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Study on genetic variability, heritability and genetic advance for quantitative 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, leaf width, leaf area, stem girth, total soluble solids, leaf:stem ratio, green fodder yield, and dry fodder yield whereas low and moderate for other characters. High PCV values were observed for total soluble solids, leaf:stem ratio, and HCN content whereas low and moderate for other characters. High GCV value was observed for none of the any character whereas low and moderate for other characters. The high genetic advance as percent of mean was observed in leaf area, total soluble solids, leaf:stem ratio, HCN content, and green 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). 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. 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].

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) [6, 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 advance etc. The parents having more genetic variability result into higher heterotic expression in F_1 and greater amount of genetic variability in segregating populations (Shekhawat *et al.*, 2001) [14, 19]. 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 *khariif*, 2019-20. The experimental material consists of 70 F_2 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 F_2 crosses were evaluated during *khariif*, 2019-20. 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 quantitative and three quality parameters. The quantitative 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 f_2 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:

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

Where,

- i = 1, 2, ----- r (replication)
- j = 1, 2, -----t (treatment)
- Y_{ij} = performance of jth variety in the ith block
- μ = population mean
- b_i = true effect of ith block
- t_j = true effect of jth treatment
- e_{ij} = random error
- r = number of replications
- t = number of treatments

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

different characters was estimated as suggested by Allard (1960).

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

Where,

GA = expected genetic advance

h_b² = heritability in broad sense

σ_{pi} = phenotypic standard deviation for ith character

K = intensity of selection, the value of which is 2.06 at 5% (Lush, 1949) [18].

B. Estimation of variability

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

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

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

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

Where,

- σ_g = Genotypic standard deviation
- σ_p = Phenotypic standard deviation
- σ_e = Environmental standard deviation
- ̄X = Grand mean

C. Estimation of heritability

The heritability in broad sense h² (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_g² = Genotypic variance
- σ_p² = Phenotypic variance

D. Genetic advance

(A) The expected genetic advance under selection for the

E. Genetic advance as percent of mean (GAM)

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

Where,

̄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 viz. plant height, number of leaves per plant, leaf length, leaf width, leaf area, stem girth, leaf:stem ratio, green fodder yield per plot, dry fodder yield per plot, total soluble solids, hydrocyanic acid content, and protein percent. 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, 20], Kadam *et al.*, (2001) [14, 19], Kumar *et al.*, (2014) [2], Agrawal *et al.*, (2005) [1], Bello *et al.*, (2007) [4], Rani *et al.*, (2009) [17], and Jadhav *et al.*, (2017) [9].

Table 2: Analysis of variance for simple RBD with respect to different characters for f₂ generation during the year 2019-20

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	879.439	16.459	476.338	3.142	1326.069	0.435
Treatments	69	2626.193**	2.857**	69.158**	1.449**	9045.043**	0.078**
Error	130	298.627	0.735	55.539	0.131	312.641	0.010
SE		9.977	0.495	4.302	0.209	10.208	0.059
SEd		14.109	0.700	6.084	0.295	14.437	0.084
SEd from mean		9.905	0.491	4.271	0.207	10.135	0.059
CD at 1%		36.853	1.829	0.002	0.772	37.708	0.219
CD at 5%		27.899	1.384	0.001	0.584	28.546	0.166
CV %		6.660	6.585	8.841	5.121	4.405	7.059

Source of variations	df	TSS (%)	Leaf:stem ratio	HCN (ppm)	Green fodder yield (kg)	Dry fodder yield (kg)	Protein (%)
Replication	2	0.496	0.005	595.743	1.199	0.410	2.748
Treatments	69	10.357**	0.006**	958.568**	1.981**	0.294**	0.974**
Error	130	0.880	0.0002	233.954	0.049	0.003	0.278
SE		0.541	0.009	8.830	0.129	0.032	0.304
SEd		0.766	0.013	12.488	0.182	0.045	0.430
SEd from mean		0.537	0.009	8.767	0.128	0.032	0.302
CD at 1%		2.001	0.034	32.619	0.476	0.119	1.125
CD at 5%		1.515	0.026	24.694	0.360	0.090	0.852
CV %		9.849	6.895	16.927	3.681	3.368	7.372

* Significant at 5% level of probability, ** Significant at 5% level of probability

