.8	0.03	-0.33	0.05	1.45	-0.67*	0.12	-0.07	0.45	0.17	0.74	-0.97**	-0.66	-6.32**
94031A x IS 18551	2.02	-0.18	2.74	-1.1	-0.82	0.24	-0.10*	0.25	-0.06	0.01	-0.04	-0.2	0.28	12.82**	0.69*	2.75**	3.36**
SE (d)	15.76	0.52	3.02	6.81	0.58	0.18	0.05	0.74	0.32	0.15	0.04	0.3	0.32	4.62	0.33	0.31	1.15
5% significant value	31.6	1.04	6.07	13.38	1.16	0.36	0.1	1.48	0.64	0.3	0.08	0.6	0.64	9.28	0.66	0.62	2.31
1% significant value	42.23	1.39	8.09	18.2	1.55	0.48	0.13	2	0.85	0.4	0.1	0.8	0.85	12.38	0.88	0.83	3.08

female parents viz. 94031A (2.63) and 31A (1.54) had significant positive GCA effect for IVDMD, with former exhibiting maximum effect. The significantly negative GCA effect was recorded in female parents 94031A (-0.82) and male parents COFS 29 (-0.34) for phenol content.

It is noteworthy that a negative GCA effect is desirable for HCN content. Among the female parents, 14A (-24.28) was found to be the best combiner, having the highest negative GCA value. Parent 31A (-8.19) have also exhibited negative significant GCA effect. Among male parents, IS 18551 (-20.60) and HJ 541 (-5.40), exhibited a significantly negative GCA effect for HCN content. Four female parents viz. 94012A (-1.64), 31A (-1.32), 126A (-0.66) and 94031A (-0.37) and three male parents i.e., HJ 541(-1.53), IS 2205 (-1.21) and SSG 59-3 (-0.61) exhibiting significant negative GCA effects for tannin content, with maximum effect shown by HJ 541.

SCA effects of crosses

For evaluating the superiority of crosses over parent, SCA effects were evaluated. The SCA effects of the various crosses are presented in Table 3.Interestingly, none of the crosses exhibited positive significance for SCA effect for plant height, tillers/ plant, leaf length and breadth. However, for leaves per plant, maximum positive significance was recorded for the cross 126A x SSG 59-3 (13.13) followed by 14A × IS 18551 (6.51).Furthermore, for stem diameter, no crosses exhibited negative and significant SCA effect. In contrast, two cross combinations i.e. 94031A × 541 (0.14) and 94012A × IS 2205 (0.11), revealed a significant and positive SCA effect for leaf: stem ratio. For the green fodder yield in 1st cut, the maximum SCA effect was recorded for the cross 31A × HJ 541 (2.93) followed by 14A × IS 2205 (2.55) and 126A × HJ 541 (1.88), respectively. The significant SCA effect was recorded for the cross 94012A × 541 (1.07) followed by 14A ×18551 (1.03), 126A × 2205 (0.83) and 126A × COFS-29 (0.66), respectively, where former exhibited maximum effect. For dry fodder yield in 1st cut, only cross 126A × HJ 541 (0.49) showed significant positive SCA effect. For the similar character in 2nd cut, the maximum SCA effect was recorded in case of cross 14A × IS 18551 (0.13) followed by 94012A × HJ 541 (0.12), 31A × IS 18551 (0.11) and 126A × IS 2205 (0.08), respectively.

Interestingly, positive SCA effect is not significant for any of the cross combination with respect to TSS, the same character for which none of the parents exhibited positive significant GCA effect. For protein yield, the maximum SCA effect was recorded for the cross 94012A × SSG 59-3 (1.45) followed by crosses 31A × IS 2205 (0.94) and 94012A × HJ 541 (0.88), respectively. For the character IVDMD, the maximum SCA effect was recorded for the cross 14A × SSG 59-3 (4.73) followed by crosses 14A x HJ 541 (4.17), 94031A × IS 18551 (3.36). Two crosses viz. 94031A × COFS 29 (-0.97) and 14A × SSG 59-3 (-0.73), respectively, revealed negative SCA effect for total phenol content. The maximum significant and negative SCA was recorded for 94031A × HJ 541(-54.75) for HCN content. For this character the crosses 14A x SSG 59-3 (-35.31) and 126A × IS 2205 (-30.82) also exhibited significant SCA value. Among all the combinations, crosses 94012A × COFS 29 (-2.66), 94012A × IS 2205 (-2.40) and 94031A × SSG 59-3 (-1.92) showed significant negative SCA effect for tannin content, with former being the best cross.

