

Characters Study of Selection Criteria and Genetic Variability in Forage Sorghum (*Sorghum bicolor* L. Moench) Genotype for Green Fodder Yield and Its Contributed Traits

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ABSTRACT

The investigation entitled “Characters Study of Selection Criteria and Genetic Variability in Forage Sorghum (*Sorghum bicolor* L. Moench) Genotype for Green Fodder Yield and Its Contributed Traits” were conducted at Crop Research Center, Modipuram, SVPUA and T, Meerut 250110 (UP) during *kharif* season 2019-20. Genetic variability studies were carried out for 33 sorghum genotypes during the years 2019-20. The analysis of variance revealed that there

was significant amount of variation for all the ten characters. Days to 50% flowering, plant height, leaf length, leaf breadth, leaf area, stem girth, leaves per plant, leaf stem ratio, total soluble solids and green fodder yield per plant was shown to have been recognized as having high heritability value. High estimate of (phenotypic coefficient of variance and genotypic coefficient of variance) PCV and GCV were observed for plant height, leaf area and green fodder yield per plant. The genetic divergence by Tocher’s method for seed yield and its component traits in sorghum genotypes. On the basis of genetic divergence under study, it is suggested that the crosses between cluster IV and cluster III, cluster II and cluster V be used for an effective in hybridization breeding program. The percent contribution of ten characters towards total genetic divergence showed that green fodder yield per plant maximum contribution to divergence followed by leaf area, leaves per plant, plant height and leaf breadth and lower contribution was made by leaf length towards the divergence.

Keywords Genetic advance, Genetic variability, Heritability, Divergence, Quantitative traits.

INTRODUCTION

Sorghum (*Sorghum bicolor* L. Moench) is a plant belonging to the family of grasses (Poaceae). Sorghum is a C₄ grass plant that diverged from maize

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approximately 15 million years ago, making it the fifth most important cereal grain produced world wide (Doggett 1988). Although sorghum is well adapted to tropical and subtropical climates, most of its acreage is in drought-prone, semi-arid tropical regions of the world. Under such harsh environmental conditions, sorghum is produced primarily for human consumption and then as animal feed and fodder. The ploidy varies in Para sorghum from $2n = 10$ to $2n = 40$ and most of species in *Stiposorghum* are diploid with $2n = 10$, while *S. interjectum* has $2n = 30, 40$ and *S. plumosum* has $2n = 10, 20, 30$ (Garber 1950, Lazarides *et al.* 1991, Dillon *et al.* 2007). Appropriate selection strategies to identify genotypes with desirable traits are essential for successful plant breeding programs. Analysis of variability among traits and the identification of associations among various traits contributing to yield would facilitate successful development of high yielding varieties. However, crop selection alone cannot be effective in developing varieties, so make the suitable varieties by selection toward yield and farmer preferred characteristics. The identification of yield related traits could result in more effective selection for green fodder yield and farmer preferred traits. The high level of genetic diversity and characterization of accessions integrated into world collections is essential in order to classify, manage exotic germplasm, collect and ultimately utilize the different genetic improvement of the crop.

Plant genetic resources are essential for future food security to meet the needs of Uttar Pradesh. Greater use of this diversity in sorghum breeding applications, to develop broad genetic base varieties, will lead to sustainable sorghum production. A good understanding of genetic diversity among accessions will allow accurate breeding. Therefore, genetic variants threaten sorghum diversity. The aim of the survey was to assess the level of genetic diversity and genetic variation studies for production, feeding and nutritional quality in forage sorghum.

MATERIALS AND METHODS

The experimental material used in present investigation consisted of 33 advance lines of sorghum are enlisted below:

These genotypes are-

Sl. No.	Genotype	Sl. No.	Genotype	Sl. No.	Genotype
1	HC-541	12	Pant chari-3	23	CSV-14
2	Pant chari-8	13	Pant chari-5	24	CSV-13
3	Pusa chari-6	14	HC-573	25	Bundela chari
4	HC-171	15	HC-308	26	HJ-513
5	HC-136	16	Pusa chari-9	27	CSV-12
6	Pratap Raj Jowar-1	17	Pant chari-4	28	HC-260
7	MP chari	18	SSG59-3	29	CSV-28
8	HJ-541	19	Pusa chari-23	30	CSV-20
9	Pusa chari-615	20	Versha	31	PJ-1430
10	Pant chari-6	21	CSV-15	32	CSV-27
11	Pant chari-2	22	Pant chari-7	33	CSV-23

