



Study of Genetic Diversity in Forage Sorghum [*Sorghum bicolor* (L.) Moench]

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Analysis of genetic divergence through Mahalanobis D^2 statistics exhibited considerable genetic diversity among genotypes. The thirty genotypes of forage sorghum were grouped into 6 clusters. The cluster II (14 genotypes) and cluster I (7 genotypes) having the maximum number of genotypes. This envisaged that the genotypes grouped within a particular cluster were more or less genetically similar to each other and apparent wide diversity was mainly due to the remaining genotypes distributed over rest of the other clusters. Percent contribution and expression of characters towards the genetic divergence play an important role in selecting the superior genotypes among diverse genotypes. Plant height had maximum contribution towards the genetic divergence followed by green fodder yield, leaf stem ratio and number of leaves per plant and remaining characters noted very low contribution percent towards the genetic divergence. Maximum intra cluster distance was recorded in cluster IV, indicating greater genetic divergence

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between the genotypes belonging to these clusters and crosses involving genotypes viz., CSV-15, CSV-17, Pant Chari-8, CSV-16 and Pant Chari-7 are suggested. Crosses in the above combinations are expected to provide enough genetic variability to select high green fodder yield and stable segregates in the segregating generations.

Keywords: *Sorghum bicolor*; sorghum; genetic divergence; inter-cluster distance; cluster mean.

1. INTRODUCTION

“Sorghum is the most important food and fodder crop of dry land agriculture. Sorghum grains are important as food and as livestock feed. The stem and foliage are used as a green fodder, hay, silage and pasture. The stems are also used as fuel and building material. Sorghum is used in preparation of different types of food and unleavened bread is the most common food made from sorghum flour. The dough is sometimes fermented before the bread is prepared, and the grains boiled to make a porridge or gruel. It is also used in the preparation of biscuit. Beer is prepared from sorghum grain in many parts of Africa. In India it is grown over an area of 16 million hectare with total production of about 11.60 million tons. In spite of premier position occupied by India 717 kg per hectare in the world millets scenario, per hectare yields are very low as compared to world average. This wide gap is an eye opener to intensify the breeding programme at national level. This may be due to limited geographical distribution of *rabi* sorghum confined to Indian sub continent and inadequate utilization of available genetic diversity” [1]. “The total area, production and productivity of jowar are 5.65 million hectare, 4.41 million tones and 780 Kg per hectare respectively in India and the total area, production and productivity are 0.16 million hectare, 0.11 million tones and 677 Kg per hectare in U.P. respectively” [2]. “The area under high forage yielding varieties is negligible in western Uttar Pradesh. Hence, it is essential to develop superior varieties with a significant superiority in term of green fodder yield. D^2 -statistics as multivariate analysis is a powerful tool in the estimating genetic divergence in crop plants. Being a numerical estimate this method has an added advantage over other as it permits precise comparisons among all possible traits of population in a group and its commutation offers the automatic removal of the effects of correlations among the genetic variables involved to its efficiencies and usages. D^2 -statistics as multivariate analysis is a powerful tool in the estimating genetic divergence in crop plants. Being a numerical estimate this method

has an added advantage over other as it permits precise comparisons among all possible traits of population in a group and its commutation offers the automatic removal of the effects of correlations among the genetic variables involved to its efficiencies and usages. The utility of Mahalanobis's generalized distance (D^2) is not only limiting factor for determining the degree of divergence in different populations but also for selecting genetically diverse parents for an efficient breeding programme” [3].

2. MATERIALS AND METHODS

Thirty diverse genotypes of forage sorghum were grown in randomized block design with three replications during the *khari* 2017 at Crop Research Centre of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U.P.). Each plot comprised of four rows of 5 m length, with row to row and plant to plant spacing of 30 cm and 10 cm, respectively. Observations on ten quantitative characters namely days to 50% flowering, plant height, leaf length, leaf breadth, leaf area, stem girth, number of leaves per plant, leaf stem ratio, total soluble solids and green fodder yield were recorded from five plants in each replication. The mean values were transformed in to uncorrelated linear function for Mahalanobis D^2 analysis. The genotypes were grouped in to different clusters per Tocher's method Rao, [4]), whereas intra and inter cluster distances were computed.

3. RESULTS AND DISCUSSION

In the present study thirty genotypes of forage sorghum were subjected to D^2 analysis using ten component characters. Consequently six clusters were formed. From the pattern of clustering it could be inferred that sufficient divergence was present to enable the formation of individual clusters. The clustering pattern is suggestive of the fact that geographic diversity is not efficient index of genetic diversity. Therefore Mahalanobis D^2 analysis of quantitative characters is a powerful tool for measuring genetic divergence among the material selected even from the same