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 11.47 ton/ha in cross ICSA 469 A X 01 K 733 to 25.17 ton/ha in cross ICSA 293 x 01 K 733 with general mean of 20.22 ton/ha. The dry fodder yield was lowest in cross ICSA 467 X CSV 15 (3.00 ton/ha) while it was highest in cross ICSA 469 A X 04 K 700 (8.13 ton/ha) with a general mean of 5.55 ton/ha. The mean values for plant height varied between 191.733 cm to 32.1766 cm in the cross SPA2 94012 X 04 K 700 and cross ICSA 467 X CSV 15, respectively with a general mean of 259.453 cm. The range of mean values for number of leaves per plant was between 11.03 in cross ICSA 293 X PC-5 to 15.50 in cross ICSA 467 X 04 K 693 with a general mean of 13.02. The range of mean values for leaf length ranged from 71.70 cm to 94.20 cm in cross ICSA 467 X 01 K 733 and cross 11 A2 X 04 K 668 respectively with a general mean of 84.29 cm. The mean value of leaf width was found between 5.10 cm in cross SPA2 94012 X 04 K 700 to 7.53 cm in cross

ICSA 469 A X 04 K 668 with a general mean of 7.07 cm. The range of mean values for leaf area was between 258.98 cm² to 560.39 cm² in cross SPA2 941012 X 04 K 700 and cross HB 94004 A X 04 K 700 with a general mean of 401.33 cm². The range of mean values for stem girth was found between 1.10 cm in cross SPA2 94012 X 04 K 700 to 1.91 cm in cross ICSA 469 A X CSV 15 with a general mean of 1.46 cm. The range of mean values for TSS % was found between 5.40% to 15.23% in cross HB 94004 A X CSV 15 and cross 993100 A X PC 5 with a general mean of 9.52 %. The range of mean values for leaf stem ratio was 0.16 to 0.36 in cross ICSA 271 X 04 K 668 and ICSA 271 X PC 5 respectively with a general mean of 0.23. The mean value of HCN content was found between 63.98 ppm in cross ICSA 293 X 04 K 693 to 151.46 ppm in cross HB 94004 A X 04 K 668 with a general mean 90.36 ppm. The mean value of protein percent was found between 5.90 % in cross ICSA 467 X UPMC 8 to 8.54% in cross SPA2 94012 X 04 K 693 with a general mean of 7.15 %.

