



Study of Genetic Variability and Fodder Yield Components in Forage Sorghum (*Sorghum bicolor* L. Moench)

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ABSTRACT

The present investigation consists of 34 sorghum genotypes and the experiment was conducted during Kharif-2015 in Randomized Block Design with three replications. The data were recorded for 12 quantitative characters to study genetic variability, heritability and genetic advance. On the basis of mean performance, high green fodder yield per plot was exhibited by the genotype HJ-513. Analysis of variance among 34 genotypes showed a significant difference for all characters studied. The highest genotypic coefficient of variation (GCV) & phenotypic coefficient variation (PCV) was observed for a number of leaves per plant, leaf stem ratio and green fodder yield indicating that these characters could be used as a selection for crop improvement. On the basis of high estimates of heritability coupled with high genetic advance was observed for plant height, leaf length, leaf area, number of leaves per plant, leaf stem ratio and green fodder yield indicating a predominance of additive gene effects and possibilities of effective selection for the improvement of these characters.

Keywords: *Sorghum, Genetic variability, Heritability and Genetic Advance.*

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INTRODUCTION

Sorghum (*Sorghum bicolor* L. Moench) is one of the most important cereal crop grown in Africa, Asia, USA, Australia, and Latin America. Its importance after wheat, maize, rice and barley is because of its good adaptation to a wide range of ecological conditions, low input cultivation and diverse uses [2]. In India, it is third major cereal after rice and wheat and it is most important food crop grown under rainfed conditions. Knowledge of genetic diversity of a crop usually helps the breeder in choosing desirable parents for the breeding program and gene introgression from distantly related germplasm. The more diverse genotypes or accessions can be crossed to produce superior hybrids with resistance to abiotic and biotic stresses. Understanding the wealth of genetic diversity in sorghum will facilitate the further improvement of this crop for its genetic architecture [3]. Sorghum is an important *Kharif* fodder crop of India. It has a potential to produce high green fodder yield and therefore, needs to be developed. To exploit its potentiality for fodder yield, several genetic improvement techniques have been done. Fodder yield, the most important and polygenically controlled complex character, is also governed by many physiological changes within the plant and also influenced by many environments in which the plant is grown. Hence it is not an easy character for selection. The success of the breeding program depends upon the quantum of genetic variability available for exploitation and the extent to which the desirable characters are heritable. Variability refers to the presence of differences among the individuals of plant population. Variation results due to difference either in genetic constitution of the individual of a plant population or an environment, they have grown. The existence of variability is essential for improvement

of genetic material. The total area, production and productivity of sorghum are 6.08 million hectares, 4.24 million tones and 0.70 metric tons per hectare respectively in India [1].

MATERIAL AND METHOD

The material for the present investigation consists of 34 sorghum genotypes were grown in a Randomized block design with three replications during *Kharif*- 2015 at the Crop Research centre, Chirodi of Sardar Vallabhbhai Patel University of Agriculture, Technology, Meerut. The experiment was sown on 5 June 2015 in a 4-row plot of 5-meter length. The row to row spacing was 30 cm and plant to plant distance was 10 cm. Five representative plants for each genotype in each replication were randomly selected to record observations on days to 50% flowering, days to milking stage, plant height, leaf breadth (cm), leaf length (cm), leaf area (cm²), stem girth (mm), number of leaves per plant, Leaf stem ratio, total soluble solids (%), Protein content (%), green fodder yield (Kg/Plot). The variability was estimated as per procedure for analysis of variance suggested by Panse and Sukhatme [4]. PCV and GCV were calculated by the formula given by Burton [5]. Heritability in a broad sense (h^2) by Burton and De Vane [6] and genetic advance were calculated by using the procedure given by Johnson *et al.* [7].

