Original Research Article

Genetic Divergence Studies in Sorghum (*Sorghum bicolor* L.) Land Races for Yield and Yield Parameters

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A B S T R A C T

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The multivariate analysis based on Mahalanobis's D^2 statistic (D^2 values) grouped the 26 accessions in to 6 clusters Cluster I and cluster II were the largest and consisted of 11 accessions whereas, remaining three clusters had only one accession each i.e. 23 (local land race from Buldhana), 17 (sel. from Gulbhendi local), 13 (yellow pericarp land race from Latur) and 11(sel. from yellow pericarp land race) indicated their genetic distinctness from rest of the genotypes. The intra and inter cluster distances among the 26 accessions revealed that the maximum divergence were observed between the clusters III and IV (D=34.11) followed by I and VI (D=32.17), II and IV (31.51). The cluster IV recorded highest % threshed grains and seed yield seed yield and highest mean test weight (PVR 101 SG and PVR 102 SG) whereas, cluster II (LLR from Sindkheda, Dudh mogra local) recorded highest mean plant height and test weight, respectively. The cluster I recorded lowest mean for days to 50% flowering and highest mean fodder yield (184.20). First three PCs i.e. PC I, PC II and PC III, contributed 57.92, 23.04 and 6.45 % of total variance. Cluster I comprised of genotypes with high threshable grains (%) ranging between 70.0 to 97.6%, whereas, genotypes manifesting lower threshable grain (%) were grouped into cluster II. Among rest of the clusters, comprising single genotype each, cluster III and cluster IX were exhibited medium threshable grain percentage and best taste, respectively. The D^2 analysis carried out thus helped to identify the diverse accessions from the available germplasm for the use in crop improvement programmes.

Introduction

Sorghum is the third most important cereal crop cultivated extensively in India after wheat and rice. Sorghum grown in *rabi* season is characterized by its excellent grain quality, exclusively utilized for human consumption and hence fetches higher market price as compared to *kharif*. Normally sorghum is consumed in the form of *Roti,* unleavened bread, but now days it is also consumed as *hurda* (roasted grains separated from sorghum panicles at dough

stage) in Maharashtra region. *Hurda* (sweet grain sorghum) fetches higher price as compared to normal grain sorghum thus benefiting farmers and consumers. Traditionally Maldandi and Gulbhendi are used as hurda purpose genotype which has less sweetness and difficulty in threshing at dough stage (40 to 60% grain recovery). So there is need to develop genotypes suitable for table purpose sweet grain sorghum (*hurda*) having easy threshability (90-100%

grain recovery) and sweetness at milky/dough stage. Understanding of genetic diversity of a species is fundamental in any crop improvement programme. For such species, in general the parents with more genetic divergence are expected to yield heterotic hybrids in addition to generating a broad spectrum of variability in segregating generations. The D^2 statistic is a useful multivariate statistical tool for effective discrimination among various genotypes on the basis of genetic divergence (Murty and Arunachalam, 1966; Sonawane and Patil, 1991). Hence, an attempt has been made to study the genetic divergence in available germplasm of sweet grain sorghum for percent threshed grains and fodder yield and its components to provide a basis for selection of parents for hybridization.

Materials and Methods

Twenty four genotypes of sweet grain sorghum collected from sorghum growing areas of Maharashtra, having different geographical origins and representing the spectrum of variation along with two sweet grain sorghum varieties were used in this study. These genotypes were evaluated at Sorghum Research Station, Vasantrao Naik Marathwada Krishi Vidyapeth, Parbhani, Maharashtra during *rabi* season of 2015-16 in a randomized block design with two replications. Each entry was planted in 4 rows of 4m length keeping 45 and 15 cm spacing between and within rows. Total eight observations were recorded *viz.* plant stand at harvest, days to 50% flowering, Plant height, % threshable grains, seed yield per plant, 100-seed weight, fodder yield, and taste. Percent threshed grains and taste were recorded at the time of ideal stage of harvest for sweet grain sorghum i.e. at milk dough stage. The analysis of variance for the individual character and analysis of covariance for character pairs were carried

out as described by Cochran and Cox (1957). Wilk's V criterion was used to test the significance of pooled differences in mean values of the nine characters studied (Singh and Chaudhary, 1977). Divergence was estimated by the multivariate analysis using Mahalanobis's (1936) and D^2 statistic as described by Rao (1952). On the basis of D^2 values obtained, the variables were grouped into different clusters by employing Tocher's method (Rao, 1952). The percent contribution of each character to the total divergence was calculated by ranking each character on the basis of transformed uncorrelated values. Finally, the percent contribution for each character was calculated by taking total number of ranks of all the characters to hundred. The data were analyzed statistically using the software WINDOSTAT, developed by INDOSTAT services Ltd. Hyderabad, India.

