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GENETIC VARIABILITY AND DIVERSITY STUDIES IN SORGHUM GERMPLASMS FOR GRAIN YIELD AND YIELD COMPONENTS

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ABSTRACT

The genetic diversity and variability are an essential prerequisite for improving the genetic makeup of any crop. Thus, the study was carried out to assess the both genetic variability and diversity for seventeen morphological traits associated with yield in hundred and one germplasm accessions with seven checks. The result of genetic variability revealed that grain yield per plant recorded high phenotypic coefficient of variation and genotypic coefficient of variation. High heritability coupled with high genetic advance was observed for flag leaf area, chlorophyll index, panicle length of branches, dry fodder yield per plant and grain yield per plant. Cluster analysis grouped the germplasm accessions into four major clusters based on mean data in which cluster I had the largest accessions followed by cluster II and III. The least number of accessions were found in cluster IV with nine accessions. The accessions from cluster I and IV can be used for hybridization programme as these accessions will have two extreme mean values thereby generates more variation upon hybridization. Principal component analysis revealed that the seven components were found to have eigen value more than one. Among the morphological traits associated with grain yield, maximum divergence was contributed by days to 50 per cent flowering, days to maturity and hundred seed weight. Hence, importance must be given to these traits.

Key words : Sorghum germplasm, Genetic variability, Diversity analysis, Principal component analysis.

Introduction

Sorghum is one of the fifth most important cereal crop in world besides rice, wheat, maize and barley. In India, it is the third important crop after rice and wheat (Mahajan and Wadikar, 2011). It is a dual-purpose crop which can be used for food and fodder. Mostly rainfed sorghum is used for human consumption. Sorghum is mostly cultivated in arid and semi-arid regions of the world (Rohman *et al*., 2004). It is known to be a climate-resilient crop as it has the ability to adapt to varied environmental conditions especially in drought prone regions. It serves as a source of raw material for starch, fibre, biofuels, alcohol and other products (Ahamed *et al.*, 2015). Analysis of genetic variability is the foremost criteria for any breeder to carryout effective breeding programme. Variability for yield traits can be estimated by Phenotypic coefficient of variance (PCV) and Genotypic coefficient of variance (GCV). Of these two parameters, GCV estimates heritable variation while PCV estimates non-heritable variation (Zinzala *et al*., 2018). Inheritance of polygenic trait can be ensured by heritability. As heritability is influenced by environment, estimates of heritability alone will not help in effective selection. Hence estimation of heritability along with genetic advance will enhance the outcome of selection for superior individuals (Al-naggar *et al.*, 2018).

Information on genetic diversity helps in selection of diverse parents for hybridization. It aids us to combine the favorable alleles for various agronomic traits to produce superior hybrids. Jain and Patel (2016) implied that PCA is done to identify the key contributing traits for yield which shows maximum diversity. These traits will be further utilized in breeding programme. Hence, the present study aimed to estimate genetic variability, heritability and genetic advance along with genetic diversity in order to identify key heritable traits and for the selection of superior parental combinations among sorghum germplasm accessions.

Materials and Methods

The experimental materials include 101 germplasm with seven checks and the experiment was laid out during *Kharif* 2018 in Department of Millets, Tamil Nadu Agricultural University, Coimbatore. The Augmented design II was followed with 4m row length and spacing of 45 cm × 15 cm. From each entry, five plants were tagged for recording observations on biometric traits. Mean of five plants from each entry were used for statistical analysis. Observations were recorded on the following traits *viz.*, plant height (cm), stem diameter (cm), leaf length (cm), leaf width (cm), flag leaf length (cm), flag leaf width (cm), flag leaf area (cm), chlorophyll index, number of leaves, number of nodes, panicle length (cm), panicle length of branches (cm), days to 50 per cent flowering (no. of days), days to maturity (no. of days), dry fodder yield per plant (g), hundred seed weight (g) and grain yield per plant (g). The analysis of variance was performed and significance for these characters was studied. The coefficient of variation was calculated for all the traits to compare the variability. The phenotypic (PCV) and genotypic coefficient of variation (GCV) were estimated by following Falconer and Scott (1967), broad sense heritability (H^2) by Lush (1940) and genetic advance as per cent of mean (GAM) by Johnson *et al.* (1955) using R studio version 1.4.1717 © 2009-21 package. The diversity analysis was done using R studio version 1.4.1717 © 2009-21 package and principal component analysis was carried out using STAR software.

