

Genetic Variability for Agronomic Traits in Sorghum Minicore Collection

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Abstract – Sorghum is a major cereal crop globally with economically important uses such as food, feed, fodder, fuel, and fiber. Crop improvement and precision breeding can be achieved by understanding and utilizing the variability in sorghum germplasm collection. A total of 242 germplasm accessions of sorghum minicore were assessed for the extent of variability, trait associations and genetic diversity. Sorghum minicore collection was evaluated for agronomic traits in two post-rainy seasons at ICRISAT- Patancheru, India. Large variability was observed for agronomic traits and strong associations between the traits studied. The 242 minicore accessions were grouped into six clusters under a hierarchical dendrogram. Genotypes from diverse clusters can be used in crossing programs to combine desirable traits and can be used as donors in breeding programs.

Keywords – Sorghum Minicore, Genetic Diversity, Correlation, Clusters.

I. INTRODUCTION

Sorghum [(*Sorghum bicolor* L.) Moench] is one of the five major cultivated species in the world acting as a dietary staple for 500 million people in 30 countries [1] grown in Africa, Asia, USA, Australia, and Latin America. It has several economically important potential uses such as food, feed, fodder, fuel, and fiber and is well adapted to diverse agro-ecologies subjected often to abiotic stresses such as drought, aluminum toxicity, low fertility and salinity. Knowledge of genetic diversity of a crop helps the breeder in choosing desirable parents for the breeding program and gene introgression from distantly related germplasm. Superior hybrids with resistance to biotic and abiotic stresses can be produced with the availability of diverse genotypes. Understanding of the genetic diversity in sorghum will facilitate further improvement of this crop for its genetic architecture [2]. In the present study 242 sorghum minicore germplasm accessions were investigated for variability, trait associations and diversity analysis by evaluating the accessions for agronomic traits. It aimed to characterize the germplasm for certain useful agro-morphological traits. The identified accessions may prove to be important donors for further breeding programs.

II. MATERIALS AND METHODS

The sorghum minicore collection comprising of 242 global germplasm accessions was used as the plant material for this study. The sorghum minicore collection represents all the basic five races (*caudatum* 16.1%, *durra* 12.4%, *guinea* 12%, *kafir* 8.7%, *bicolor* 8.3%) and 10 intermediate races (*caudatum-bicolor* 12.4%; *guinea-*

caudatum 11.2%; *durra-caudatum* 7.9%; *durra-bicolor* and *kafir-caudatum* each 2.9%; *kafir-durra* 1.7%; *guinea-kafir* 1.2%; and *guinea-bicolor*, *guinea-durra*, and *kafir-bicolor* each 0.8%) [3].

The genotypes were evaluated at International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India for two seasons, post-rainy 2013 and 2014. The experiments were conducted in alpha lattice design with two replications, each genotype planted in two rows of 2 m length, spaced at 60 cm between the rows. Plant to plant distance was maintained at 15 cm. Observations were recorded on whole plot wise for days to 50 per cent flowering, plant height (m) and plot-wise for fresh biomass yield (t ha⁻¹), dry biomass yield (t ha⁻¹), grain yield (g), tiller number and lodging score. Lodging was visually scored immediately prior to harvest with a score of 1=no lodging and a score of 10=complete lodging.

Analysis of Variance (ANOVA) was done using Statistical Analysis Systems (SAS) version 9.2 [4]. Pearson correlations were performed in the proc comp of R. The hierarchical clustering was performed on the Euclidean distance matrix utilizing Ward's linkage method measuring the un-weighted pair-group method with arithmetic averages (UPGMA) using R [5].

III. RESULTS AND DISCUSSION

The pooled season mean performance and ANOVA of sorghum minicore collection showed high variability for the traits studied (**Table 1**). Large variability exists in sorghum germplasm for various agronomic traits that can be effectively used in crossing programs for developing improved products. Highly significant genotype x environment was observed for all agronomic traits. In the present study high heritability was noticed for the agronomic traits. The high heritability observed for these traits indicated that these traits were less subjected to environmental influences. These results are in concordance with previous report of [6] where germplasm lines were used to assess morphological and yield traits.

Days to 50 Percent Flowering

The mean flowering time was 56 days with a high heritability of 65% and significant genotype x environment (GxE). High heritability was observed for flowering time in forage sorghum [7]. This study showed a large variability in flowering time which was earlier reported by Upadhyaya et al., 2009 in sorghum minicore collection.

Plant Height

The plant height mean was 2m with 45% heritability and significant G×E. Similar high heritability in forage sorghum genotypes was observed [7].

