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Assessment of genetic variability, heritability and genetic advance for yield and quality traits in forage sorghum [*Sorghum bicolor* (L.) Moench]

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Abstract

The present investigation was carried out with 70 F₂ crosses of forage sorghum in completely randomized block design with 3 replications at GBPUAT, Pantnagar under normal sown condition. The observations were recorded on nine yield contributing traits and three quality traits. The statistical analysis for genetic variability was done using ANOVA, h^2 , GCV, PCV and GA. The analysis of variance revealed significant difference among the crosses with respect to different yield and quality traits. The results of the present study indicated that high heritability values were observed in plant height, number of leaves, leaf width, leaf area, green fodder yield, and dry fodder yield and moderate for others. High GCV and PCV values were observed for leaf: stem whereas low and moderate for other characters. The high genetic advance was observed in plant height, leaf area, stem girth, total soluble solids, leaf: stem ratio, hydrocyanic acid content, green fodder yield, and dry fodder yield whereas low and moderate for others.

Keywords: Variability, GCV, PCV, GA and h^2

Introduction

Sorghum is one of the most important and widely grown crops in the world having the area of 41.14 million hectare with the production of about 58.72 million tonnes globally whereas 5.00 million hectare and 4.50 million tonnes grain production in India (USDA Foreign Agricultural Services, 2019) [23].

Sorghum is known by various names in Africa, such that *guinea-corn*, *dawa* or *sorgho* in West Africa, *durra* in the Sudan, *mshelia* in Ethiopia and Eritrea, *mtama* in East Africa, *kaffir corn* in South Africa and *amabele* or *mabele* in several countries in Southern Africa. In the Indian sub-continent, it is known as *jowar* (Hindi), *cholam* (Tamil Nadu), *jonna* (Andhra Pradesh) and *jola* (Karnataka). Five basic races of cultivated sorghum are recognized as *Bicolor*, *Guinea*, *Kafir*, *Durra* and *Caudatum* (Harlan and De Wet, 1972) [5].

It has extensive variability of usage such as forage sorghum, grain sorghum and sweet sorghum, providing food, fodder, feed, fuel and fiber. The crop is mainly grown in tropical and subtropical areas because of its drought tolerance capacity, and quick growing habit, good palatability where agro-climatic conditions such as rainfall, temperature and soil are variable. Much of the crop is grown in the stress-prone and marginal areas of the semi-arid tropics, mainly on small holdings. In Northern Western India, it is grown for meeting the major fodder requirement of *kharif* and summer seasons.

Nutritionally, among the *kharif* fodders, sorghum is a crop *par excellence* with starch (63-68%), potential of high digestibility (50-60%), dry matter (20-35%), sugars (8-17%), crude protein (7.5-10.0%), calcium (0.53%), phosphorus (0.24%), and crude fiber (30-32%) (Sheoran *et al.*, 2000) [20]. Beside the higher content of carbohydrates, it has iron (Fe) and vitamin B₃ contents which are higher than maize and rice. It is a major staple food of many countries in Asia and Africa, sorghum is now a major feed crop in the United States, Argentina, Mexico, South Africa, and Australia (Miller and Kebede, 1984) [16].

Genetic variability and relationship among different individuals is a prerequisite for any successful breeding programme. Genetic variability of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced forage production. Genetic variability explains the genetic differences between different populations within a species or between species. Genetic variability can be estimated by assessing the different genetic parameters like analysis of variance, heritability and genetic

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advance etc. The parents having more genetic variability result into higher heterotic expression in F₁ and greater amount of genetic variability in segregating populations (Shekhawat *et al.*, 2001) [19].

Precise information on nature and degree of genetic variability helps the plant breeder in selecting the genetically diverse parents for the purposeful hybridization. (Arunachalam, 1981) [3]. Genetic improvement of yield especially in self-pollinated crops depends on nature and amount of genetic variability (Joshi and Dhawan, 1966) [12]. One of the important approaches to sorghum breeding is hybridization and subsequent selection. Parents' choice is the first step in plant breeding program through hybridization. In order to obtain transgressive segregants, genetic variability between parents is necessary (Joshi *et al.*, 2004) [13]. The higher genetic variability between parents, the higher heterosis in progeny can be observed (Joshi and Dhawan, 1966) [12]. Estimation of genetic variability is one of appropriate tools for parental selection in sorghum hybridization programs. Appropriate selection of the parents is essential to be used in crossing nurseries to enhance the genetic recombination for potential yield increase. In view of the above, there is need to screen the variability of forage sorghum crosses based on yield and quality parameters to find

out their suitability in different breeding programmes.