The experiment was conducted according to a Randomized Block Design (RBD). All the recommended crop cultivation practices were followed to raise a good crop of sorghum with 4 row plot of 5 meter length. The row to row spacing was 30 cm and plant to plant distance was 10 cm respectively. Observations were recorded on yield and yield attributing characters. All the observations were taken from each plot, on randomly five selected plants from each genotype. The data were recorded for the following characters viz., days to 50% flowering, plant height, leaf length, leaf breadth, leaf area, stem girth, leaves per plant, leaf stem ratio, total soluble solids and green fodder yield per plant. The mean values of genotypes in each replication were used for statistical analysis. The steps involved in the analysis of variance were as described by Fisher (1955). The genotypic and phenotypic coefficients of variation were calculated as per the formula suggested by Burton and Devane (1952). GCV and PCV values were categorized as low (0-10%), moderate (11-20%) and high (> 20%) as indicated by Sivasubramaniam and Madhavamenon (1973). Heritability (as broad sence) was calculated as per Allard (1960). The heritability percentage was categorized as low (0-30%), moderate (30 -60 %) and high (>60%) as given by Johnson *et al.* (1955) and genetic advance as per Johnson *et al.* (1955) were also worked out. The genetic advance was categorized as low (0-10%), moderate (11 – 20%) and high (>20%) as suggested by Johnson *et al.* (1955). The multivariate analysis of genetic divergence using Mahalanobis D^2 statistics was first suggested by Rao (1952).

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance revealed significant differences for all 10 studied traits in the 33 forage sorghum genotypes shown in Table 1 and indicated that the mean value of square clusters due to genotype was highly significant for all the studied characters viz., days to 50% flowering, plant height, leaf length, leaf breadth, leaf area, stem girth, leaves per plant, leaf stem ratio, total soluble solids and green fodder yield per plant. The results of the present study are in agreement with the Khadakabhavi *et al.* (2014), Yadav *et al.* (2019), Singh *et al.* (2019) and Prasad and Sridhar (2020) who had also reported the high variability in sorghum for different traits.

Coefficient of variation

In the study of phenotypic coefficient of variance (PCV) is higher than genotypic coefficient of variance (GCV) for all the characters while the differences between phenotypic coefficient of variance and genotypic coefficient of variance are smaller that indicated that environmental impact of factor is less (Table 2). The high phenotypic and genotypic coefficient of variance was observed with green fodder yield (28.95, 28.88) followed by leaf area (27.94, 27.68), plant height (26.79, 25.78) and leaf stem ratio (20.04, 19.49).

Heritability analysis

The high heritability (>60%) in broad sense was revealed for all the traits (Table 2) namely, days to 50% flowering, plant height, leaf length, leaf breadth,

leaf area, stem girth, leaves per plant, leaf stem ratio, total soluble solids and green fodder yield per plant. The finding of heritability was in consonance with the finding of by Singh *et al.* (2016), Jimmy *et al.* (2017), Rajarajan *et al.* (2018) and Wadikar *et al.* (2018).

Genetic advance analysis

Estimates of genetic advance expressed as percent of mean was highly (>20%) observed (Table 2) for plant height, leaf breadth, leaf area, stem girth, leaves per plant, leaf stem ratio, total soluble solids and green fodder yield per plant which indicates that good response for selection based on *per se* performance of these traits. Similar result was also noted by earlier workers Malik *et al.* (2015), Kalpande *et al.* (2018), Karadi and Kajjidoni (2019) and Dev *et al.* (2019).

The present study revealed high heritability combined with high genetic gain as percentage mean for most of the characters, indicating the presence of significant genetic variation and additive gene effects. Moreover, it is always desirable to compute broad sense heritability in conjunction with genetic advance because the information of heritability coupled with genetic advance help to explain the role of phenotypic variance.

Divergence analysis

In present investigation based on D² values (Tables 3 - 5) thirty three genotypes of sorghum were grouped into six clusters using ten component characters. Among the clusters (Table 4), cluster I was the largest with fifteen genotypes, cluster II and V had 4 genotypes each, cluster III with 7 genotypes, cluster IV had 1 genotype and cluster VI with 2 genotypes

Table 1. Analysis of variance (ANOVA) for ten characters of thirty three genotypes in forage sorghum (*Sorghum bicolor* L. Moench). *, ** Significant at 5% and 1% level, respectively.