geographic region. Out of the 6 clusters, cluster I with 7 genotypes, cluster II had 14 genotypes, cluster III and cluster IV with 1 genotypes each, cluster V had 4 genotypes and cluster VI with 3 genotype based on present investigation, it was concluded that in general, there was parallelism between genetic and geographic diversity (Table-2 and Fig. 1). The cluster III and cluster IV represented by single genotypes which independently diverged from others. These genotypes may be very unique and useful in breeding point of view. Fourteen varieties grouped under Cluster II indicating their proximity and narrow genetic base. This view point has been supported by the work of More et al. [5] and Ahalawat et al. [6]. The intra cluster distance among various clusters recorded maximum intra cluster distance (Table-1) for cluster IV (163.164) and lowest intra cluster distance was noted for cluster V (54.781). The maximum intra cluster distance was because of wide genetic diversity among its genotypes. The chance of developing good segregates by crossing the genotypes of the same cluster showing low value for intra cluster distance are very low. Therefore, it would be logical to attempt crosses between the genotypes of clusters separated by larger inter cluster distances. The little diversity and selection of parents within the cluster having higher mean for a particular character may also be useful for further developing high yielding forage sorghum varieties. Average inter cluster D^2 values among 30 genotypes exhibited maximum inter cluster distance (Table-1) values between cluster IV and VI (1019.496) followed by cluster I and VI (1006.879), cluster V and VI (901.703), cluster III and VI (870.167), cluster II and VI (495.045) and cluster I and IV (396.294). This clearly indicates that the genotypes included in these clusters are having broad spectrum of genetic diversity and could very well be used in hybridization programme of forage sorghum for improving fodder yield. Maximum inter cluster distance was recorded between cluster IV (CSV-17) and cluster VI (Pant Chari-8, CSV-16, Pant Chari-7) that are used in hybridization programme while minimum inter cluster distance was observed between clusters IV and V (169.065) which indicates that the genotype (HC-171, UP Chari-2, Pusa Chari-9, Pant Chari-4 in cluster IV and Pant Chari-8, CSV-16, Pant Chari-7 in cluster V) of these clusters had close relationship and hence, may not be emphasized upon to be used in hybridization programme. The comparison of cluster means for ten traits under

study attributes considerable genetic differences between the clusters regarding one or more characters. Cluster I exhibited maximum values of cluster mean for days to 50% flowering and total soluble solids. Cluster II revealed high mean values for leaf length, leaf breadth, leaf area, stem girth and green fodder yield. Cluster III estimated maximum values of cluster mean for plant height, and number of leaves per plant. Cluster VI recorded high mean values for leaf stem ratio. These findings indicated that the genotypes having high mean values for respective traits gathered in the clusters showing high cluster mean for respective trait. Individually, the genotypes from the respective clusters would be exploited according to the objective of the breeding programme. Therefore, the elite genotypes CSV-15, CSV-17, Pant Chari-8, CSV-16 and Pant Chari-7 may be involved in crossing for developing fodder yield. Classification of the germplasm into divergent groups based on inter cluster distances, *per se* performance and selection of parents from diverse clusters was reported in several studies Damor et al. [7]; Ahalawat et al. [6] and Rohila et al. [8]. Crosses suggesting parents belonging to most divergent clusters would be expected to manifest maximum heterosis and also wide variability of genetic architecture. Thus the crosses between the genetically diverse genotypes of cluster III characterized by plant height, number of leaves per plant and leaf stem ratio with genotype CSV-15, Cluster IV with genotype CSV-17, and Cluster VI with genotype like Pant Chari-8, CSV-16 and Pant Chari-7 (Table-3) are expected to show high heterosis and are also likely to produce new recombinants with desired characters and may be rewarding and effective in forage sorghum improvement programme. Hence, the above identified five genotypes as potential parents can be utilized in further breeding programme in which the above attributes will be considered for selection to achieve the best result of the breeding programme suggested by Thant et al. [9] and Deep et al. [10]. Percent contribution of leaf stem ratio followed by green fodder yield, plant height and number of leaves per plant contributed most towards genetic divergence (Table-4). Remaining traits contributed very little or did not contribute at all towards genetic divergence. These results are somewhat in accordance with the findings of Singh et al. (2017), Tesfaye [11]; Ahalawat et al. [6]; Rohila et al. [8] and Rathod et al. [12].

Table 1. Average intra and inter cluster (D^2 value) distance in thirty genotype of forage sorghum (*Sorghum bicolor* L. Moench)

Clusters	I	II	III	IV	V	VI
I	87.423	223.267	231.287	396.294	178.809	1006.879
II		118.170	213.279	330.843	177.294	495.045
III			84.924	328.313	213.438	870.167
IV				163.164	169.065	1019.496
V					54.781	901.703
VI						132.690

Bold values are intra cluster distance

Table 2. Distribution of thirty genotypes of forage sorghum (*Sorghum bicolor* L. Moench)

Clusters number	No. of genotypes	Genotypes
I	7	SPV-15, UP Chari-1, SPV-815, Pant Chari-2, Raj.Chari-1,HJ-541, Pant Chari-5
II	14	UP Chari-3, UP Chari-4, MP Chari, Pant Chari-6, CSV-84, HC-136, ICSV-700, HC-308, HC-260, SSG-59-3, G-48, Versa, HJ-513, Pant Chari-3
III	1	CSV-15
IV	1	CSV-17
V	4	HC-171, UP Chari-2, Pusa Chari-9, Pant Chari-4
VI	3	Pant Chari-8, CSV-16, Pant Chari-7