Materials and Methods

The initial research related to screening was carried out in the experimental area of Instructional Dairy Farm, Nagla, G.B. Pant University of Agriculture and Technology, Pantnagar, District U. S. Nagar, Uttarakhand during *kharif*, 2018-19. The experimental material consists of 70 F₂ crosses of forage sorghum (Table-1). The experiment was laid out in randomized complete block design (RBD) with three replications under normal sown condition. All the seventy F₂ crosses were evaluated during *kharif*, 2018-19. Each entry was planted in 3 meter long four rows plot. The rows were spaced 25 cm apart. All the recommended package of practices for sorghum was followed to raise a healthy crop. The observations were recorded on nine yield and three quality parameters. The yield parameters were plant height (PH), number of leaves per plant (NL), leaf length (LL), leaf width (LW), leaf area (LA), stem girth (SG), leaf:stem ratio (L:S), green fodder yield per plot (GFY), dry fodder yield per plot (DFY) whereas quality parameters were total soluble solids (TSS), hydrocyanic acid content (HCN), and protein percent (PP). The statistical analysis was performed by Indostat Hyderabad.

Table 1: List of F₂ Crosses

SI. No.	Cross	SI. No.	Cross
1.	ICSA467 X CSV15	36.	ICSA 271 X CSV15
2.	ICSA467 X PC5	37.	ICSA 271 X PC5
3.	ICSA467 X 04K693	38.	ICSA 271 X 04K693
4.	ICSA467 X 04K700	39.	ICSA 271 X 04K700
5.	ICSA467 X 01K733	40.	ICSA 271 X 01K733
6.	ICSA467 X UPMC8	41.	ICSA 271 X UPMC8
7.	ICSA467 X 04K668	42.	ICSA 271 X 04K668
8.	11A2 X CSV15	43.	993100A X CSV15
9.	11A2 X PC5	44.	993100A X PC5
10.	11A2 X 04K693	45.	993100A X 04K693
11.	11A2 X 04K700	46.	993100A X 04K700
12.	11A2 X 01K733	47.	993100A X 01K733
13.	11A2 X UPMC8	48.	993100A X UPMC8
14.	11A2 X 04K668	49.	993100A X 04K668
15.	HB 94004A X CSV15	50.	ICSA276 X CSV15
16.	HB 94004A X PC5	51.	ICSA276 X PC5
17.	HB 94004A X 04K693	52.	ICSA276 X 04K693
18.	HB 94004A X 04K700	53.	ICSA276 X 04K700
19.	HB 94004A X 01K733	54.	ICSA276 X 01K733
20.	HB 94004A X UPMC8	55.	ICSA276 X UPMC8
21.	HB 94004A X 04K668	56.	ICSA276 X 04K668
22.	SPA2 94012 X CSV15	57.	ICSA293 X CSV15
23.	SPA2 94012 X PC5	58.	ICSA293 X PC5
24.	SPA2 94012 X 04K693	59.	ICSA293 X 04K693
25.	SPA2 94012 X 04K700	60.	ICSA293 X 04K700
26.	SPA2 94012 X 01K733	61.	ICSA293 X 01K733
27.	SPA2 94012 X UPMC8	62.	ICSA293 X UPMC8
28.	SPA2 94012 X 04K668	63.	ICSA293 X 04K668
29.	ICSA469 X CSV15	64.	SP 55609A X CSV15
30.	ICSA469 X PC5	65.	SP 55609A X PC5
31.	ICSA469 X 04K693	66.	SP 55609A X 04K693
32.	ICSA469 X 04K700	67.	SP 55609A X 04K700
33.	ICSA469 X 01K733	68.	SP 55609A X 01K733
34.	ICSA469 X UPMC8	69.	SP 55609A X UPMC8
35.	ICSA469 X 04K668	70.	SP 55609A X 04K668