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

Sl. No.	F ₂ Cross	PH (cm)	NL	LL (cm)	LW (cm)	LA (cm ²)	SG (cm)	TSS (%)	L:S	HCN	GFY (kg/plot)	GFY (ton/ha)	DFY (kg/pot)	DFY (ton/ha)	PP (%)
1	ICSA467 X CSV15	204.83	14	89.2	8.27	490.82	1.63	8.73	0.27	117.41	4.15	13.83	0.9	3.00	6.86
2	ICSA467 X PC5	216.13	13.33	90.23	6.97	402.36	1.48	8.07	0.32	98.07	7.44	24.80	1.58	5.27	6.81
3	ICSA467 X 04K693	236.6	15.5	86.63	8.47	407.14	1.58	7.73	0.29	69.35	6.47	21.57	1.32	4.40	6.62
4	ICSA467 X 04K700	253.4	14.1	84.07	7	392.58	1.43	7.07	0.27	71.78	6.11	20.37	1.2	4.00	6.55
5	ICSA467 X 01K733	260.07	14.73	71.7	7.57	394.84	1.49	7.9	0.33	109.62	5.55	18.50	1.23	4.10	6.95
6	ICSA467 X UPMC8	255	14.5	75.5	7.4	403.62	1.47	8.57	0.24	103.51	6.14	20.47	1.3	4.33	5.9
7	ICSA467 X 04K668	254.2	13.93	78.47	7.6	419.82	1.48	7.9	0.26	98.01	7.14	23.80	1.96	6.53	7.72
8	11A2 X UPMC8	211.93	13.57	81.03	7.1	416.44	1.53	9.73	0.32	97.83	5.96	19.87	1.29	4.30	7.35
9	11A2 X 04K700	218.67	13.6	82.6	6.57	424.52	1.48	7.07	0.29	108.29	6.91	23.03	1.43	4.77	7.84
10	11A2 X CSV15	230	13.77	83.97	6.27	371.51	1.32	11.23	0.24	110.67	6.05	20.17	1.3	4.33	7.35
11	11A2 X 01K733	281.1	14.5	83.93	7.63	455.3	1.58	8.23	0.26	96.28	7.04	23.47	1.46	4.87	7.63
12	11A2 X 04K693	252.9	13.93	88.27	7.07	425.9	1.38	6.4	0.28	150.87	7.09	23.63	1.41	4.70	6.15
13	11A2 X 04K668	236.03	15.03	94.2	6.63	419.47	1.45	6.73	0.32	70.72	6.05	20.17	1.22	4.07	7.57
14	11A2 X PC5	216.87	14.2	84.17	8	483.89	1.43	10.73	0.32	93.01	7.52	25.07	1.59	5.30	6.45
15	HB 94004A X 04K668	282.03	13.03	87.2	6.83	427.13	1.48	9.73	0.26	151.47	5.38	17.93	1.63	5.43	6.13
16	HB 94004A X 04K693	277.3	12.7	86.93	6.83	402.27	1.31	9.4	0.22	84.42	6.14	20.47	1.58	5.27	6.06
17	HB 94004A X PC5	261.47	14.17	92	8.13	546.5	1.65	10.73	0.27	94.93	6.44	21.47	1.65	5.50	6.7
18	HB 94004A X CSV15	261	13.6	89.9	8.4	504.47	1.62	5.4	0.26	84.49	5.22	17.40	1.32	4.40	7.99
19	HB 94004A X 04K700	262.97	14.77	83.33	8.27	560.39	1.79	9.4	0.26	84.67	5.66	18.87	1.63	5.43	6.7
20	HB 94004A X 01K733	305.4	12.37	80.6	6.7	345.35	1.52	8.4	0.2	78.15	7.49	24.97	2.14	7.13	7.68
21	HB 94004A X UPMC8	264.8	13.27	82.9	7.3	396.4	1.48	8.73	0.23	95.73	4.08	13.60	1.1	3.67	7.53
22	SPA2 94012 X PC5	256.63	13.5	88.7	7.3	445.34	1.58	10.73	0.27	132.48	6.22	20.73	1.61	5.37	6.93
23	SPA2 94012 X CSV15	266.2	12.77	82.3	7.03	380.13	1.36	10.4	0.25	97.5	5.7	19.00	1.87	6.23	7.82
24	SPA2 94012 X 04K668	252.1	12.13	84.67	6.2	363.3	1.21	10.9	0.26	120.96	6.63	22.10	2.03	6.77	7.91
25	SPA2 94012 X 04K693	262.07	11.17	87.33	6.03	350.78	1.28	10.07	0.19	122.17	5.8	19.33	1.91	6.37	8.67
26	SPA2 94012 X 01K733	256.07	13.37	82.57	6.9	384.96	1.48	9.73	0.24	96.17	6.17	20.57	1.62	5.40	6.79
27	SPA2 94012 X 04K700	191.73	11.6	78.77	5.1	258.98	1.11	10.73	0.24	78.28	5.13	17.10	1.71	5.70	7.04
28	SPA2 94012 X UPMC8	221.1	11.23	84.07	7.13	420.29	1.46	9.73	0.19	113.98	6.32	21.07	2.02	6.73	7.02
29	ICSA469A X UPMC8	256.2	13.5	84.43	6.5	370.14	1.22	10.73	0.25	69.87	4.36	14.53	1.19	3.97	6.65
30	ICSA469A X 04K693	279.9	13.43	87.63	6.73	403.99	1.44	8.9	0.17	77.2	5.94	19.80	1.72	5.73	6.49
31	ICSA469A X 04K700	291.53	12.43	85.2	6.5	363.34	1.24	9.73	0.21	83.67	7.49	24.97	2.44	8.13	7.38
32	ICSA469A X 01K733	292.67	12.77	81.6	7.6	419.79	1.74	8.4	0.18	85.42	3.44	11.47	1.06	3.53	7.57
33	ICSA469A X CSV15	321.77	13.8	81.8	8.17	462.61	1.91	9.9	0.23	76.22	5.05	16.83	1.56	5.20	6.68
34	ICSA469A X PC5	281.43	12.83	93.37	7.53	497.96	1.56	9.73	0.21	84.17	7.19	23.97	1.9	6.33	6.95
35	ICSA469A X 04K668	236.43	12.1	87.57	8.8	522.5	1.69	10.4	0.22	72.82	6.16	20.53	1.99	6.63	6.84
36	ICSA271 X 04K693	251.4	12.5	79.87	6.23	330.78	1.45	9.4	0.18	70.07	5.63	18.77	1.63	5.43	7.91
37	ICSA271 X PC5	210.13	12.57	90.87	7.1	433.11	1.47	10.9	0.36	84.33	6.11	20.37	1.95	6.50	7.01
38	ICSA271 X CSV15	291.53	14.23	83.83	7.3	404.64	1.52	8.57	0.24	71.89	5.88	19.60	1.73	5.77	6.15
39	ICSA271 X 04K700	275.43	14.17	78.97	7.4	396.11	1.67	7.23	0.19	83.34	5.8	19.33	1.69	5.63	6.79
40	ICSA271 X UPMC8	273.9	13.3	88.7	6.97	435.07	1.54	6.73	0.24	70.38	5.81	19.37	1.61	5.37	6.5
41	ICSA271 X 04K668	294.07	13.43	86	7.33	429.03	1.53	9.4	0.16	71.96	6.27	20.90	1.47	4.90	7.51
42	ICSA271 X 01K733	311.1	12.9	79.47	7.1	370.71	1.62	10.73	0.2	93.93	6.19	20.63	2.01	6.70	7.55
43	993100A X 04K700	236.57	12.8	79.53	7.27	389.02	1.47	10.73	0.19	66.06	6.08	20.27	1.69	5.63	6.95
44	993100A X PC5	271.23	11.77	91.8	6.77	400.48	1.41	15.23	0.17	66.41	5.58	18.60	1.72	5.73	6.69
45	993100A X 04K693	303.33	12.5	89.33	7.4	410.83	1.4	11.57	0.21	82.12	6.08	20.27	1.95	6.50	7.29
46	993100A X UPMC8	226.17	11.57	81.67	7.03	386.29	1.41	7.73	0.21	91.95	5.79	19.30	1.83	6.10	7.12