Table 3. Cluster means values for ten characters in forage sorghum (*Sorghum bicolor* L. Moench)

Character	Days to 50% flowering	Plant height (cm)	Leaf length (cm)	Leaf breadth (cm)	Leaf area (cm ²)	Stem girth (mm)	No. of leaves per plant	Leaf stem ratio (w/w)	Total soluble solids (%)	Green fodder yield (q/ha)
I	87.111**	247.184	67.762	5.989	272.329	16.578	9.711*	0.364	9.533**	545.367*
II	80.933	197.790	69.963**	6.528**	327.463**	16.880**	10.427	0.181*	9.260	601.441**
III	86.667	321.007**	67.598	5.476*	258.851	15.600	11.444**	0.427	8.102*	547.313
IV	80.593*	222.296	67.052	6.429	318.525	16.504	9.948	0.291	8.381	567.342
V	83.500	192.632*	68.547	6.470	311.182	16.123	9.867	0.368	8.780	563.886
VI	83.056	208.580	66.474*	5.509	240.623*	15.533*	10.311	0.485**	7.921	549.533

*Minimum cluster mean values; **Maximum cluster mean value

Table 4. Contribution of different characters in creating diversity in forage sorghum (*Sorghum bicolor* L. Moench) based on Mahalanobis's D² analysis

S.N.	Characters	Contribution (%)
1	Days to 50% flowering	2.300
2	Plant height (cm)	40.460
3	Leaf length (cm)	0.080
4	Leaf breadth (cm)	1.150
5	Leaf area (cm ²)	1.840
6	Stem girth (mm)	0.230
7	No. of leaves per plant	20.000
8	Leaf stem ratio (w/w)	24.370
9	Total soluble solids (%)	0.460
10	Green fodder yield (q/ha)	29.200

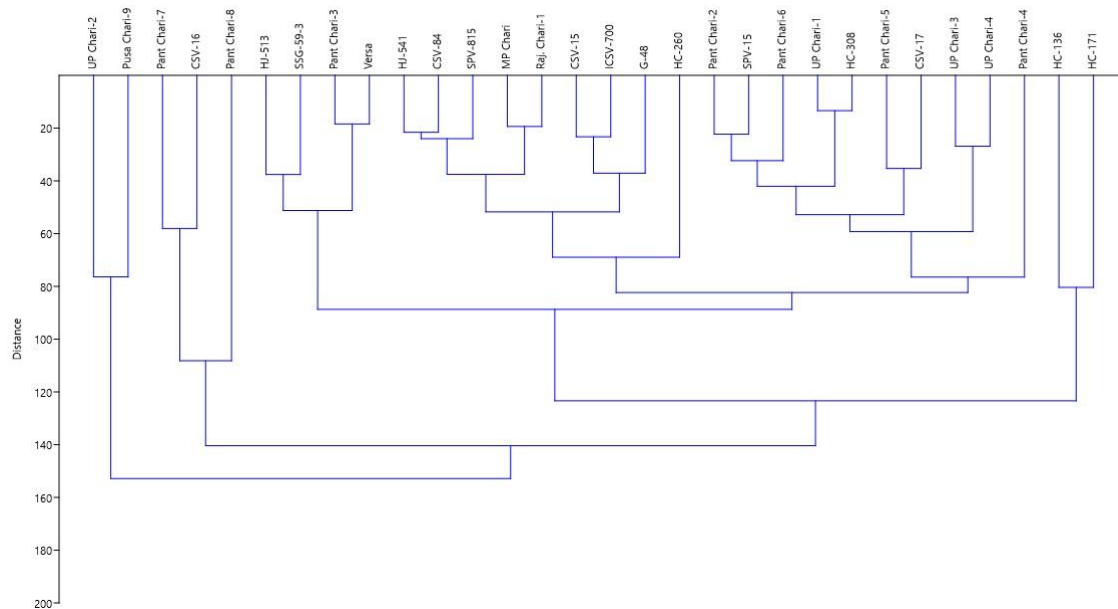


Fig. 1. Dendrogram of thirty genotypes of sorghum

4. CONCLUSION

D² were used for selection of genetically diverse and superior genotypes. Exceptionally good genotypes with one or more of the traits seemed desirable. Inter-crossing of different groups will lead to more opportunities for crossing, which releases potential masked variability by disrupting undesirable relationships. Crosses suggesting parents belonging to most divergent clusters would be expected to manifest maximum heterosis and also wide variability of genetic architecture. Genetic divergence study suggested that crosses between the genetically diverse genotypes of cluster III characterized by plant height, number of leaves per plant and leaf stem ratio with genotype CSV-15, Cluster IV with genotype CSV-17 and Cluster VI with genotype like Pant Chari-8, CSV-16 and Pant Chari-7 are

expected to show high heterosis or better hybrid vigour in F₁ or better hybrids and also for good recombinants in segregating population effective in forage sorghum improvement programme. Hence, the above identified five genotypes as potential parents can be utilized in further breeding programme in which the as above attributes can be considered for selection to achieve the best result of the breeding programme.

CONFERENCE DISCLAIMER

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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