(A) Analysis of variance and means: Characters under study were analyzed using analysis of variance to test whether treatments were differing significantly among themselves. The model is as follows:

$$Y_{ij} = \mu + b_i + t_j + e_{ij}$$

Where,

$i = 1, 2, \dots, r$ (replication)

$j = 1, 2, \dots, t$ (treatment)

Y_{ij} = performance of j^{th} variety in the i^{th} block

μ = population mean

b_i = true effect of i^{th} block

t_j = true effect of j^{th} treatment

e_{ij} = random error

r = number of replications

t = number of treatments

$$\text{Restrictions are } \sum_{i=1}^r b_i = 0 \text{ and } \sum_{j=1}^t t_j = 0$$

(B) Estimation of variability

$$\text{CV (\%)} = \frac{\text{Standard deviation}}{\text{Mean}} \times 100$$

$$\text{Genotypic coefficient of variation (GCV \%)} = \frac{\sigma_g}{\bar{X}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV \%)} = \frac{\sigma_p}{\bar{X}} \times 100$$

$$\text{Environmental coefficients of variation (ECV \%)} = \frac{\sigma_e}{\bar{X}} \times 100$$

Where,

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

σ_e = Environmental standard deviation

\bar{X} = Grand mean

(C) Estimation of Heritability: The heritability in broad sense h^2 (b) was estimated for each character as the ratio of genotypic variance to phenotypic variance by the formula:

$$\text{Heriheritability (\%)} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

(D) Genetic Advance: The expected genetic advance under selection for the different characters was estimated as suggested by Allard (1960).

$$GA = h_b^2 \times \sigma_{pi} \times K$$

Where,

GA = expected genetic advance

h_b^2 = heritability in broad sense

σ_{pi} = phenotypic standard deviation for i^{th} character

K = intensity of selection, the value of which is 2.06 at 5% (Lush, 1949).

(E) Genetic advance as per cent of mean (GAM)

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where

\bar{X} = General mean of the character

Results and Discussion:

Analysis of variance for yield and quality traits: The analysis of variance was carried out for all the characters in Randomized Block Design and the result are presented in the Table 2. The mean sum of square of the differences among the treatments is highly significant for all the yield and quality characters under timely sown condition. This type of result indicated existence of inherent genetic differences among genotypes for different characters. The analysis of variance revealed significant difference among the genotypes which validated further on the basis of genetic and statistical analysis of the data. It revealed that mean squares due to genotypes were found to be significant for all the characters. The findings of present study were found similar with the findings of Desai *et al.*, (2000) [6], Kadam *et al.*, (2001) [14], Kumar *et al.*, (2014), Agrawal *et al.*, (2005) [1], Bello *et al.*, (2007) [4], Rani *et al.*, (2009) [17], and Jadhav *et al.*, (2017) [9]. The mean performance of 70 F₂ crosses has been listed in Table 3. The mean performance of different genotypes for green fodder yield was found to range between 11.00 ton/ha in cross ICSCA 469 X 01 K 733 to 24.72 ton/ha in cross ICSCA 293 x 01 K 733 with general mean of 19.78 ton/ha. The dry fodder yield was lowest in cross ICSCA 467 X CSV 15 (2.66 ton/ha) while it was highest in cross ICSCA 469 A X 04 K 700 (7.81 ton/ha) with a general mean of 5.23 ton/ha. The mean values for plant height varied between 190.73 cm to 320.67 cm in the cross SPA2 94012 X 04 K 700 and cross ICSCA 467 X CSV 15, respectively with a general mean of 258.326 cm. The range of mean values for number of leaves per plant was between 13.00 in cross ICSCA 467 X CSV 15 to 10.17 in cross SPA2 94012 X UPMC 8 with a general mean of 12.002. The range of mean values for leaf length ranged from 70.67 cm to 93.17 cm in cross ICSCA 467 X 01 K 733 and cross 11 A2 X 04 K 668 respectively with a general mean of 83.308 cm. The mean value of leaf width was found between 4.77 cm in cross SPA2 94012 X 04 K 700 to 8.47 cm in cross ICSCA 469 A X 04 K 668 with a general mean of 6.737 cm. The range of mean values for leaf area was between 257.95 cm² to 559.36 cm² in cross SPA2 941012 X 04 K 700 and cross HB 94004 A X 04 K 700 with a general mean of 400.306 cm². The range of mean values for stem girth was found between 0.97 cm in cross SPA2 94012 X 04 K 700 to 1.78 cm in cross ICSCA 469 A X CSV 15 with a general mean of 1.327 cm. The range of mean values for TSS % was found between 5.17 to 15.00 in cross HB 94004 A X CSV 15 and cross 993100 A X PC 5 with a general mean of 9.29. The range of mean values