Correlation analysis

The phenotypic correlation coefficients among 18 characters are presented in Table 4. The correlation analysis revealed GFY 1st cut had significant positive correlation with PH (0.498**; 0.267**), DFY 1st (0.929**; 0.843**) and DH 35 (0.235*; 0.229*) at both genotypic and phenotypic level; and had significant negative correlation with SD (-0.272**; -0.247**) and IVDMD (-0.253**; -0.207*) at both genotypic level and phenotypic level, respectively. Similarly GFY 2nd cut had significant positive correlation with TP, DFY 2nd and IVDMD at both the level and significant positive correlation with PH, LSR and TSS at genotypic level only.

The component characters were also found to be correlated among themselves. The character DFY 1st cut had significant positive correlation with PH, DFY 2nd, DH 35 and DH total at both genotypic and phenotypic level; and both DFY 1st and DFY 2nd had significant negative correlation with SD and HCN at genotypic level only. This negative association could be used to select desirable genotypes with low anti-nutritional factors. PH and TP had significant positive association at genotypic level. Significant positive correlation was observed among the characters LL, LB and SD at phenotypic level.

Among studied quality attributes, significant negative correlation was observed between phenol content with tannin content and IVDMD at both genotypic and phenotypic level. In addition, significant positive correlation was observed in case of tannin content with PY, Ph and IVDMD was noticed at both the levels (i.e., genotypic and phenotypic), and HCN

with PY and IVDMD at genotypic level. TSS had significant positive correlation with TP, LP, SD, LSR, GFY 2nd and tannin content; and negative correlation with LL, DFY 2nd cut, PY, HCN and IVDMD at genotypic level. Similarly, HCN is significant and negatively correlated with tannin content at both the level.

DISCUSSION

The primary objective of heterosis breeding is to achieve a quantum jump in yielding ability of crop plant. For the exploitation of heterosis in a fodder crop, high degree of heterosis for fodder yield and its components is a pre-requisite. The negative heterosis is important for some morphological character *viz.* stem diameter and anti-nutritional factors.

The cross 14A × HJ 541 exhibited the highest heterosis for number of leaves/plant (89.23%) over the check CSH 24MF. The hybrid 14A × HJ 541 (30.13%) exhibited high heterosis for number of leaves/plant and for protein content over check SSG 59-3. 126A × HJ 541 was recorded for the maximum heterosis for the dry fodder yield in the 1st cut (146.22%) over CSH 24MF and IVDMD (18.75%) over the check SSG 59-3. The hybrid 126A × HJ 541 exhibited high heterosis for GFY in 2nd cut (61.22%) and DFY in 2ndcut (177.36%) over the check SSG 59-3 and significant negative heterosis for tannin content (-87.16%). Similar findings were reported by Soujanya *et al.,* (2018).

Similarly, 31A × COFS 29 exhibited the highest heterosis for TSS (23.92%) over the check CSH 24MF and 94012A × IS 18551, 31A × COFS 29 and 14A × IS 18551 had high negative heterosis indicating their potential to be used in future. For protein content the highest heterosis was recorded for 14A × COFS 29 (56.57%) followed by 126A × COFS 29 (31.25) and 14A × HJ 541 (30.13) over the check SSG 59-3. A significantly high positive heterosis for protein content was also reported by Parmar *et al.* (2019) in their studies. The cross 94031A x COFS 29 (-15.48%) exhibited maximum negative heterosis for phenol content over the first check SSG 59-3. Other hybrids worth mentioning are 94031A × IS 2205 (-13.64%), 94031A × SSG 59-3 (-12.87%) and 94031A × HJ 541 (-9.07%).