Fresh Biomass yield

Fresh biomass yields had high heritability of 73% with significant G×E interactions with similar results in 188 RIL population of sorghum [8] The mean for fresh biomass yield was 13.9 tha⁻¹.

Dry Biomass Yield

Dry biomass yields had high heritability of 80% with significant G×E interaction and a mean dry weight 6.1 tha⁻¹. Similar results were observed in RIL population of sorghum [8]

Grain Yield

The mean grain yield was 3.4 tha⁻¹ with 44% heritability and significant G×E.

Number of Tillers

The mean number of tillers was 1 with 50% heritability. As in our present study high G×E was also observed for tiller number in sorghum hybrids [(9), (10)] Heritability of 50% was observed for tillering which was similar to findings of [10] in sorghum hybrids.

Lodging

Lodging score had a mean of 1 with 40% heritability and significant G×E. In the preset study mean lodging was 1.8 and similar lodging means were observed in lentil. High G×E interaction and heritability was also similar to lentil [11] High lodging has also been observed in flax [12].

All traits showed moderate to high heritability and had significant G×E interaction.

Table 1: Mean performance of sorghum minicore entries for agronomic traits over post-rainy seasons 2013 and 2014 at ICRISAT, Patancheru, India

Traits	Across season		
	Mean (SE±)	H ²	G×E
Days to 50% flowering	56 (5.5±)	65	59.5
Plant height (m)	2.0 (0.3±)	45	0.1
Fresh biomass yield (tha ⁻¹)	13.9 (3.8±)	73	33.7
Dry biomass yield (tha ⁻¹)	6.1 (1.7±)	80	5.4
Grain yield (tha ⁻¹)	3.4 (0.9±)	44	1.9
Number of tillers	1 (0.6±)	50	1.0
Lodging	1.8 (0.9±)	40	1.9
SPAD	27.9 (2.3±)	50	77.1 ^{ns}

H²- broad sense heritability; SE- standard error; G×E- genotype × environment; ns- non-significant @ p > 0.01

Correlation Studies

The trait associations were studied by correlation studies across seasons (**Table 2**). Among the agronomic traits studied flowering time had significant positive correlation with plant height (0.29**), fresh biomass (0.59**), dry biomass yield (0.49**) and grain yield (0.2*). Plant height had a positive correlation to fresh (0.29**) and dry biomass yields (0.25**). Flowering showed significant positive correlation to fresh and dry biomass yields explaining the fact that late flowering leads to longer maturity duration that enables accumulation of higher biomass content in sorghum [13] Significant positive correlation between plant height and flowering time has been reported earlier [(14), (15)] Significant positive correlation of sorghum dry biomass yield with plant height was reported [(16), (17), and (18)] A trend similar to our studies significant positive correlation was observed between plant height and maturity duration in 242 accessions of sorghum minicore collection by [19] In previous studied sweet sorghum genotypes showed

positive correlation between fresh and dry biomass yields [20] similar to the observations in this study. Grain yield was positively correlated to flowering time [21] Significant negative correlation was observed between flowering time and lodging (-0.21**). Lodging showed significant negative correlation to dry biomass yield which is in accordance with previous studies in sweet sorghum [22] The biomass yields reduced with lodging and showed significant negative correlation for fresh (-0.28**) and dry biomass (-0.28**) yields.

Fresh biomass yield had a positive correlation with dry biomass yield (0.75**) whereas number of tillers contributed significantly to both fresh (0.21**) and dry biomass yields (0.2**). Tillering had a significant positive correlation with dry biomass yield similar to the findings in sorghum varieties [18] Rice also showed similar results where higher biomass was calculated with the increase in the number of tillers [23]

Table 2: Correlation coefficients of agronomic traits in sorghum minicore accessions over post-rainy seasons 2013 and 2014 at ICRISAT, Patancheru, India.

	DDF	PH	FSY	DSY	TILL	LS	SFS	GY	SPAD
DDF	1	0.29**	0.59**	0.49**	-0.11	-0.21**	-0.03	0.2**	-0.03
PH		1	0.29**	0.25**	-0.05	0.1	0.06	-0.02	0.02
FSY			1	0.75**	0.21**	-0.28**	-0.1	0.11	0
DSY				1	0.2**	-0.28**	-0.09	0.1	-0.01
TILL					1	0.05	0.27**	-0.03	-0.05
LS						1	0.09	-0.07	0.12
SFS							1	-0.03	0.05
GY								1	0.03
SPAD									1

< 0.05 = *

< 0.01 = **

DDF= days to 50% flowering, PH= plant height, FBY= fresh biomass yield, DBY= dry biomass yield, TILL= number of tillers, LS= Lodging score, SFS= shoot fly score, GY= grain yield SPAD= soil plant analysis development