for leaf stem ratio was 0.15 to 0.35 in cross ICSA 271 X 04 K 668 and ICSA 271 X PC 5 respectively with a general mean of 0.21. The mean value of HCN content was found between 62.95 ppm in cross ICSA 293 X 04 K 693 to 150.43 in cross HB 94004 A X 04 K 668 with a general mean 89.327 ppm. The mean value of protein percent was found between 5.77% in cross ICSA 467 X UPMC 8 to 8.54% in cross SPA2 94012 X 04 K 693 with a general mean of 7.03%.

Success of any breeding programme depends upon the extent of variability present in the breeding population. The estimation of variability is of utmost importance in a crop for the identification of lines which can generate further variability so that artificial selection of desirable diverse genotypes may be made. Some of the very useful variations would go unutilized if not be identified by the breeder during selection process.

Table 2: Analysis of variance for simple RBD with respect to different characters for F₂ generation during the year 2018-19.

Source of Variations	df	Plant Height (cm)	No. of Leaves	Leaf Length (cm)	Leaf Width (cm)	Leaf Area (cm ²)	Stem Girth (cm)
Replication	2	751.072	0.224	104.203	0.289	1350.149	0.007
Treatments	69	2623.116**	2.893**	69.897**	1.449**	9045.043**	0.078**
Error	130	296.604	0.123	59.177	0.102	312.64	0.005
SE		9.943	0.202	4.441	0.184	10.208	0.042
SEd		14.061	0.286	6.281	0.261	14.437	0.060
SEd from mean		9.872	0.201	4.409	0.183	10.135	0.042
CD at 1%		36.728	0.749	0.001	0.682	37.708	0.157
CD at 5%		27.804	0.567	0.002	0.516	28.546	0.119
CV %		6.666	2.928	9.234	4.750	4.417	5.577

Table 2: Continued...

Source of Variations	df	TSS (%)	Leaf:stem Ratio	HCN (ppm)	Green Fodder Yield (kg)	Dry Fodder Yield (kg)	Protein (%)
Replication	2	0.051	0.044	375.403	1.847	0.052	2.937
Treatments	69	10.357**	0.006**	958.568**	1.981**	0.294**	0.974**
Error	130	0.810	0.0002	233.954	0.049	0.003	0.237
SE		0.519	0.009	8.830	0.129	0.032	0.281
SEd		0.735	0.013	12.428	0.182	0.045	0.397
SEd from mean		0.516	0.009	8.767	0.128	0.032	0.279
CD at 1%		1.920	0.036	32.619	0.476	0.119	1.038
CD at 5%		1.453	0.27	24.694	0.360	0.090	0.786
CV %		9.687	7.731	17.123	3.764	3.583	6.927

* Significant at 5% level of probability

** Significant at 1% level of probability

Table 3: Mean performance of yield and quality traits in F₂ crosses forage sorghum.

