

GENETIC DIVERSITY AMONG FORAGE SORGHUM (*SORGHUM BICOLOR* L. MOENCH) GENOTYPES

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(Received : 20 March 2022; Accepted : 05 April 2022)

SUMMARY

The study was conducted on 25 forage sorghum genotypes (*Sorghum bicolor* L. Moench) were evaluated for their genetic diversity based on 18 morpho-biochemical characters. Genotypes grown in Randomized Block Design during *kharif* season to categorize them for fodder and quality traits. The mean squares were observed to be highly significant for all the 18 characters studied. This also indicated its suitability for further statistical analysis for all the character studied. The genotypes were grouped in to six clusters indicating high genetic divergence among them. Based on their inter-cluster distance and cluster mean for the various characters, it could be inferred that cluster I, followed by IV, II, and III were the most divergent from the other cluster. These genotypes can be utilised for hybridization programmes. These traits *viz.* Green fodder yield, dry fodder yield, IVDMD and plant height upto base of flag leaf contributed highly towards the genetic divergence among genotypes studied.

Key words : Sorghum, variability, genetic divergence, inter-cluster distance, cluster mean

Sorghum (*Sorghum bicolor* L. Moench) was originated in Africa is one of the five top cereals crops and extremely drought tolerant. This ability makes it an excellent choice for cultivation in semi-arid and arid areas. It is one of the major multi-purpose crops grown for forage and grain purpose. In India, the yield of sorghum varies from state to state with varying rainfall, soil types and seasons. In northern parts, it can be grown during summer and *kharif* season while in southern parts it can be grown throughout the year. It is a quick growing habit, high yield, regeneration potential, better palatability, digestibility and drought tolerance makes it good choice of fodder for farming community on which the livestock industry depends.

In India, the area under cultivated sorghum was 4.82M ha with a production of 4.77 MT and productivity 989 kg/ ha (Indostat, 2020). In Haryana, the area under sorghum was 29.90 thousand hectares with a production of 15.74 thousand tons and productivity 528 kg/ ha ((Indostat, Haryana 2020). Sorghum is widely grown for fodder in states like Rajasthan, Punjab, Haryana, Uttar Pradesh, Delhi and Gujarat.

Brown midrib (*bmr*) is a visible marker that is associated with the reduction of lignin in corn, sorghum and pearl millet. Intensity of the coloration

is not a measure of reduction in lignin content although it is an indicator that the *bmr* gene is present. There are at least four genes that exist in sorghum, which produces a brown midrib reaction. Three of these genes were identified at Purdue University in 1978 and others exist in World Collection of Sorghum (Porter *et al.*, 1978). Brown midrib sorghum had the highest mean crude protein and a very high IVTD % (in-vitro true digestibility). Normal sorghum had the lowest crude protein, highest lignin content and the highest ADF % (Acid Detergent Fiber) and NDF % (Neutral Detergent Fiber) value. Normal sorghum had the lowest IVTD %. TDN (Total Digestible Nutrients), ADF and NDF value for *bmr* hybrids were more desirable than standard genotype.

Palatability in *bmr* materials has been improved over conventional sorghum. These improvements make *bmr* a very attractive characteristic of forage crops. Lignin is negative factor of digestibility having negative correlation between lignin and IVDMD. *Bmr* genotypes contain low amount of lignin. For better efficiency of livestock, both the quantitative production of fodders and their quality play significant role (Ahmad *et al.*, 2015). Keeping above points in view we have studied *bmr* and non-*bmr* genotypes of sorghum for fodder yield and quality.

METHODS AND MATERIALS

Twenty-five forage sorghum genotypes Bmr1, Bmr-2, Bmr3, Bmr-4, Bmr-5, COFS 29, HJ 513, HC 260, IS 2205, IS 2389, Duggi, CSV 21F, S 490, S 437, S 651, G 46, SSG 59-3, HC 136, HC 171, HJ 541, PC 5, PC 7, PC 8, ICSV 700, HC 308 were used in present study. The material was collected from Forage Section, Department of Genetics and Plant Breeding CCSHAU, Hisar. The field experiment was conducted at Research Area of Forage Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar in Ramandomized Block Design during *kharif* season. Morphological observations were recorded on different quantitative variables. Statistical analyses were carried out according to methods given by Al-Jibouri *et al.*, (1958), Dewey and Lu (1959), Panse and Sukhatme (1967).

Quality parameters: -

TABLE 1
Observations recorded on quality parameters

S. No.	Parameter	Method
1	NDF (Neutral Detergent Fiber) (%)	Goering and Van Soest (1970)
2	ADF (Acid Detergent Fiber) (%)	Goering and Van Soest (1970)
3	Lignin (%)	Goering and Van Soest (1970)
4	Crude Protein (%)	Micro-Kjeldhal's method
5	IVDMD (%)	Tilley and Terry (1971)
6	DDM (Digestible dry matter) (q/ha)	IVDMD (%) × DFY/100
7	Protein yield (q/ha)	C.P(%) × DFY/100

RESULTS AND DISCUSSION

Analysis of variance revealed the significant differences among genotypes for all characters under study. Based on D² statistics and Tocher's method 25 genotypes were grouped into 6 clusters with a variable number of entries revealing considerable amount of genetic diversity in the material (Table 2).

