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DIVERSITY ANALYSES OF FORAGE TRAITS IN SORGHUM (*SORGHUM BICOLOR* L.) GERMPLASM

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SUMMARY

Sorghum germplasm including TNAU released varieties, dual purpose sorghum, forage sorghum, sweet sorghum, Maldhandi collections, ICRISAT lines and Tamil Nadu Local land races were evaluated for forage traits during the *Rabi* 2016 to study the divergence using multivariate (D^2) analysis. Results revealed four distinct cluster indicates that the germplasm had variation between group of cluster. The intra-cluster distances in all the four clusters were registered low, indicating that the genotypes within the same cluster were closely related for its forage value. The highest inter-cluster distance was observed between cluster I (14 genotypes) and cluster IV (2 genotypes) and the lowest between the cluster II (25 genotypes) and III (85 genotypes). The clustering pattern revealed that genetic diversity was not necessarily correlated with geographical origins but depends on forage traits viz., plant height, leaf area index, leaf area and stem thickness. The grouping of accessions into different clusters describes the breeder to identify and select the diverse genotypes, which can be used as the donor parents in breeding programme to realize heterosis. Intercrossing of divergent groups leads to wide genetic base in the base population and greater opportunities for crossing over to occur, which releases hidden variability by breaking the close linkages.

Key words : Sorghum, forage sorghum, Leaf are index, diversity, cluster analysis

Sorghum (*Sorghum bicolor* L.) is highly drought adopted crop which serves as excellent source of food, feed, green and dry fodder and biofuel is mainstay of dry land farmers in semi-arid tropics owing to assured grains and fodder even under low input and receding moisture regimes. Sorghum is resilient to different kinds of situation and it can be grown in a range of diverse ecosystem. It is also the base crop which many inter- and sequence cropping systems are built upon. Sorghum is cultivated in 100 countries in the world, covering area in America, Africa, Asia and Pacific. Sorghum is the third important cereal in India after rice and wheat. In Africa the crop is second in importance after maize. Fifty-nine percent of world sorghum area is in Africa. The developing countries in Asia and Africa contribute more than 70% of total sorghum production in the world. Asia alone contributes 45% of the world sorghum production. Sorghum production in Asia is concentrated mainly in India and China which accounts for 86%. During the last few years, sorghum yields has declined due to the major production constraints such as inadequate and/or erratic rainfall, poor soil fertility, pest and disease invasions and high temperatures. Hence, it is important to increase the sorghum yield under fragile environment to meet the growing demand due to expanding population growth. In addition to that genetic gain from past three decades are very less and revealed that parents used in the breeding programmes are has narrow genetic base. Hybridization involving genetically diverse parents is known to provide an opportunity for bringing together gene constellations resulting in desirable transgressive segregants in advanced generations. However, postulation of rational criteria for identification of such parents is still a live problem in plant breeding. To consider geographic diversity among the parents as an index of genetic diversity has been acclaimed and equally disclaimed in numerous reports. However, reports on genetic diversity among the *rabi* sorghum are very limited.

In the present study, D^2 analysis has been applied to assess the diversity among the 126 sorghum genotypes, to identify the divergent types suitable for hybridization programme. Diversity analysis provides information on deciding choice of parents from distantly related clusters to secure yield from distantly

related clusters to secure yield improvement in sorghum. The aim of the present study is to assess the sorghum genotypes for its divergence based on quantitative traits. This could help in identification of superior genotypes to improve sorghum genetic gains in breeding programmes.

MATERIALS AND METHODS

The material for the present study comprised of 126 genotypes includes TNAU released varieties, dual purpose sorghum, forage sorghum, sweet sorghum, Maldhandi collections, ICRISAT lines and Tamil Nadu Local land races. All the materials were sourced from Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore.

The present study was carried out at Millet Breeding Station and New Area Farm, Department of Millets, Tamil Nadu Agricultural University, Coimbatore during *Rabi* 2016 –17. Each accession was sown in randomized block design with the two replications. The row length is four meter with the spacing of 45cm between the rows and 15cm between the plants. The experiment was laid out in black cotton soil and the recommended package of practices was followed for raising a good crop. In each accession, five plants were selected randomly and used for collecting data on days to 50% flowering, days to maturity, plant height (cm), ear head length (cm), leaf area (cm^2), leaf area index, number of nodes, stem thickness (cm), peduncle length (cm), single plant yield (g). The mean of traits were subjected to statistical analysis.