Sl. No.	Cross	PH	NL	LL	LW	LA	SG	TSS	L:S	HCN	GFY (Kg/plot)	GFY (ton/ha)	DFY (Kg/plot)	DFY (ton/ha)	PP
1	ICSA467 X CSV15	204.25	13.50	88.69	8.10	490.30	1.57	8.62	0.26	116.89	4.08	13.40	0.85	2.67	6.80
2	ICSA467 X PC5	215.57	12.82	89.72	6.80	401.84	1.42	7.95	0.31	97.56	7.37	24.37	1.53	4.93	6.75
3	ICSA467 X 04K693	236.02	14.98	86.12	8.30	406.62	1.52	7.62	0.29	68.84	6.41	21.13	1.27	4.07	6.56
4	ICSA467 X 04K700	252.80	13.60	83.55	6.83	392.06	1.37	6.95	0.27	71.27	6.04	19.93	1.15	3.67	6.49
5	ICSA467 X 01K733	259.53	14.23	71.18	7.40	394.32	1.42	7.78	0.32	109.10	5.48	18.07	1.18	3.77	6.89
6	ICSA467 X UPMC8	254.38	13.97	74.98	7.23	403.11	1.41	8.45	0.23	102.99	6.07	20.03	1.25	4.00	5.84
7	ICSA467 X 04K668	253.85	13.42	77.95	7.43	419.31	1.42	7.78	0.25	97.49	7.07	23.37	1.91	6.20	7.66
8	11A2 X UPMC8	211.43	13.07	80.52	6.93	415.92	1.47	9.62	0.31	97.32	5.89	19.40	1.24	3.97	7.29
9	11A2 X 04K700	218.17	13.10	82.08	6.40	424.01	1.42	6.95	0.29	107.77	6.84	22.57	1.38	4.43	7.78
10	11A2 X CSV15	229.52	13.27	83.45	6.10	370.99	1.25	11.12	0.24	110.15	5.98	19.73	1.25	4.00	7.29
11	11A2 X 01K733	280.60	13.97	83.42	7.47	454.78	1.52	8.12	0.25	95.77	6.97	23.03	1.41	4.53	7.56
12	11A2 X 04K693	252.42	13.43	87.75	6.90	425.38	1.31	6.28	0.27	150.36	7.02	23.20	1.36	4.37	6.08
13	11A2 X 04K668	235.53	14.53	93.68	6.47	418.95	1.38	6.62	0.31	70.21	5.98	19.73	1.17	3.73	7.50
14	11A2 X PC5	216.37	13.72	83.65	7.83	483.38	1.37	10.62	0.32	92.49	7.46	24.63	1.54	4.97	6.39
15	HB 94004A X 04K668	281.50	12.52	86.68	6.67	426.61	1.41	9.62	0.26	150.95	5.32	17.50	1.58	5.10	6.07
16	HB 94004A X 04K693	276.75	12.20	86.42	6.67	401.75	1.24	9.28	0.22	83.91	6.07	20.03	1.53	4.93	6.00
17	HB 94004A X PC5	260.90	13.67	91.48	7.97	545.98	1.59	10.62	0.26	94.41	6.37	21.03	1.60	5.17	6.64
18	HB 94004A X CSV15	260.50	13.10	89.38	8.23	503.95	1.56	5.28	0.25	83.97	5.15	16.93	1.27	4.07	7.92
19	HB 94004A X 04K700	262.48	14.27	82.82	8.10	559.88	1.72	9.28	0.25	84.15	5.59	18.43	1.58	5.10	6.64
20	HB 94004A X 01K733	304.87	11.85	80.08	6.53	344.83	1.46	8.28	0.20	77.64	7.43	24.53	2.09	6.80	7.62
21	HB 94004A X UPMC8	262.73	12.75	82.38	7.13	395.88	1.42	8.62	0.22	95.21	4.01	13.13	1.05	3.33	7.47
22	SPA2 94012 X PC5	256.12	13.00	88.18	7.13	444.82	1.51	10.62	0.27	131.97	6.15	20.27	1.56	5.03	6.87
23	SPA2 94012 X CSV15	265.67	12.27	81.78	6.87	379.62	1.29	10.28	0.24	96.99	5.63	18.57	1.82	5.90	7.75
24	SPA2 94012 X 04K668	251.55	11.62	84.15	6.03	362.79	1.14	10.78	0.25	120.44	6.57	21.67	1.98	6.43	7.85
25	SPA2 94012 X 04K693	261.53	10.63	86.82	5.87	350.26	1.21	9.95	0.19	121.65	5.73	18.90	1.86	6.03	8.60
26	SPA2 94012 X 01K733	255.53	12.83	82.05	6.73	384.44	1.42	9.62	0.23	95.66	6.10	20.10	1.57	5.07	6.73
27	SPA2 94012 X 04K700	191.23	11.10	78.25	4.93	258.46	1.04	10.62	0.24	77.77	5.07	16.67	1.66	5.37	6.98
28	SPA2 94012 X UPMC8	220.58	10.70	83.55	6.97	419.78	1.39	9.62	0.19	113.46	6.25	20.60	1.97	6.40	6.95
29	ICSA469A X UPMC8	255.67	12.97	83.92	6.33	369.63	1.15	10.62	0.24	69.36	4.29	14.07	1.14	3.63	6.58