The highest amount of negative heterosis for the character HCN was recorded for the hybrid 126A × IS 18551 (-32.98%) over the second check CSH 24MF. Other crosses which showed negative heterosis over the second check are 14A × SSG 59-3 (-24.40%) and 14A × HJ 541 (-11.02%). The hybrid 31A × HJ

541 was recorded for the highest amount of negative heterosis for tannin content over first and second check. Other crosses viz., 94012A × IS 2205 (-82.56%), 94031A × IS 2205 (-77.91%) also exhibited negative heterosis over the second check.

Analysis of combing ability

The combining ability analysis indicated the presence of considerable variation among the hybrids and parents for all the characters under study. The magnitude of SCA variance was greater than GCA variance for all the characters, indicated pre-dominance of non-additive gene action in the inheritance of all characters of interest, is an important for the exploitation of heterosis through hybrid breeding. Several authors also reported the predominance of SCA variance in forage sorghum for fodder yield and its component characters by Pandey *et al.* (2013) and Dehinwal *et al.* (2017).

GCA effects of parents

The breeding value of the parental genotypes is reflected by GCA effect and is beneficial in identifying superior genotypes to be used for developing populations. The parents with best GCA effect for the various characters under study are presented in Table 5.

SCA effects of crosses

Specific combining ability effects symbolize the non-reliable component of the genotypic value arising due to contribution from dominance deviation and interaction deviation. Hence, SCA effect is the main reason for the exploitation of heterosis in F$_1$. Promising crosses for the various characters for SCA effect are presented in Table 5.

Correlation analysis

Correlation studies provide information about the importance of different traits for direct and indirect selection. The characters had positive correlation with GFY may prove to be helpful in increasing the green fodder yield of the crop. Simultaneous improvement of fodder yield and quality is one of prime objectives of majority of the sorghum breeder and to achieve these objectives, plant characters that are associated with fodder yield and quality should be selected simultaneously. Plant breeders could use these significant correlations in breeding programme for developing high yielding nutritious genotypes to meet the growing demand quality green fodder.Significant positive association of GFY with PH (Bibi *et al.* 2016)

TABLE 4

Estimates of Phenotypic correlation coefficient for different morphological and quality parameters

Parameters	PH	TP	LP	LL	LB	SD	LSR	GFY 1st	GFY 2nd	DFY 1st	DFY 2nd	TSS	PY	HCN	Ph	Tan	IVDMD
PH	1																
TP	0.14	1															
LP	0.38**	0.28**	1														
LL	0.48**	-0.11	0.25**	1													
LB	-0.12	-0.55**	-0.21*	0.24**	1												
SD	0.04	-0.20*	-0.11	0.27**	0.40**	1											
LSR	-0.48**	-0.07	-0.15	-0.25**	0.02	-0.37**	1										
GFY 1st	0.26**	0.00	0.04	0.07	-0.12	-0.24**	-0.06	1									
GFY 2nd	0.17	0.19*	0.13	0.01	-0.33**	-0.17	-0.17	0.09	1								
DFY 1st	0.25**	-0.00	0.05	0.16	-0.12	-0.27**	-0.00	0.84**	0.18*	1							
DFY 2nd	0.13	0.17	0.13	0.04	-0.32**	-0.21*	-0.09	0.09	0.94**	0.28**	1						
TSS	0.10	0.12	0.14	0.09	-0.07	-0.38**	0.19*	0.07	-0.13	0.16	-0.13	1					
PY	-0.02	0.04	0.15	-0.09	-0.07	-0.06	-0.09	-0.06	0.11	0.01	0.17	-0.08	1				
HCN	-0.21*	-0.32**	-0.15	-0.09	0.25**	0.16	0.02	-0.01	-0.11	-0.14	-0.16	-0.18*	-0.29**	1			
Ph	0.28**	0.12	0.35**	0.07	-0.08	-0.02	-0.16	0.09	-0.06	0.04	-0.03	-0.02	0.05	-0.06	1		
Tan	0.10	0.26**	0.33**	-0.01	-0.30**	-0.18*	-0.15	-0.14	0.07	-0.10	0.11	0.18	0.33**	-0.19*	0.21*	1	
IVDMD	-0.33**	-0.26**	-0.33**	-0.15	0.25**	0.25**	0.15	-0.20*	0.20*	-0.16	0.18	-0.31**	0.02	0.16	-0.24**	-0.35**	1

PH=Plant height (cm);TP=Tillers per plant;LP=Leaves per plant;LL=length of leaf (cm);LB=Leaf breadth (cm);SD=Stem diameter (cm);LSR=Leaf : Stem ratio;GFY1st and 2nd =Green fodder yield in 1st and 2nd cut (kg/plot);DFY in 1st and 2nd cut= Dry fodder yield in 1st and 2nd cut (kg/plot);TSS=Total Soluble Solids (0 brix);CP=Protein Content (%);HCN=Hydrocyanic acid content (µg/gm);Ph=Phenol content (mg/gm);Tan=Tannin.