Results and Discussion

The analysis of variance showed highly significant differences among the accessions for all the characters studied indicating the presence of considerable variability in the experimental material. The percent contribution of different characters to the total diversity is presented in the Table 1. Threshed grained weight contributed enormously (54.15%) to the total variation followed by plant stand at harvest (18.46%) and plant height (12.31%).

Clustering pattern on D^2 values

The multivariate analysis based on Mahalanobis's D^2 statistic (D^2 values) grouped the 26 accessions in to 6 clusters (Table 2). The clustering pattern obtained in the present study revealed that genetic diversity was not necessarily associated with geographical origin (Table 2). Katiyar and Singh (1990), Arora *et al.,* (1991) and Singh

et al., (2001) have also reported the similar results in Faba Beans, Guar and Sorghum, respectively. Cluster I and cluster II were the largest and consisted of 11 accessions. Whereas, remaining four clusters had only one accession each i.e. 23, 17, 13 and 11 indicated their genetic distinctness from rest of the genotypes (Fig. 1). The intra and inter cluster distances among the 26 accessions (Table 3) revealed that the maximum divergence was observed between the clusters III and IV (D=34.11) followed by I and VI (D=32.17), II and IV (31.51). Five clusters (I, II, III, IV and V) have shown their maximum divergence from cluster VI. The maximum amount of heterosis is expected from the crosses with parents belonging to the most divergent clusters as has been reported by Katiyar and Singh (1990), Arora *et al.,* (1991) and Umakanth *et al.,* (2003). The inter cluster distance between clusters V and III was minimum (D=11.96) than intra cluster distance between cluster II (14.1).

Cluster means

The cluster means for nine characters (Table 4) revealed considerable variation among the clusters. The data revealed considerable differences among the clusters for most of the characters studied. Cluster IV exhibited highest % threshed grains (92.6%) and seed yield (1.2 kg/plot) ((PVR 101 SG and PVR 102 SG) whereas, cluster II (Jute local from Sindkheda, dist. Buldhana and Dudh mogra local from Solapur) recorded highest mean plant height (173.45 cm) and test weight (3.02 g) respectively. The cluster I recorded lowest mean for days to 50% flowering (72.10) and highest mean fodder yield (4.2 kg/plot). The data on inter cluster distances and *per se* performance of genotypes were used to select genetically diverse and agronomically superior genotypes. The genotypes, exceptionally good with respect

to one or more characters were desirable. On the basis of mean performances, the local genotype PVR 101 SG recorded highest threshed grain (%) and fodder yield and had considerable diversity therefore, it can be selected as a promising line. Intercrossing of divergent groups would lead to wide genetic base in the base population and greater opportunities for crossing over to occur, which in turn may release hidden variability by breaking close linkage (Thody, 1960).

The progenies derived from such crosses are expected to show wide variability, providing greater scope for isolating transgressive segregants in the advanced generations. Hence, these genotypes may be used repeatedly in the crossing programmes to recover transgressive segregants, which can be either released as a variety or can be utilized in the genetic enhancement of Sorghum crop.

Principal component analysis

Total four principle components, accounting 94.15 of total variance were obtained from principle component analysis. First three PCs i.e. PC I, PC II and PC III, contributed 57.92, 23.04 and 6.45 % of total variance. The results obtained from PCA were further corroborated by cluster analysis using UPGMC (Unweighted Paired Group Method using Centroids). Twenty six sweet grain sorghum cultivars were classified into seven morphologically distinct clusters (Fig. 2). UPGMC proved to be useful in showing high internal (within cluster) homogeneity and external (between clusters) heterogeneity within cultivars, as previously reported by Florence (2010) and Mohammadi and Prasana (2003). The resulting clusters were well resolved in terms of morphological characteristics. Cluster I comprised of genotypes with high threshable grains (%) ranging between 70.0

to 97.6%, whereas, genotypes manifesting lower threshable grain (%) were grouped into cluster II. Among rest of the clusters, comprising single genotype each, cluster III and cluster IV were exhibited medium threshable grain percentage and best taste, respectively. So genotypes from these may be utilized as *hurda* (sweet grain sorghum) purpose sorghum by evaluating in multilocation trials for grain yield, tender grain taste and threshability at dough stage. According to Li *et al.,* 2002 diversity analysis based on phenotypic values may not be the perfect representation of natural grouping of cultivars. More reliable results can be obtained after employing suitable molecular markers such as SSR by reducing environmental effects or experimental errors. The discriminating power principle of component analysis is not conclusive due to the small number of traits evaluated and their susceptibility to environmental conditions. The D^2 analysis carried out thus helped to identify the diverse accessions from the available germplasm for the use in crop improvement programmes.