Diversity and Construction of Phenotypic Dendrogram

The data on ten traits for 126 sorghum genotypes under drought stress condition were subjected to Multivariate hierarchical cluster analysis. Cluster analysis was performed using INDOSTAT services Ltd (version 8.5), Hyderabad, India, further the tree diagram based on elucidation distances was developed by TOCHER clustering method. The D^2 statistics was calculated according to Mahalanobis (1936) and Rao (1952). Average inter and intra cluster distances were estimated as per the procedure outlined by Singh and Choudhary (1977).

RESULTS AND DISCUSSION

Genetic diversity analysis was made in 126 sorghum germplasm at Department of Millets, TNAU, Coimbatore during *rabi* 2017 in order to find out diversity present in breeding materials of sorghum for forage traits. Significant differences were observed among the genotypes for ten quantitative traits had justified the relative contributions of these traits to the diversity. Based on D^2 statistics and Tochers method, the 126 genotypes were grouped into four clusters and each cluster revealing considerable amount of genetic diversity among the material. It was observed that cluster III had maximum number of genotypes *i.e*. 85 followed by cluster II with 25 genotypes, cluster I genotypes had 14 genotypes and cluster IV had 2 genotypes. (Table.1 *and* Figure 1). The formation of solitary clusters may be due to the gene flow or intensive natural/human selection for diverse adaptive complexes (Sujatha and Pushapavalli, 2015). Genotypes which had sweetness were found clustered in separately as Cluster I and II. The genotypes which had grain sorghum and local land races were found grouped in cluster III. (Rajarajan and Ganesamurthy, 2014). Further, Drought tolerant rainfed adopted TNAU released variety APK 1 grouped in cluster IV. The clustering pattern is not based on evolution and relatedness but purely on forage traits *viz*., plant height, leaf area index, leaf area, leaf length, and leaf breadth.

The grouping of accessions into different clusters describes the breeder to identify and select the diverse genotypes, which can be used as the donor's parents in breeding programme to realize heterosis. Selection within the cluster may not be rewarded good genetic gain because those lines mostly derived from same origin or possess similar morphological features or sister lines. Intercrossing of divergent groups leads to wide genetic base in the base population and greater opportunities for crossing over to occur, which releases hidden variability by breaking the close linkages (Thoday, 1960). Alternatively the donors identified can be utilized as elite genetic stocks/pre breeding lines for imparting the corresponding traits.

The diagonal values are denoted as intra cluster values. The Intra cluster distances of all the clusters are expressed as nil. Hence there is no variation present within the members of same cluster. The inter cluster distance between clusters 1 and 2 is 2238.619, 1 and 3 is 776.714, 1 and 4 is 6570.904 and between clusters 2 and 3 is 1538.182, 2 and 4 is 4332.313 and between cluster 3 and 4 is 2794.546. (Table 3).

Blum and Sullivan (1986) evaluated sorghum and millet landraces for their genetic variation

TABLE 1
Cluster representation of Sorghum gremplasms

S. No.	Cluster No.	Number of Germpalsm	Name of Germplasm
1	CLUSTER 1	14	EG 55, KO5 SS 310, KO5 SS 60, KO5 SS 44, KO5 SS 262, KO5 SS 311, IS 4617, Chinna Vellai Cholam, VS 1564, SPV 527, MTRS 708, KO5 SS 259, SO3 220
2	CLUSTER 2	25	CO 30, ISVAT 1021, GR 315, KO5 SS 747, SSV 84, EG 16, ENT 1, SO3 814, LGR 69, EG 3, IS 6422, KO5 SS 524, Vellai Cholam, SO3 696, SPV 413, EG 13
3	CLUSTER 3	85	IS 132, AS 1, EG 97, CO 18, AS 3850, KO5 SS 215, SPV 313, EG 50, MS 26445, APK 1, MS 26445, IS 31, SO3 791, IS 1501, CO 30, SO3 719, Irrugu cholam, IS 1251, KO5 SS 810, SPV 7942, MS 8430, M 26269, EG 15, AS 6191, GR 104, SPV 527, MS 7851, SO3 77, SO3 77, K 8, SO3 839, IS 5476, BS 68, SO3 885, EG 51, AS 4660, K 8, K 8, SO3 266, APK 1, SO3 538, SO3 885, K 8, R 836, IS 3569, SPV 521, KO5 SS 924, EG 3, GR 422, GR 306, Dharmapuri cholam, KO5 SS 211, MR 38, IS 3238, SO3 773, SPV 721, AS 3866, SPSSV 39, KO5 SS 60, IS 2870, SO3 464, ACM 8, GR 322, KO5 SS 314, SPV 738, COS 28, EG 77, KO5 SS 234, MR 38, MS 8351, IS 296, IS 5469, EG 79, IS 3952, EG 73, ACM 6, MS 7904, IS 167, Karuppu Cholam
4	CLUSTER 4	2	APK 1, SO3 464
	Total	126	126