30	ICSA469A X 04K693	279.32	12.92	87.12	6.57	403.47	1.37	8.78	0.16	76.68	5.87	19.37	1.67	5.40	6.43
31	ICSA469A X 04K700	290.97	11.93	84.68	6.33	362.82	1.18	9.62	0.20	83.16	7.43	24.53	2.39	7.80	7.32
32	ICSA469A X 01K733	292.12	12.27	81.08	7.43	419.27	1.67	8.28	0.18	84.90	3.37	11.03	1.01	3.20	7.51
33	ICSA469A X CSV15	321.22	13.27	81.28	8.00	462.09	1.84	9.78	0.22	75.70	4.98	16.40	1.51	4.87	6.61
34	ICSA469A X PC5	280.88	12.33	92.85	7.37	497.45	1.49	9.62	0.21	83.65	7.12	23.53	1.85	6.00	6.89
35	ICSA469A X 04K668	235.88	11.57	87.05	8.63	521.98	1.63	10.28	0.21	72.30	6.09	20.10	1.94	6.30	6.77
36	ICSA271 X 04K693	250.83	12.00	79.35	6.07	330.26	1.39	9.28	0.17	69.56	5.57	18.33	1.58	5.10	7.85
37	ICSA271 X PC5	209.60	12.05	90.35	6.93	432.60	1.40	10.78	0.36	83.82	6.04	19.90	1.90	6.17	6.94
38	ICSA271 X CSV15	290.97	13.73	83.32	7.13	404.13	1.45	8.45	0.23	71.37	5.82	19.17	1.68	5.43	6.09
39	ICSA271 X 04K700	274.88	13.65	78.45	7.23	395.60	1.60	7.12	0.18	82.83	5.73	18.90	1.64	5.30	6.73
40	ICSA271 X UPMC8	273.38	12.80	88.18	6.80	434.55	1.48	6.62	0.23	69.86	5.74	18.93	1.56	5.03	6.44
41	ICSA271 X 04K668	293.53	12.93	85.48	7.17	428.51	1.46	9.28	0.16	71.44	6.21	20.47	1.42	4.57	7.44
42	ICSA271 X 01K733	310.55	12.37	78.95	6.93	370.19	1.56	10.62	0.19	93.41	6.12	20.20	1.96	6.37	7.49
43	993100A X 04K700	236.02	12.28	79.02	7.10	388.50	1.41	10.62	0.18	65.55	6.01	19.80	1.64	5.30	6.89
44	993100A X PC5	270.68	11.25	91.28	6.60	399.97	1.35	15.12	0.17	65.90	5.51	18.13	1.67	5.40	6.63
45	993100A X 04K693	302.82	12.00	88.82	7.23	410.31	1.34	11.45	0.20	81.60	6.01	19.80	1.90	6.17	7.22
46	993100A X UPMC8	225.58	11.05	81.15	6.87	385.77	1.34	7.62	0.21	91.44	5.73	18.87	1.78	5.77	7.06
47	993100A X CSV15	221.95	11.93	86.35	6.80	391.13	1.47	12.12	0.20	81.21	6.21	20.47	1.99	6.47	7.66
48	993100A X 04K668	191.28	11.38	78.85	6.13	314.89	1.17	10.62	0.21	78.90	6.47	21.33	1.95	6.33	7.17
49	993100A X 01K733	260.68	11.67	78.05	6.30	333.09	1.11	6.45	0.17	73.87	5.82	19.17	1.90	6.17	7.79
50	ICSA276 X 04K693	228.88	12.12	83.35	7.23	414.86	1.41	8.62	0.29	95.71	6.29	20.73	1.68	5.43	7.36
51	ICSA276 X UPMC8	271.42	11.73	82.35	7.23	407.16	1.46	11.12	0.16	91.37	5.99	19.77	1.92	6.23	7.11
