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Assessment of genetic diversity in forage sorghum [*Sorghum bicolor* (L.) Moench] for fodder yield and its component traits using D^2 statistics

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Abstract
Sixteen genotypes of Sorghum [*Sorghum bicolor* (L.) Moench] were evaluated in a Randomized Block Design with three replications at NEBCRC, GBPUA and T, Pantnagar, Uttarakhand. The objective of preent study was to measure the genetic divergence for yield and yield related components by using Mahalanobis D^2 method. The observations were recorded for 13 different traits and results revealed that seven different clusters were obtained. The cluster I was largest and contained the maximum number of genotypes i.e 9 followed by cluster IV (2) while the cluster II, cluster III, cluster V, cluster VI and cluster VII each contained one genotype, respectively. Highest inter cluster distance was recorded between cluster IV and V (26.37). The higher inter cluster distance as compared to intra cluster distance suggested the presence of sufficient amount of genetic divergence among genotypes under studied. Maximum inter-cluster distance was obtained between cluster V and IV, which indicated that the genotypes belonging to these clusters could be used as parental material under a hybridization programme for getting desirable/transgressive segregants. The characters green fodder yield per plant, plant height, protein and TSS was found as major contributing characters towards the genetic divergence.

Keywords: Sorghum, diversity, yield, D Square

Introduction
Sorghum [*Sorghum bicolor* (L.) Moench], 2n=2x=20, a C_4 plant of family *Poaceae*, is a major feed, food and fodder crop throughout the world. 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) [8]. In India, it is grown for food, feed and fodder purpose on an area of around 5.02 million hectares with 4.80 million tons of grain production per annum (USDA Foreign Agriculture Service, 2018). In any plant breeding programme one of the major objectives is the generation of genetic variability as well as its exploitation. Genetic diversity refers to the amount of differences present between or within species. The presence of adequate genetic diversity provides ample opportunities to develop superior varieties. Diversity assessment helps plant breeders to choose the most genetically divergent genotypes that upon hybridization can give rise to desirable progenies in segregating generations. The parents having more genetic distant relationship result into higher heterotic expression in F_1 and greater amount of genetic variability in segregating populations (Shekhawat *et al*., 2001) [7]. In sorghum, lot of genetic diversity is present in the primary, secondary and tertiary gene pool however there is a need to make genuine efforts to assess available diversity. Hence the present investigation was conducted to estimate the magnitude of genetic diversity present among the elite sorghum genotypes.

Material and Methods
The present experiment was conducted during *kharif* 2020-21 by using 16 genotypes of sorghum grown in a Randomized Block Design (RBD) with three replications at Norman E. Borlaug Crop Research Centre, GBPUA and T, Pantnagar, Uttarakhand (Table 1). Recommended agronomic practices were adopted to raise the uniform crop stand and to minimize the effects of environmental variations. Observations were recorded on 13 different characters *viz*., *viz.*, Days to 50% flowering, Plant height (cm), Leaf length (cm), Leaf width (cm), Stem girth (cm), Number of leaves per plant, Number of nodes per plant, Leaf area index

(cm^2), HCN, Protein, TSS, Green fodder yield per plant and Dry fodder yield per plant respectively. The data recorded for various yield and attributing attributes were subjected to estimation of genetic diversity using the Mahalanobis D^2statistics (Mahalanobis, 1936) [5]. The clusters were prepared by following the Tocher's method Rao (1952) [6].

Table 1: List of elite sorghum genotypes used in present study

S. No.	Genotypes	S. No.	Genotypes
1	UP Chari-2	9	CSV-15
2	Pant Chari-6	10	CSV-17
3	Pant Chari-14	11	CSV-24SS
4	PC 2018-157	12	SPV 1725
5	PC 2018-259	13	SSG 59-3
6	PC 2018-264	14	HJ 513
7	PC 2018-265	15	IS 10302
8	PC 2018-352	16	IS 20399