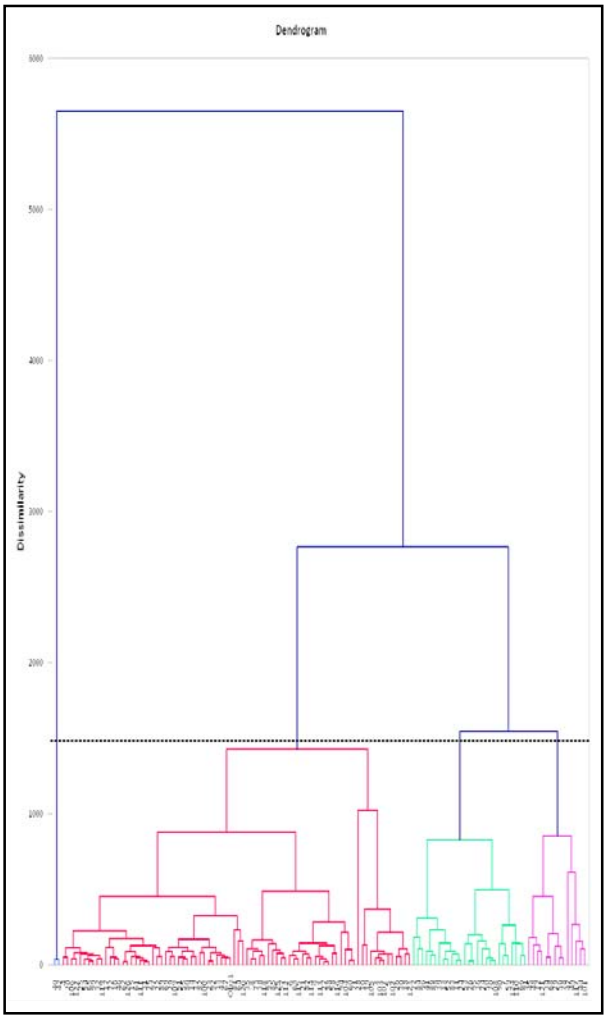

Fig. 1. Dendrogram depicting the clustering pattern among 126 sorghum genotypes.

TABLE 2
Inter cluster and Intra cluster distance

	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	0	2238.619	3776.714	6570.904
Cluster 2		0	1538.182	4332.313
Cluster 3			0	2794.546
Cluster 4				0

associated with the mechanism of dehydration avoidance and dehydration tolerance. The measured variables indicated a general trend for greater drought resistance. Chantereau *et al.* (1989) distinguished traditional landraces in to three groups using 25 agro morphological traits: viz., (1) durra race, hardy and adapted to dry zones; (2) two sub-groups corresponding to the *guinea* and *bicolor* races, hardy and adapted to wet zones; and (3) the *kafir* and *caudatum* cultivars, high yielding and adapted to intermediate zones. Ezeaku *et al.* (1999) used multivariate methods to classify accessions of sorghum. Clustering pattern showed that geographic diversity, though important but was not the only factor responsible for determining genetic divergence. Rao *et al.* (1996) evaluated morphological and agronomic characters of 4000 accessions from major sorghum growing states of India. They considered the characters like days to flowering, plant height, panicle length and grain quality, worthy of exploitation. They were having good quality large grain and hence they can be used as parents for yield improvement in sorghum.