TABLE 5

Promising female and male parents having good gca effect and crosses with good specific combining ability for different characters

Characters	Female parents	Male parents	Promising hybrids
Plant height (cm)	-	-	-
No. of tillers per plant	-	-	-
No. of leaves per plant	14A (3.99**)	IS 18551 (7.76*)	126A x SSG 59-3 (13.13**), 14A x IS 18551 (6.51*)
Leaf length (cm)	-	-	-
Leaf breadth (cm)	31A(1.01**)	-	14A x HJ 541 (1.72**), 126A x IS 2205 (0.63**)
Stem diameter (cm)	94031A (-0.32**), 126A (-0.19*)	HJ 541 (-0.19*)	94031A x SSG 59-3 (-0.42*)
Leaf: Stem ratio	94031A (0.11**)	-	94031A x HJ 541 (0.14**), 94012A x IS 2205 (0.11*)
GFY in 1st cut (kg/plot)	14A (0.82*)	SSG 59-3 (1.87**)	31A x HJ 541 (2.93**), 14A x IS 2205 (3.55**)
GFY in 2nd cut (kg/plot)	94031A (0.38**)	HJ 541 (0.97*)	94012A x SSG 59-3 (1.07**), 14A x IS 18551 (1.03**)
GFY in 2nd cut (kg/plot)	14A (0.17*)	SSG 59-3 (0.30**)	14A x HJ 541 (0.49**)
DFY in 2nd cut (kg/plot)	94031A (0.07**)	SSG 59-3 (0.03*)	14A x HJ 541 (0.13**), 31A x IS 18551 (0.11**)
TSS (0 brix)	-	-	-
Protein yield (%)	14A (0.88*)	IS 18551 (-20.69**), HJ 541 (-5.40*)	94012A x SSG 59-3 (1.45**), 31A x IS 2205 (0.94)
HCN content (µg/g)	14A (-24.28**), 31A (-8.19**)	COFS 29 (-0.34*)	94031A x HJ 541 (-54.75), 14A x SSG 59-3 (-35.31**)
Total phenol (µg/g)	94031A (-0.82**)	-	94031A x COFS 29 (-0.97*), 14A x SSG 59-3 (-0.73**)
Tannin (mg/g)	94012A (-1.64**), 31A (-1.32**)	HJ 541 (-1.53**), IS 2205 (-1.21**)	94012A x COFS 29 (-2.66**), 94012A x IS 2205 (-2.40)
IVDMD (%)	94031A (2.63**), 31A (1.54**)	HJ 541 (1.31*)	14A x SSG 59-3 (4.73**), 14A x HJ 541 (4.17**)

and DFY (Bhardwaj *et al.* 2017) was also reported in earlier studies. Positive and significant correlation of GFY with forage yield components has also been reported by Amare *et al.* (2015) and Vijaylaxmi *et al.,* 2019. The significant negative correlation of GFY with IVDMD was also reported by Prakash *et al.* (2010). Significant positive correlation was observed among the characters LL, LB and SD at phenotypic level. Parmar *et al.,* 2019 reported significant positive association between PH and TP, LB and SD. A positive genotypic correlation between two desirable traits makes it easy to improve both the traits under consideration at once.

CONCLUSION

It was evident from the study that various cross combinations were extensively studied for their potentials in improvement of sorghum quality and other important traits. Some parents were identified with good combining abilities for the yield and yield attributing characters. Considering green fodder yield as most important parameter, it might be concluded that the hybrids 31A × SSG 59-3, 126A × IS 2205 and14A × SSG 59-3 were found performing better for green fodder production and have potential to meet the growing fodder demand and could also be analyzed by molecular approach too to confirm their reliability.

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