Table.1 Percentage contribution of different characters to the total diversity

Source	Times ranked first	Contribution (%)
Plant stand at harvest	60	18.46
Days to 50% flowering	3	0.92
Plant height	40	12.31
% threshable tender grains	176	54.15
grain yield per plant	11	3.38
100-seed weight	19	5.85
Fodder yield	14	4.31
Tender grain Taste score	2	0.62

Table.2 Clustering pattern of 55 Sorghum accessions and their geographical origin based on D^2 statistics

Cluster	No. of accessions	Genotypes
I	11	Phule Madhur, Gulbhendi, Safed Mani, Lal chikani (land races from Dhule), PVR 101 SG, PVR 109 SG, PVR 106 SG, yellow pericarp land race from Latur dist., Satpani Sindkheda (land races from Buldhana dist.), PVR 102 SG, PVR 105 SG,
II	11	Dudh Mogra, sweet grain sorghum land race fromMarsul, dist. Buldhana, PVR 108 SG, Sahyadri local, Jute local (land race from Sindkheda dist. Buldhana), PVR103 SG, Hurda-2, PVR 107 SG, PVR 104 SG, PVR 110 SG.
III	1	Wani local land race from Vidarbha region
IV	1	Hurda-1(sel. From Gulbhendi local)
V	1	Selection from Yellow pericarp sorghum land race.
VI	1	Yellow pericarp sorghum (Piwali local)

Table.3 Intra and inter cluster distances based on D^2 values for 26 accessions

Cluster	I	II	III	IV	V	VI
I	9.99	23.9	30.13	17.1	23.42	32.17
II		14.1	17.43	31.51	18.1	29.25
III			0	34.11	11.96	21.21
IV				0	24.86	27.61
V					0	15.16
VI						0

Table.4 Cluster means for eight characters in sorghum based on D^2 values

Cluster	Plant stand at Harvest	Days to 50% Flowering	Plant ht. (cm)	threshable Grains (%)	Grain yield (kg/plot)	100 grain Wt. (g)	Fodd. Yield (kg/plot)	Tender grain taste score (1-5)
I	76.18	72.1	170.14	89.91	1.10	2.50	4.05	2.36
II	75.82	74.2	173.45	18.23	1.12	3.02	3.91	5.55
III	66.00	81.5	103.00	80.00	1.18	2.62	3.25	7.00
IV	47.00	75.0	141.00	92.60	1.20	2.76	3.10	6.00
V	51.50	74.0	103.00	28.00	0.54	2.83	3.10	4.00
VI	21.00	79.5	90.00	12.50	1.19	2.26	4.60	5.00