47	993100A X CSV15	222.5	12.43	85.2	6.97	391.64	1.53	12.23	0.21	81.72	6.27	20.90	2.04	6.80	7.72
48	993100A X 04K668	191.83	11.9	79.37	6.3	315.4	1.24	10.73	0.22	79.42	6.53	21.77	2	6.67	7.23
49	993100A X 01K733	261.27	12.17	78.57	6.47	333.6	1.18	6.57	0.18	74.38	5.88	19.60	1.95	6.50	7.85
50	ICSA276 X 04K693	229.43	12.63	83.87	7.4	415.38	1.48	8.73	0.29	96.23	6.36	21.20	1.73	5.77	7.42
51	ICSA276 X UPMC8	271.97	12.23	82.87	7.4	407.67	1.53	11.23	0.17	91.89	6.06	20.20	1.97	6.57	7.18
52	ICSA276 X 04K668	302.63	12.43	79.43	7.17	374.66	1.68	10.07	0.16	92.69	5.83	19.43	1.4	4.67	6.63
53	ICSA276 X 01K733	279.43	11.9	82.1	6.87	380.69	1.31	8.73	0.17	88.31	6.16	20.53	1.71	5.70	7.62
54	ICSA276 X CSV15	285.33	11.67	81.87	7.6	384.31	1.46	13.9	0.21	93.14	6.93	23.10	2.31	7.70	7.11
55	ICSA276 X 04K700	273.43	12.3	72.77	7.7	375.32	1.36	10.23	0.22	92.66	6.09	20.30	1.41	4.70	6.96
56	ICSA276 X PC5	264.5	12.8	89.33	8.6	490.4	1.91	11.23	0.21	92.21	6.19	20.63	1.59	5.30	7.62
57	ICSA293 X 04K668	236.33	11.87	90.17	6.83	412.5	1.35	10.4	0.29	82.58	6.09	20.30	1.64	5.47	6.87
58	ICSA293 X CSV15	243.17	12.23	87.53	7.13	421.23	1.55	10.23	0.22	99.22	5.17	17.23	1.58	5.27	7.69
59	ICSA293 X UPMC8	238.33	12.83	87.23	6.23	346.17	1.27	9.73	0.24	95.37	5.59	18.63	1.82	6.07	8.57
60	ICSA293 X 04K693	236.3	12.07	82.8	6.37	336.01	1.29	5.73	0.24	63.99	4.13	13.77	1.17	3.90	7.49
61	ICSA293 X PC5	255.43	11.03	80.63	7.07	373.4	1.47	9.73	0.21	97.53	6.05	20.17	1.74	5.80	7.16
62	ICSA293 X 01K733	261.6	12.23	83.6	7.1	400.09	1.37	10.73	0.2	91.93	7.55	25.17	2.11	7.03	6.53
63	ICSA293 X 04K700	284.67	13.1	87.5	6.83	396.71	1.22	10.4	0.23	82.74	6.38	21.27	1.66	5.53	7.54
64	SP 55609A X CSV15	250.7	12.53	91	6.9	389.1	1.33	6.07	0.23	69.06	5.99	19.97	1.98	6.60	7.19
65	SP 55609A X 04K693	286.33	13.13	80.1	6	306.43	1.34	12.23	0.33	72.79	7.08	23.60	1.6	5.33	7.5
66	SP 55609A X UPMC8	286.8	13.27	82.8	6.43	343.38	1.56	10.73	0.24	86.69	6.14	20.47	1.67	5.57	6.53
67	SP 55609A X 01K733	256.97	13.03	84.57	5.8	334.38	1.23	10.4	0.21	92.54	6.37	21.23	1.96	6.53	7.61
68	SP 55609A X 04K700	281.43	13.07	74.4	6.43	308.08	1.24	7.73	0.21	100.64	6.22	20.73	2.06	6.87	7.02
69	SP 55609A X 04K668	319.8	14.27	83.03	6.57	354.83	1.52	9.73	0.2	90.87	6.44	21.47	2.05	6.83	7.79
70	SP 55609A X PC5	288.17	13.6	92.97	6.33	381.51	1.48	13.23	0.22	83.99	6.46	21.53	1.44	4.80	7.46
	Mean	259.45	13.02	84.29	7.07	401.34	1.46	9.53	0.24	90.36	6.07	20.23	1.67	5.57	7.16
	C.V.	6.66	6.59	8.84	5.12	4.41	7.06	9.85	6.9	16.93	3.68	12.27	3.37	11.23	7.37