52	ICSA276 X 04K668	302.08	11.93	78.92	7.00	374.14	1.61	9.95	0.16	92.17	5.76	18.97	1.35	4.33	6.57
53	ICSA276 X 01K733	278.88	11.37	81.58	6.70	380.18	1.24	8.62	0.16	87.80	6.09	20.07	1.66	5.37	7.55
54	ICSA276 X CSV15	284.77	11.13	81.36	7.43	383.79	1.39	13.78	0.21	92.62	6.86	22.63	2.26	7.37	7.05
55	ICSA276 X 04K700	272.88	11.80	72.25	7.53	374.80	1.29	10.12	0.21	92.14	6.02	19.87	1.36	4.37	6.90
56	ICSA276 X PC5	263.95	12.28	88.82	8.43	489.88	1.84	11.12	0.20	91.69	6.12	20.20	1.54	4.97	7.56
57	ICSA293 X 04K668	235.77	11.35	89.65	6.67	411.98	1.29	10.28	0.29	82.07	6.02	19.87	1.59	5.13	6.81
58	ICSA293 X CSV15	242.62	11.73	87.02	6.97	420.72	1.48	10.12	0.21	98.70	5.11	16.80	1.53	4.93	7.62
59	ICSA293 X UPMC8	237.77	12.30	86.72	6.07	345.65	1.20	9.62	0.24	94.85	5.52	18.20	1.77	5.73	8.51
60	ICSA293 X 04K693	235.75	11.57	82.28	6.20	335.50	1.23	5.62	0.24	63.47	4.07	13.33	1.12	3.57	7.42
61	ICSA293 X PC5	254.92	10.52	80.12	6.90	372.88	1.40	9.62	0.21	97.01	5.98	19.73	1.69	5.47	7.09
62	ICSA293 X 01K733	261.05	11.73	83.08	6.93	399.58	1.31	10.62	0.20	91.41	7.48	24.73	2.06	6.70	6.47
63	ICSA293 X 04K700	284.10	12.58	86.98	6.67	396.19	1.15	10.28	0.22	82.22	6.32	20.83	1.61	5.20	7.48
64	SP 55609A X CSV15	250.15	12.00	90.48	6.73	388.58	1.26	5.95	0.22	68.54	5.93	19.53	1.93	6.27	7.13
65	SP 55609A X 04K693	285.77	12.62	79.58	5.83	305.91	1.27	12.12	0.32	72.28	7.01	23.13	1.55	5.00	7.43
66	SP 55609A X UPMC8	286.23	12.75	82.28	6.27	342.87	1.49	10.62	0.24	86.18	6.08	20.03	1.62	5.23	6.46
67	SP 55609A X 01K733	256.43	12.53	84.05	5.63	333.87	1.16	10.28	0.20	92.02	6.30	20.77	1.91	6.20	7.55
68	SP 55609A X 04K700	280.88	12.57	73.88	6.27	307.56	1.18	7.62	0.20	100.12	6.15	20.27	2.01	6.53	6.96
69	SP 55609A X 04K668	319.23	13.77	82.52	6.40	354.31	1.45	9.62	0.19	90.36	6.37	21.03	2.00	6.50	7.73
70	SP 55609A X PC5	287.57	13.10	92.45	6.17	381.00	1.41	13.12	0.21	83.48	6.39	21.07	1.39	4.47	7.40
	Mean	258.89	12.51	83.80	6.90	400.82	1.39	9.41	0.23	89.84	6.00	19.78	1.62	5.23	7.09
	Range Lowest	191.23	10.52	71.18	4.93	258.46	1.04	5.28	0.16	63.47	3.37	11.00	0.85	2.66	5.84
	Range Highest	321.22	14.98	93.68	8.63	559.88	1.84	15.12	0.36	150.95	7.48	24.72	2.39	7.81	8.60