Source of variation	df	Days to 50% flowering	Plant height (cm)	Leaf length (cm)	Leaf breadth (cm)	Leaf area (cm ²)	Stem girth (mm)	Leaves per plant	Leaf stem ratio	Total soluble solids (%)	Green fodder yield per plant (g)
Replication	2	38.25	1.72	1.81	0.12	240.21	0.03	0.91	0.08	0.15	2.61
Treatment	32	151.00**	7064.15**	82.74**	2.86**	9874.90**	8.40**	7.50**	0.12**	6.67**	23959.17**
Error	64	10.35	1.27	0.83	0.04	94.54	0.04	0.32	0.02	0.32	2.01

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

Characters	GCV (%)	PCV (%)	Heritability (%)	Genetic advance	Genetic advance (as % of mean)
Days to 50% flowering	8.30	9.17	81.92	12.77	15.47
Plant height (cm)	25.78	26.79	99.95	39.93	42.79
Leaf length (cm)	7.27	7.38	97.04	10.60	14.76
Leaf breadth (cm)	15.14	15.44	96.19	1.96	30.59
Leaf area (cm ²)	27.68	27.94	97.18	29.95	35.90
Stem girth (mm)	9.94	9.99	98.69	3.42	20.34
Leaves per plant	14.73	15.68	88.22	2.99	28.50
Leaf stem ratio	19.59	20.04	95.59	0.13	39.46
Total soluble solids (%)	17.48	17.61	98.57	3.04	35.75
Green fodder yield per plant (g)	28.88	28.95	99.97	18.06	34.76

Table 3. Average intra and inter cluster (D2 value) distance in thirty three genotype of forage sorghum (*Sorghum bicolor* L. Moench). Bold values are intra cluster distance.

Clusters	I	II	III	IV	V	VI
I	1.93	2.36	3.23	6.73	2.90	5.76
II		2.15	4.47	7.75	4.09	5.91
III			2.27	7.04	3.15	4.52
IV				1.01	6.71	7.29
V					1.42	4.89
VI						2.13

which concluded that in general, there was parallelism between genetic and geographic diversity. Cluster IV is represented by a single genotype that differs

Table 4. Distribution of thirty three genotypes of forage sorghum (*Sorghum bicolor* L. Moench).

Clusters number	No. of genotypes	Genotypes
I	15	HC-171, MP chari, Pant chari-6, Pant chari-3, Pant chari-5, Pant chari-4, Versha, CSV-15, CSV-14, CSV-13, Bundela chari, CSV-12, CSV-28, CSV-20 and CSV-23
II	4	Pant chari-2, Pusa chari-9, SSG59-3 and CSV-27
III	7	Pant chari-8, Pusa chari-6, Pusa chari-615, HC-573, HC-308, Pant chari-7 and PJ-1430
IV	1	Pratap Raj Jowar 1
V	4	HC-541, HC-136, HJ-541 and HC-260
VI	2	Pusa chari-23 and HJ-513

Table 5. Contribution of different characters in creating diversity in forage sorghum (*Sorghum bicolor* L. Moench) based on Mahalanobis's D² analysis.

Sl.No.	Characters	Contribution (%)
1	Days to 50% flowering	2.55
2	Plant height (cm)	8.66
3	Leaf length (cm)	0.99
4	Leaf breadth (cm)	8.02
5	Leaf area (cm ²)	10.87
6	Stem girth (mm)	1.55
7	Leaves per plant	9.22
8	Leaf stem ratio	5.94
9	Total soluble solids (%)	3.69
10	Green fodder yield per plant (g)	11.12

independently from other genotypes. The formation of isolated clusters may be due to complete isolation preventing gene flow or intensive natural/human selection on different adaptive complexes. These genotypes may be very unique and useful in breeding point of view. Fifteen varieties grouped under Cluster I indicates their proximity and narrow genetic base. This view point has been supported by the work of Shivani and Sreelakshmi (2013), Elangovan *et al.* (2014), Elangovan and Kiran (2015) and Umakanth *et al.* (2019).

CONCLUSION

The accomplishment of any breeding program objective depends upon the extent of genetic variability in base population and it is essential to subject a population for selection to achieve improvement in a particular trait. In the present study the analysis of variation shows highly significant differences among the genotypes for characters studied viz., days to 50% flowering, plant height, leaf length, leaf breadth, leaf area, stem girth, leaves per plant, leaf stem ratio, total soluble solids and green fodder yield per plant would be important for bringing on crop improvement. High estimate of PCV and GCV were observed for the plant height, leaf breadth, leaf area, stem girth, leaves per plant, leaf stem ratio, total soluble solids and green fodder yield per plant. The PCV and GCV for green fodder yield per plant showed more differences between these two mean and showed more interaction of environment for expression of characters. The magnitude of phenotypic coefficients of

variation in selected sorghum genotypes was higher than that of the genotypic coefficients of variation, indicating that environmental factors are influencing studied characters. Studies on heritability and genetic advance revealed for plant height, leaf breadth, leaf area, stem girth, leaves per plant, leaf stem ratio, total soluble solids and green fodder yield per plant may be improved through simple selection procedures. Genotypes Pratap Raj Jowar-1, Pusa Chari-23, HJ-513, Pant Chari-2, Pusa Chari-9, SSG59-3 and CSV-27 have been proved to be major contributors to its economic superiority and parents may be involved in crossing program for developing high yielding varieties in forage sorghum.

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