* 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

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.

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, leaf width, leaf area, stem girth, total soluble solids, leaf:stem ratio, green fodder yield, and dry fodder yield whereas moderate for number of leaves per plant, 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.

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	10.736	6.457	2.528	9.376	13.443	10.297	18.653	19.049	17.199	13.224	18.700	6.730
PCV	12.634	9.223	9.195	10.684	14.146	12.485	21.094	20.258	24.132	13.727	19.001	9.982
h^2	0.722	0.490	0.076	0.770	0.903	0.680	0.782	0.884	0.508	0.928	0.969	0.455
h^2 (%)	72.20	49.00	7.60	77.00	90.30	68.00	78.20	88.40	50.80	92.80	96.90	45.50
G.A. (5%)	48.758	1.213	1.207	1.198	105.614	0.256	3.238	0.087	22.818	1.593	0.632	0.669
G.A. (1%)	62.486	1.554	1.546	1.536	135.349	0.328	4.149	0.111	29.243	2.041	0.810	0.857
G.A.M. (5%)	18.793	9.313	1.431	16.950	26.315	17.496	33.980	36.897	25.252	26.243	37.911	9.346
G.A.M. (1%)	24.084	11.935	1.834	21.723	33.724	22.422	43.547	47.286	32.362	33.631	48.585	11.978

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 value was observed for none of the character, 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. High PCV values were observed for total soluble solids, leaf:stem ratio and hydrocyanic acid content, moderate for plant height, leaf width, leaf area, stem girth, green fodder yield per plant, and dry fodder yield per plant whereas low for characters number of leaves per plant, leaf length, 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 leaf area, total soluble solids, leaf:stem ratio, hydrocyanic acid content, green fodder yield and dry fodder yield, moderate for plant height, leaf width, whereas low for number of leaves per plant, leaf length, and protein percent. 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) ^[2], Malik *et al.*, (2015) ^[15], Supriya *et al.*, (2015) ^[15], and Ahlawat *et al.*, (2018) ^[2].

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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