Cluster Analysis

The relationship among the 242 sorghum minicore accessions based on their genetic relatedness was clustered in a dendrogram based on the mean values of the agronomic traits studied. Unweighted Pair Group Method with Arithmetic Mean (UPGMA) derived dendrogram, dividing the material into two major clusters at 4.5 (y-axis). The second group was further divided at approximately 3.5 (y-axis) whereas the first group divided at 1.3 (y-axis). The cutoff on the dendrogram was taken at 1.2 where six distinct clusters observed in the sorghum minicore set (Fig. 1). The maximum numbers of accessions fell in Cluster III with 70 accessions and minimum number in cluster I with 24 accessions. Cluster II and VI had 42 and 41 accessions respectively. Cluster IV consisted of 35 accessions and V had 33 accessions. Most of the early flowering (<50 days) genotypes were clustered in cluster III followed by cluster IV and VI. Genotypes with good plant height (>2m) were found in Cluster II followed by cluster VI. Both high fresh biomass yield (>25tha⁻¹) and high dry biomass yield (>10 tha⁻¹) accessions were grouped in cluster II. High grain yielding

genotypes were observed in cluster 1 and IV. All genotypes with more than 2 tillers were grouped in cluster II and I. Most of the high lodging genotypes were found in cluster V and VI. High SPAD (>50) genotypes were clustered maximum in cluster III followed by cluster II, IV and VI. Clustering the 242 sorghum minicore germplasm accessions following UPGMA using the data from agronomic traits divided the genotypes in to six distinct clusters. Genotypes with similar agronomic traits do not always fall in the same cluster. Genotypes with good plant height were found in clusters II and VI whereas most of the high biomass yielding genotypes was in cluster II. The distribution of genotypes into various clusters was at random suggesting that the genetic diversity was not related to geographic density. Similar results were reported in genetic diversity studied in rabi sorghum [2] and 44 sorghum minicore accessions [24]. The genotypes from diverse clusters from this study can be used in crossing programs to develop agronomically superior genotypes.

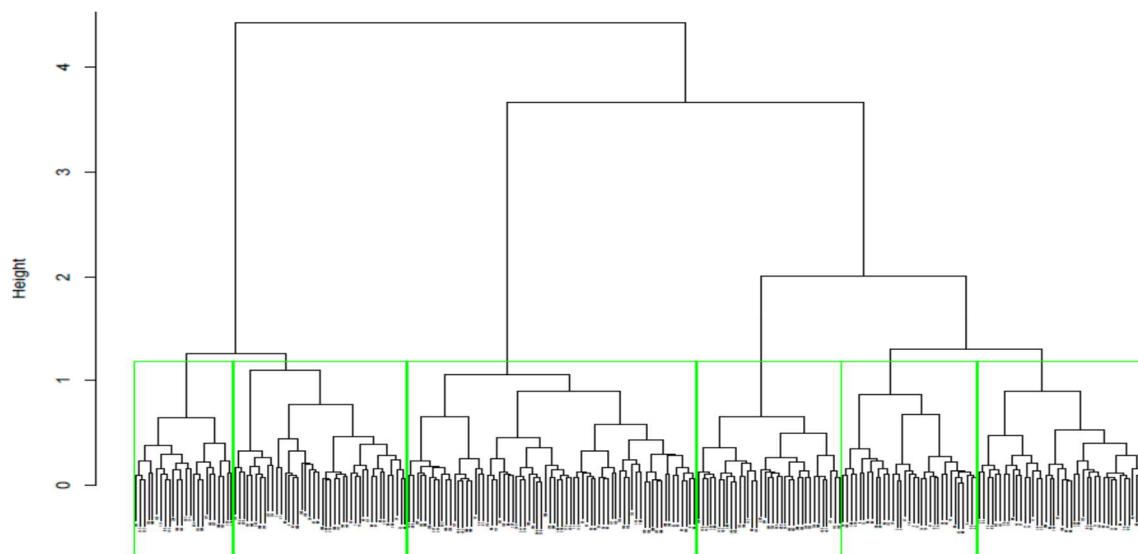


Fig. 1: UPGMA dendrogram representing the agronomic traits of 242 sorghum minicore genotypes

Fig.1: UPGMA dendrogram representing the agronomic traits of 242 sorghum minicore genotypes

IV. CONCLUSION

This study reports the presence of large variability for agronomic traits in the sorghum minicore collection. Significant trait associations were observed along with diversified clusters. Minicore accessions from diverse clusters can be used to combine the desired traits to develop elite genotypes in the breeding program.

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