* PH- Plant height, NL-Number of leaves per plant, LL- Leaf length, LW- Leaf width, LA-Leaf area, SG-Stem girth, L:S- Leaf:stem ratio, GFY- Green fodder yield per plot, DFY- Dry fodder yield per plot, TSS- Total soluble solids, HCN- Hydrocyanic acid content, PP- Protein percent.

Heritability, GCV, PCV and GA: The coefficient of variation at genotypic (GCV), phenotypic (PCV) level and genetic advance are presented in Table 4. Robinson *et al.* (1949) [18] classified heritability values as high (>60%), moderate (30-60%) and values less than 30% low. Accordingly, the results of the present study indicated that high heritability values were observed in plant height, number of leaves per plant, leaf width, leaf area, stem girth, total soluble solids, leaf:stem ratio, green fodder yield, and dry fodder yield whereas moderate for hydrocyanic acid content and protein percent, low for leaf length. High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from selection.

Deshmukh *et al.* (1986) [7] classified PCV and GCV values as low (0-10%), moderate (10-20%) and high (20% and above) values. According to this classification, high GCV values were observed for the characters leaf:stem ratio, moderate for plant height, leaf area, stem girth, total soluble solids,

hydrocyanic acid content, green fodder yield and dry fodder yield, whereas low for number of leaves per plant, leaf length, leaf width, and protein percent.

Falconer and Mackay (1996) [8] classified genetic advance as percent of mean as low (0-10%), moderate (10-20%) and high (20% and above). Genetic advance as percent of mean (at 5%) was observed high for plant height, leaf area, stem girth, total soluble solids, leaf:stem ratio, hydrocyanic acid content, green fodder yield and dry fodder yield, moderate for number of leaves per plant, leaf width, and protein percent whereas low for leaf length. Genetic advance as percent of mean (at 1%) was observed high for plant height, leaf width, leaf area, stem girth, total soluble solids, leaf:stem ratio, hydrocyanic acid content, green fodder yield, and dry fodder yield, moderate for number of leaves per plant and protein percent whereas low for leaf length. Heritability and genetic advance are important selection parameters. The estimate of genetic advance is more useful as a selection tool when coupled with heritability estimates (Johnson *et al.*, 1955) [11]. The estimates of genetic advance help in understanding the type of gene

action involved in the expression of various quantitative characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action (Singh and Narayanan, 1999) [21]. The

findings of present study on genetic variability parameters were observed similar with the findings of Jain and Patel (2012) [10], Kumar (2014), Malik *et al.*, (2015) [15], Supriya *et al.*, (2015) [22], and Ahlawat *et al.*, (2018) [2].

Table 4: Genetic variability parameters for different yield and quality traits in F₂ crosses of forage sorghum.

Parameters	PH	NL	LL	LW	LA	SG	TSS	L:S	HCN	GFY	DFY	PP
GCV	10.78	8.006	2.269	9.946	13.478	11.754	19.192	20.44	17.398	13.521	19.892	7.051
PCV	12.675	8.525	9.509	11.023	14.183	13.01	21.498	21.853	24.411	14.035	20.213	9.884
h^2	0.723	0.882	0.057	0.814	0.903	0.816	0.797	0.875	0.508	0.928	0.969	0.509
h^2 (%)	72.3	88.2	5.7	81.4	90.3	81.6	79.7	87.5	50.8	92.8	96.9	50.9
G.A. (5%)	48.79	1.859	0.929	1.246	105.614	0.29	3.281	0.086	22.818	1.593	0.632	0.729
G.A. (1%)	62.527	2.382	1.191	1.596	135.349	0.372	4.204	0.111	29.243	2.041	0.81	0.934
G.A.M. (5%)	18.887	15.489	1.115	18.489	26.383	21.876	35.293	39.382	25.545	26.832	40.329	10.361
G.A.M. (1%)	24.205	19.85	1.429	23.694	33.811	28.035	45.23	50.47	32.737	34.387	51.684	13.278

Summary and Conclusion

The analysis of variance revealed significant difference among the genotypes which validated further on the basis of genetic and statistical analysis of the data. It revealed that mean squares due to genotypes were found to be significant for all the characters. The wide range of mean performance was observed in different crosses. The range of heritability, GCV, PCV and genetic advance as percent of mean was observed from low to high in different yield and quality parameters. The traits which had desired value of variability parameters and mean performance can be utilized in crop improvement programme. This study generally indicated that there was significance genetic variability among the genotypes studied. Thus, there is an opportunity of direct selection of superior crosses for different yield contributing and quality traits in crop improvement programme.

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