RESULTS AND DISCUSSION

Genetic variability in any crop is pre-requisite for selection of superior genotypes over the existing cultivars. The analysis of variance for different characters indicated the existence of highly significant differences for all the 12 characters study at 1% level of significance suggesting each and every genotype are genetically divergent from each other and there is ample scope for selection of characters from these diverse sources for yield and its components (Table 1). These findings were in accordance with the findings of Vedansh *et al.* [11] and Khandelwal *et al* [9]. A wide range of variance was observed for all the 12 characters. In general the phenotypic coefficient of variance was higher than genotypic coefficient variance for all yield and its contributing characters indicate the influence of environmental factors on these traits. The highest PCV and GCV was recorded for number of leaves per plant (25.037 and 28.177) followed by leaf stem ratio (25.929 and 25.516) and green fodder yield (26.762 and 26.607), Similar results were also reported by Jain and Patel [13], Malik *et al.* [10], Khandelwal *et al* [14] and Ranjith *et al.* [8]. Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV is presenting table-2 among all traits and high values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for these traits suggested the possibility of improvement through selection of these attributes. Closely relationship between GCV and PCV was found in all the characters and PCV values were slightly greater than GCV, revealing very little influence of environment for their expression. The amount of genetic variation considered alone will not be of much use to the breeder unless supplemented with the information on heritability estimate, which gives a measure of the heritable portion of the total variation. It has been suggested by Burton and Devane [6] that the GCV along with heritability estimate could provide a better picture of the amount of advance to be expected by phenotypic selection. Since the genetic advance is dependent on phenotypic variability and heritability in addition to selection intensity, the heritability estimates in conjunction with genetic advance will be more effective and reliable in predicting the response to selection [7]. Heritability in a broad sense includes both additive and non-additive gene effects. While, narrow sense heritability includes only additive components [7]. In the present study, heritability in a broad sense was estimated. Highest heritability in broad sense was observed (> 60%) for all the characters viz., days to 50% flowering (96.300), days to milking stage (96.000), plant height (97.400), leaf breadth (82.900), leaf length (72.600), leaf area (81.800), stem girth (69.600), number of leaves per plant (86.200), leaf stem ratio (94.500), total soluble solids (77.300), protein content (67.200) and green fodder yield (98.100). This indicates that these characters may be most potential for further improvement. Studied have been reported earlier also by Deepalakshmi *et al.* [15], Malik *et al.* [9] and Khandelwal *et al* [14]. Maximum genetic advance expressed as a percentage of the mean was revealed high (>20%) for plant height (29.842), leaf length (23.730), leaf area (23.688), number of leaves per plant (21.378), leaf stem ratio (29.076) and green fodder yield (23.893). Moderate genetic advance as a percentage of the mean (10-20%) was observed for days to 50% flowering (10.856) and stem girth (17.472). High heritability coupled with high genetic advance was revealed plant height, leaf length, leaf area, number of leaves per plant, leaf stem ratio and green fodder yield, indicating the preponderance of additive gene effects for these traits and hence may prove useful for effective selection. High heritability coupled with the high genetic advance for some of these traits have also been reported earlier by Jain and Patel [13], Khandelwal *et al* [9], Rana *et al* [12], Khandelwal *et al* [14], and Ranjith *et al.* [8]. This indicates the substantial contribution of additive genetic variance in the expression of these traits and can be more

useful in hybridization and selection for higher grain yield and these characters are largely controlled by additive gene action.

Table-1 Analysis of variance (ANOVA) for twelve characters of forage sorghum (*Sorghum bicolor* L. Moench)

Source of variations	Replication	Treatment	Error
Green fodder yield (kg/plot)	1.087	80.323**	0.499
Protein content (%)	0.063	1.874**	0.261
Total soluble solids (%)	0.252	4.720**	0.420
Leaf stem ratio	0.001	1.007**	0.001
No. of leaves per plant	0.362	6.591**	0.333
Stem girth (mm)	1.148	10.756**	1.362
Leaf area (cm ²)	287.893	6139.580**	421.968
Leaf length (cm)	80.296	100.646**	11.206
Leaf breadth (cm)	0.083	1.097**	0.070
Plant height (cm)	7.299	4250.372**	36.473
Days to milking stage	3.362	176.667**	2.403
Days to 50% flowering	1.970	209.044**	2.586
d. f.	2	33	66