Results and Discussion

Cluster analysis by using D^2 statistics

The results revealed that on basis of D^2 values, 16 sorghum genotypes were grouped into 7 different clusters (Table 2). The cluster I was largest and contained the maximum number of genotypes i.e 9 followed by cluster IV (2) while the cluster II, cluster III, cluster V, cluster VI and cluster VII each contained one genotype, respectively. The cluster I contained 9 genotypes *viz.*, SPV 1725, IS 10302, PC 2018-264, HJ 513, Pant Chari-6, SSG 59-3, PC 2018-259, IS 20399 and CSV-15. The cluster IV contained two genotypes *viz.*, PC 2018-265 and PC 2018-352. The cluster II contained genotype PC 2018-157, cluster III contained genotype UP Chari-2, Cluster V contained genotype CSV-17, cluster VI contained genotype Pant Chari-14 and Cluster VII contained genotype CSV-24SS. The inter-cluster distance ranged from 8.77 between cluster III and cluster II to 26.37 between cluster IV and cluster V (Table 3). Highest inter cluster distance was recorded between cluster IV and V (26.37) followed by cluster VI and IV (23.24), cluster IV and VII (22.86) and cluster IV and Cluster I (21.44). The intra cluster distance was found to be maximum in cluster I (10.17) followed by cluster IV (8.17). The higher inter cluster distance as compared to intra cluster distance suggested the presence of sufficient amount of genetic divergence among genotypes under studied. This indicated that if hybridization is attempted between the genotypes included in the cluster IV and cluster V, lot of genetic diversity will be produced in the segregating generations and the selection for desirable genotypes can be practiced. The hybridization between different genotypes included in the most divergent clusters to get desirable segregants for yield and other traits is also advocated earlier by Aruna and Audilakshmi (2008) [1]; Sinha and Kumaravadivel (2016) [9]; Jain and Patel (2016) [3]; Deep *et al*., (2019) [2]; Kanbar et al., (2020) [4]. Hence, from cluster analysis it is revealed that higher inter-cluster distance than the intra-cluster distance indicated the high genetic diversity among the genotypes. The maximum intra-cluster distance was observed in cluster I which indicated existence of wide genetic divergence in comparison of the other clusters and hence the genotypes belonging to such clusters having high degree of divergence and they could produce more segregating breeding material. Maximum inter-cluster distance was obtained between cluster V and IV, which indicated that the genotypes belonging to these clusters could be used as parental material under a hybridization programme for getting desirable/transgressive segregants.

Table 2: Classification of sorghum genotypes into different clusters based on D^2 value

Cluster number	Number of genotypes	Name of Genotypes included
I	9	SPV 1725, IS 10302, PC 2018-264, HJ 513, Pant Chari-6, SSG 59-3, PC 2018-259, IS 20399, CSV-15
II	1	PC 2018-157
III	1	UP Chari-2
IV	2	PC 2018-265, PC 2018-352
V	1	CSV-17
VI	1	Pant Chari-14
VII	1	CSV-24SS

Table 3: Inter and Intra Cluster Distances among different clusters

	C1	C2	C3	C4	C5	C6	C7
C1	10.17	13.64	13.73	21.44	13.33	14.22	13.78
C2		0.00	8.77	12.53	17.86	13.99	15.31
C3			0.00	16.64	18.12	11.35	17.42
C4				8.17	26.37	23.24	22.86
C5					0.00	12.04	14.84
C6						0.00	16.62
C7							0.00

Contribution of characters to divergence

The contribution of different characters towards the divergence is being presented in Table 4. The character green fodder yield per plant (31.67%) showed maximum contribution towards divergence. The days to 50% flowering, plant height, leaf length, leaf width, number of leaves per plant, HCN, Protein, TSS and dry fodder yield per plant contributed about 2.50%, 13.33%, 1.67%, 5.00%, 1.67%, 7.50%, 13.33%, 13.33% and 10.00% respectively. Stem girth, number of nodes and leaf area contributed 0% towards divergence. Thus, the characters green fodder yield per plant, plant height (cm), protein and TSS was found as major contributing characters towards the genetic divergence.

Table 4: Contribution of different characters towards the divergence

	Character	% Variation explained
1.	Days to 50% flowering	2.50
2.	Plant height (cm)	13.33
3.	Leaf length (cm)	1.67
4.	Leaf width (cm)	5.00
5.	Stem girth (cm)	0.00
6.	Number of leaves per plant	1.67
7.	Number of nodes	0.00
8.	Leaf area (cm^2)	0.00
9.	HCN	7.50
10.	Protein	13.33
11	TSS	13.33
12	Green fodder yield per plant (g)	31.67
13	Dry fodder yield per plant (g)	10.00

Conclusion

It can be concluded from the above discussion that there is a

presence of huge amount of genetic variability in the material under investigation as seven different clusters were obtained and intra cluster distance were found to be lesser than the inter cluster distances. Maximum inter-cluster distance was obtained between cluster V and IV, which indicated that the genotypes belonging to these clusters could be used as parental material under a hybridization programme for getting desirable/transgressive segregants. The characters green fodder yield per plant, plant height, protein and TSS was found as major contributing characters towards the genetic divergence.

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