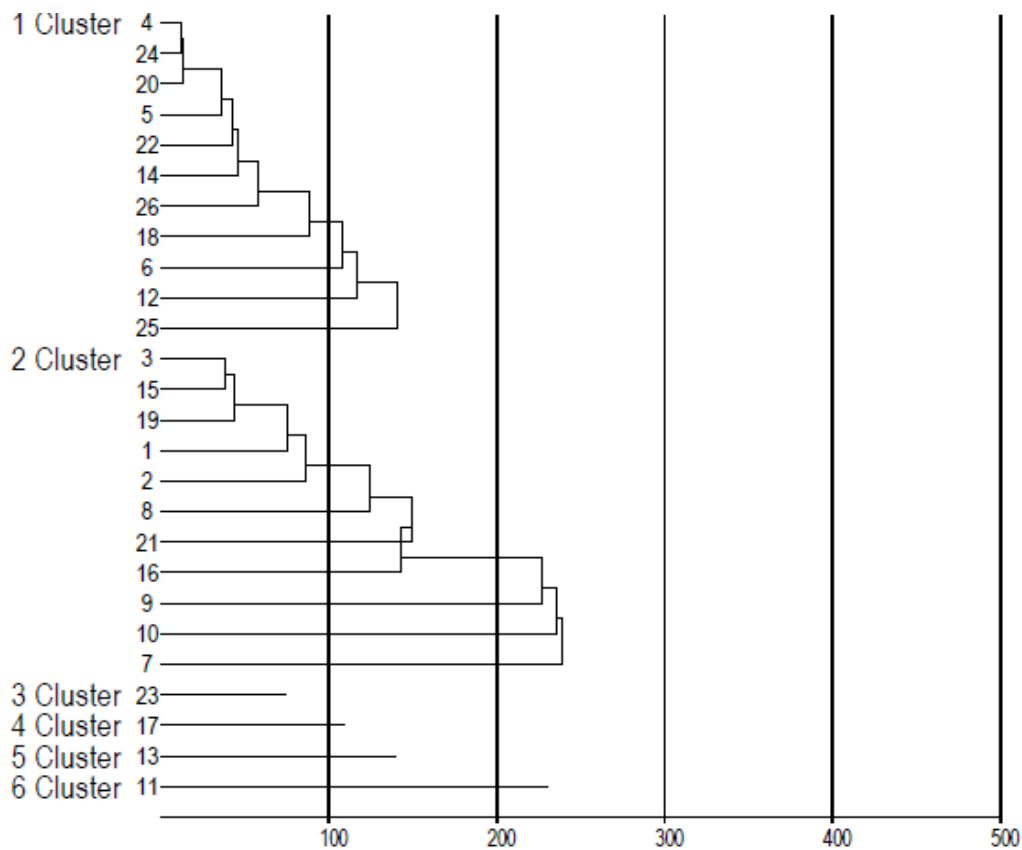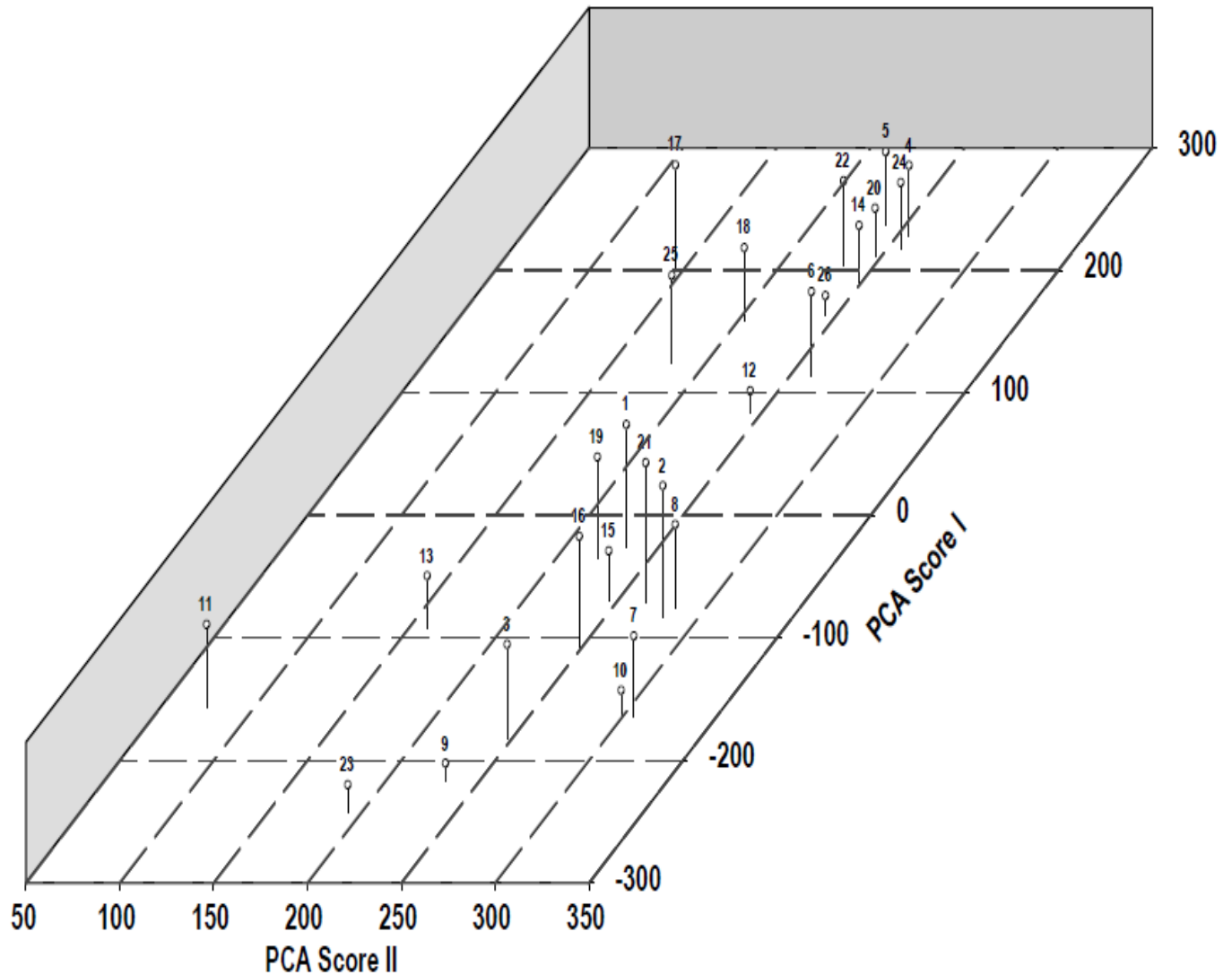**Fig.1** Clustering by Tocher's Method

Fig.2 Principle component analysis plot of 26 sweet grain sorghum genotypes

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