*, ** significant at 5% and 1% level, respectively

Table-2 Estimates of variability parameters for twelve characters in forage sorghum (*Sorghum bicolor* L. Moench)

Character	GCV (%)	PCV (%)	Heritability % (broad sense)	Genetic advance	Genetic advance (as % of mean)
Days to 50% flowering	10.312	10.504	96.300	6.776	10.856
Days to milking stage	8.188	8.356	96.000	5.385	6.529
Plant height (cm)	14.673	14.862	97.400	26.222	29.842
Leaf breadth (cm)	8.436	9.265	82.900	1.097	5.826
Leaf length (cm)	7.818	9.170	72.600	20.589	23.730
Leaf area (cm ²)	12.708	14.045	81.800	21.373	23.688
Stem girth (mm)	10.160	12.171	69.600	3.043	17.472
No. of leaves per plant	28.177	25.037	86.200	22.762	21.378
Leaf stem ratio	25.516	25.929	94.500	20.097	29.076
Total soluble solids (%)	5.917	8.101	77.300	2.168	8.834
Protein content (%)	1.222	3.682	67.200	1.238	8.960
Green fodder yield (kg/plot)	26.607	26.762	98.100	20.527	23.893

CONCLUSION

In the present investigation which included 34 genotypes of sorghum was carried out in order to study the nature and amount of variability, heritability and genetic advance for 12 quantitative characters. On the basis of mean performance, high green fodder yield per plot was exhibited by the genotype HJ-513. Analysis of variance among 34 genotypes showed a significant difference for all characters studied. The highest genotypic coefficient of variation (GCV) & phenotypic coefficient variation (PCV) was observed for

a number of leaves per plant, leaf stem ratio and green fodder yield, which indicates that scope of importance with respect to these characters through selection. High heritability coupled with high genetic advance as percent of mean estimated for plant height, leaf length, leaf area, number of leaves per plant, leaf stem ratio and green fodder yield, indicating the preponderance of additive gene effects for these traits and hence may prove useful for effective selection.

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APPENDIX-I
Mean performance of forage sorghum (*Sorghum bicolor* L. Moench) genotypes for twelve characters