Ayana and Bekele (1998) studied 415 accessions consisting of 391 landraces collected from

different geographical regions in Ethiopia and Eritrea. The materials were classified on the basis of regions of origin and adaptation zones. Phenotypic variation for qualitative (categorical) characters like color of midrib, panicle shape, compactness, awn, and glume color that displayed two or more classes was estimated using the Shannon-Weaver diversity index (H'). High and comparable levels of phenotypic variation were found between the regions of origin and between the adaptation zones.

Abdi *et. al.* (2002) selected 34 sorghum landraces consisting of 1020 individual plants from Ethiopia. Morphological variation for the fourteen qualitative characters like presence of awn, endosperm texture, glume color, glume hairiness, grain colour, panicle shape, threshability and grain covering were recorded that indicated two or more phenotypic classes, when analysed using the Shannon-Weaver diversity index (H'). Phenotypic variation was found between and within each classifying variables. Mahalakshmi and Bidinger (2002) evaluated a set of 72 diverse genotypes of sorghum [*Sorghum bicolor* (L.) Moench] for their patterns of post flowering leaf senescence under terminal drought stress conditions to identify superior sources of the stay-green trait. Leaf senescence patterns were determined by fitting the logistics or linear functions to the percentage of green leaf area (per cent GLA). They identified several tropically adapted lines with the stay-green expression equivalent to those of the best-adapted temperate lines (viz., B 35 and KS 19).

Umakanth *et al.* (2002) studied the nature and magnitude of genetic divergence for yield and its components in available exotic sorghum [*Sorghum bicolor* (L) Moench] germplasm and derivatives based on the Mahalonobis D^2 statistics, which grouped the genotypes in to five clusters. Arun kumar and Biradar (2004b) estimated the genetic diversity by Mahalonobis D^2 analysis, which grouped the genotypes in to 13 clusters based on D^2 values. Nirmala *et al.* (2004) studied the genetic divergence in twenty-six genotypes of sorghum using Mahalonobis D^2 statistics revealed 8 different clusters. Rohman *et al.* (2004) studied the genetic diversity of thirty-five exotic genotypes including those from Bangladesh. He considered the characters like days to flowering, plant height, 1000-grain weight, maturity by following Mahalonobis generalized distance (D^2) (Rao, 1952). Ogunbayo *et. al.* (2005) used the single linkage clustering, the principal component axes and a morphological dendrogram to group the 40 rice accessions using 14 agro- botanical traits. The single linkage cluster classified the 40 rice accessions in to six morphological groups whereas the principal component axes in to four broad groups those have within cluster similarities and intercluster morphological variations. The dendrogram sorted out the rice accessions into seven cluster groups. Manzelli *et al.* (2005) assessed the morphological variation within the 16 sorghum accessions and grouped the accessions into clusters based upon quantitative and qualitative characters using the univariate and multivariate methods and found that the accessions Elmi Jama Cas, Masego Cas, Masego Cad and Ca*rabi* clearly represent distinct landraces with specific features which is able to grow under harsh environmental conditions and suitable for different purpose, such as grain and/or forage production. Mohanraj *et al.* (2006) estimated the genetic diversity for 55 accessions of sorghum from ICRISAT with different geographical origins using Mahalonobis D^2 statistics and multivariate analysis, which grouped the accessions into twenty-one clusters and the clustering pattern revealed that genetic diversity was not necessarily correlated with geographical origins.gruoping was done in sorghum for drought tolerant and susceptible genotypes based on early drought indices (Rajarajan *et. al*. 2016) and morpho physiological traits (Rajarajan *et. al*. 2018).

CONCLUSIONS

Clustering analysis resulted four distinct cluster indicates that the germplasm had enormous variation between group of cluster. The grouping of accessions into four different clusters describes the breeder to identify and select the diverse genotypes, which can be used as the donor's parents in breeding programme to realize heterosis. The clustering pattern is not based on evolution but purely relatedness on forage traits *viz*., plant height, leaf area index, leaf area, leaf length, and leaf breadth. More forage value genotypes are clustered in to single cluster and grain types are in other clusters. Intercrossing of divergent groups leads to wide genetic base in the base population and greater opportunities for crossing over to occur, which releases hidden variability by breaking the close linkages.

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