Cluster pattern revealed that cluster I was the largest group consisting of seven genotypes which was followed by cluster IV (six genotypes), cluster II (five genotypes), cluster III (four genotypes) and cluster V had only one genotype *i.e.* COFS 29. Grouping of genotypes in different clusters show that

TABLE 2
Group of forage sorghum genotypes D² statistics in different clusters

Cluster	Genotypes
Cluster I	BMR-1, BMR-2, BMR-3, BMR-4, BMR-5, S 437, HC 171
Cluster II	HC 260, IS 2205, PC 7, G 46, SSG 59-3
Cluster III	HJ 513, HJ 541, ICSV 700, S 651
Cluster IV	IS 2389, PC 5, PC 8, HC 308, HC 136, Duggi
Cluster V	COFS 29
Cluster VI	CSV 21F, S 490

TABLE 3
Average intra and inter-cluster D² values for six clusters in sorghum genotype.

Cluster No.	I	II	III	IV	V	VI
I	5.06	5.57	6.19	5.61	8.36	7.82
II		4.08	5.42	5.48	7.62	7.64
III			5.08	5.35	8.36	6.28
IV				4.14	7.6	7.02
V					0	11.38
VI						3.57

bmr lines exists in cluster I and COFS 29 in cluster V. Bmr is highly-quality forage species which has higher digestibility than conventional sorghum.

Agarwal *et al.*, (2002) reported similar results, who studied genetic divergence of 41 genotypes of sorghum in which genotypes were grouped into 5 non overlapping clusters.

Average intra and inter-cluster D² (Table 3) and Fig. 1 revealed that values among all genotypes solitary clusters showed the intra-cluster value of 0.00, while cluster III (5.08) showed maximum intra-cluster distance. The inter-cluster D² values ranged from 5.35 to 11.38. Minimum inter-cluster D² values were observed between clusters III and IV, indicating the close relationship among the genotypes included in these clusters. Maximum inter-cluster values were observed between clusters V and VI. Results obtained in the present study are in line with those reported by Sinha *et al.*, (2016), Damor *et al.*, (2017) and Ahalawat *et al.*, (2018) which indicated presence of enough variability for various characters in forage sorghum conforming to the result of the present study.

Cluster-wise means for all the traits studied are presented in Table 4. The mean performance of different clusters revealed wide range of variation among these concerning different traits. The perusal of the data reveals that cluster VI comprised genotypes with high green fodder yield, dry fodder yield, plant height, crude protein, DDM. Cluster V which comprised only one genotype (COFS 29) was characterized by high no. of leaves, high no. of tillers

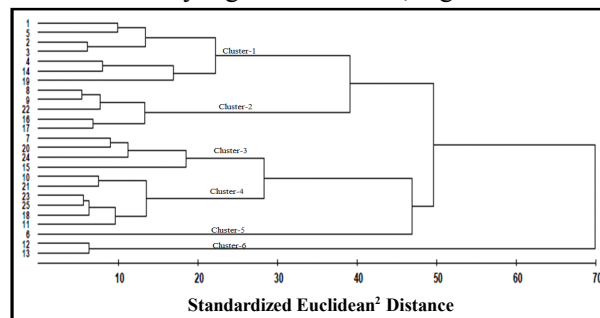


Fig. 1. Ward's minimum variance dendrogram.

TABLE 4
Cluster mean for eighteen morpho-biochemical characters of 25 sorghum genotypes

Characters	C1	C2	C 3	C 4	C 5	C 6	Mean
GFY/Plant (gm)	142.82	136.66	182.64	166.78	90.56	261.61	161.12
Natural height of plant upto base of flag leaf (cm)	139.17	192.50	190.21	147.15	173.36	220.21	167.77
No. of Leaves per plant	14.78	18.07	18.30	23.41	19.33	17.73	18.49
Stem girth (mm)	9.28	8.04	10.10	7.62	5.86	10.41	8.751
No. of tillers/plant	1.42	2.00	1.86	2.19	5.83	1.66	1.99
DFY/plant (gm)	48.88	44.76	57.18	54.58	31.36	93.63	53.64
Time of panicle emergence	82.66	66.73	78.25	81.61	101.0	85.50	79.48
Stigma length (mm)	2.31	2.23	1.85	1.62	2.40	2.18	2.05
Anther length (mm)	2.69	3.02	2.45	2.28	2.00	3.26	2.64
Panicle: length of branches (cm)	6.52	10.80	10.87	7.78	9.33	7.00	8.52
Neck of panicle above sheath (cm)	6.30	13.70	16.00	5.75	12.83	7.50	9.55
Lignin %	3.32	3.68	4.28	4.31	5.70	3.60	3.90
IVDMD %	65.12	62.14	64.97	63.46	60.26	68.18	63.03
C.P %	8.90	8.86	9.00	9.01	8.40	9.26	8.94
NDF (%)	70.48	64.86	68.60	68.07	68.06	65.98	68.02
ADF (%)	42.18	41.48	46.01	43.63	56.33	42.66	43.60
DDM (q/ha)	44.84	44.48	64.01	52.10	28.33	92.40	52.72
Protein yield(q/ha)	6.42	5.79	8.72	8.07	3.96	12.48	7.44

and low dry fodder yield and green fodder yield. The genotypes of cluster IV had a greater number of leaves, short stigma length. Low lignin was observed in cluster I which comprised of all *bmr* genotypes.

CONCLUSION

The inter-cluster distances were used to select genetically diverse and agronomically superior genotypes. The genotypes exceptionally good with one or more characters were seemed to be desirable. Inter-crossing of divergent groups would lead to greater opportunity for crossing over, which releases hidden potential variability by disrupting the undesirable linkages. The progeny derived from such diverse crosses are expected to have wide spectrum of genetic variability, providing a greater scope for isolating transgressive segregants for fodder yield and quality in advanced generations.

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