Genotypes	Days to 50% flowering	Days to milking stage	Plant height (cm)	Leaf breadth (cm)	Leaf length (cm)	Leaf area (cm ²)	Steam girth (mm)	No of Leaves per plant	Leaf stem ratio	Total soluble solids (%)	Protein content (%)	Green fodder yield (kg/Plot)
Jawahar chari-69	81.333	94.666	262.400	6.446	72.133	330.166	16.600	13.266	0.330	6.600	6.296	31.400
SSG-59-3	92.000	106.333	251.33	7.340	74.933	390.523	18.666	13.000	0.340	8.066	5.286	30.600
HC-136	102.000	111.000	262.266	7.413	70.600	371.596	18.866	12.666	0.316	7.266	8.076	34.166
HC-171	84.333	99.000	271.799	8.100	66.933	384.916	17.766	14.000	0.336	8.000	6.266	34.506
HC-260	74.000	87.000	310.600	7.093	70.466	354.922	19.466	15.133	0.410	10.133	6.500	38.500
HC-308	82.000	96.000	286.200	7.153	74.533	345.214	17.133	13.800	0.380	7.733	7.343	33.433
HJ-513	101.333	109.666	281.533	8.040	71.000	405.260	20.933	14.200	0.356	8.733	8.443	40.600
PC-7	82.333	94.000	278.733	7.193	69.466	354.704	15.400	13.533	0.276	8.133	6.420	37.000
PC-3	72.000	86.333	232.800	6.940	63.066	310.752	17.000	12.200	0.310	6.533	6.310	27.000
PC-5	93.000	104.666	271.333	6.480	74.400	342.223	20.666	13.800	0.360	7.800	6.453	30.533
U P Chari-1	73.666	86.666	282.200	7.226	62.800	322.205	17.266	13.400	0.310	6.933	6.400	26.133
U P Chari -2	92.333	103.333	272.266	7.273	71.000	366.623	18.400	11.866	0.330	7.400	6.143	32.000
CSV -15	79.333	93.000	181.933	6.386	54.733	278.030	14.066	11.333	0.290	6.800	5.606	22.666
M P- Chari	77.333	92.333	285.200	6.840	74.466	361.632	16.466	14.866	0.316	7.466	6.110	29.200
H J -541	82.000	95.333	292.533	6.933	75.600	372.366	18.800	15.066	0.410	6.733	7.153	32.266
GFS-4	70.333	82.666	238.333	6.433	64.466	294.495	17.466	12.000	0.300	10.666	6.700	28.933
GFS-5	81.666	94.000	273.800	5.666	73.33	295.034	17.533	13.933	0.273	7.266	6.643	31.300
SL - 44	73.000	86.000	265.133	7.313	66.933	347.548	16.333	13.666	0.416	6.733	5.700	30.600
COFS-29	82.600	94.000	248.800	6.986	67.466	334.722	16.200	13.133	0.316	10.466	7.120	35.400
PC-4	79.333	91.000	271.666	7.546	75.400	404.014	20.666	13.600	0.313	7.000	7.520	31.826
PC-6	72.666	86.000	241.533	7.246	68.933	354.356	17.466	12.866	0.316	6.933	6.616	28.533
Rajasthan chari-1	80.666	91.333	265.000	6.400	73.800	335.017	16.800	14.133	0.390	5.000	7.130	26.600
Rajasthan chari-2	82.200	96.666	266.466	7.233	69.000	319.645	17.866	13.800	0.390	5.333	6.553	28.800
Jawahar chari-6	90.333	103.000	279.866	7.193	74.800	381.354	15.200	13.733	0.346	6.333	5.586	40.400
SSV-84	78.000	93.000	190.866	6.133	63.266	275.480	16.000	10.333	0.290	7.066	5.940	24.666
SPV-669	69.666	82.666	186.466	7.153	67.133	340.984	13.400	11.866	0.233	6.533	5.610	24.533
Pusa chari-615	72.333	85.333	292.200	7.480	80.866	429.451	18.200	13.200	0.410	7.000	6.453	41.666
G-48	81.000	92.666	182.200	6.513	63.333	293.008	17.800	10.333	0.366	8.000	6.673	25.533
G-46	78.666	91.000	210.200	7.206	70.200	359.214	14.333	11.066	0.286	7.066	5.586	27.600
ICSV-700	69.666	83.333	190.066	5.786	61.733	253.660	16.000	9.466	0.270	7.533	5.630	24.733
Pusa chari-1	74.000	87.666	272.266	7.146	75.200	381.574	18.600	12.000	0.340	9.666	7.206	29.583
Pusa chari-6	77.666	89.333	282.600	6.280	76.333	340.369	19.266	13.333	0.306	8.000	6.420	30.600
Pusa chari -23	82.000	93.333	309.666	7.533	76.933	411.789	15.200	14.866	0.436	7.533	8.386	40.400
CSV-27	71.00	82.333	194.00	5.633	59.200	236.775	20.333	9.866	0.293	7.266	5.873	24.150
Mean	80.441	93.078	255.419	6.933	69.837	343.509	17.416	12.921	0.334	7.521	6.534	31.060
S.E.	0.928	0.895	3.486	0.153	1.932	11.859	0.673	0.333	0.006	0.374	0.295	0.408
C.D.5%	2.621	2.527	9.845	0.432	5.457	33.487	1.902	0.941	0.019	1.056	0.833	1.152
Range Lowest	69.667	82.333	181.933	5.633	54.733	236.775	13.400	9.466	0.233	5.000	5.286	22.666
Range Highest	102.000	111.000	310.600	8.100	80.866	429.451	20.933	15.133	0.436	10.666	8.443	41.666