Results and Discussion

Variability analysis

The results of phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as percent of mean were performed and presented in Table 1.

Phenotypic coefficient of variation

The phenotypic coefficient of variation was found to be high for the traits *viz.*, flag leaf area (25.63 per cent), panicle length of branches (30.20 per cent), hundred seed weight (21.08 per cent) and grain yield per plant (48.76 per cent). Plant height (17.17 per cent), stem diameter (18.48 per cent), leaf length (10.43 per cent), leaf width (14.76 per cent), flag leaf length (19.06 per cent), flag leaf breadth (18.61 per cent), chlorophyll index (15.41 per cent), number of leaves (14.66 per cent), number of nodes (14.61 per cent), panicle length (19.50 per cent) and dry fodder yield per plant (14.73 per cent) had exhibited moderate PCV. Days to flowering (9.40 per cent) and days to maturity (6.57 per cent) registered low PCV.

Genotypic coefficient of variation

Genotypic coefficient of variation was found to be high for traits *viz.*, flag leaf area (23.22 per cent), panicle length of branches (28.13 per cent) and grain yield per plant (45.46 per cent). Moderate GCV was recorded for plant height (13.08 per cent), stem diameter (13.96 per cent), flag leaf length (13.01 per cent), flag leaf breadth (13.30 per cent), chlorophyll index (14.65 per cent), number of leaves (11.25 per cent), number of nodes (11.18 per cent), panicle length (11.65 per cent), dry fodder yield per plant (12.95 per cent) and hundred seed weight (15.94 per cent). The traits *viz.*, leaf length (6.38 per cent), leaf width (9.93 per cent), days to 50 per cent flowering (8.08 per cent) and days to maturity (4.37 per cent) had registered low GCV.

Grain yield per plant recorded high phenotypic coefficient of variation and genotypic coefficient of variation. This finding was in accordance with Kalpande *et al.* (2018), Ghorade *et al.* (2015), Deepalakshmi and Ganesamurthy (2007) and Sharma *et al.* (2006). Moderate GCV and PCV for plant height were observed by Hamidou *et al.* (2018). Ghorade *et al.* (2015) reported moderate GCV and PCV for panicle length.

Heritability

High heritability was exhibited by various characters *viz.*, flag leaf area (82.02 per cent), chlorophyll index (90.40 per cent), panicle length of branches (86.77 per cent), days to 50 per cent flowering (73.74 per cent), dry fodder yield per plant (77.30 per cent) and grain yield per plant (86.94 per cent). Moderate heritability was exhibited by plant height (58.02 per cent), stem diameter (57.11 per cent), leaf length (37.35 per cent), leaf width (45.24 per cent), flag leaf length (46.59 per cent), flag leaf breadth (51.12 per cent), number of leaves (58.89 per cent), number of nodes (58.60 per cent), panicle length (35.72 per cent), days to maturity (44.16 per cent) and hundred seed weight (57.14 per cent).

Genetic advance as percent of mean

Genetic advance as percent of mean were found to be high for plant height (20.52 per cent), stem diameter (21.74 per cent), flag leaf area (43.31 per cent), chlorophyll index (28.70 per cent), panicle length of branches (53.99 per cent), dry fodder yield per plant (23.45 per cent), hundred seed weight (24.82 per cent) and grain

Table 1 : Coefficient of variation, heritability and genetic advance as percent of mean for morphological traits associated with yield and yield contributing traits.

Traits	**PCV (%)**	**GCV (%)**	**H^2 (%)**	**GAM (%)**
Plant height (cm)	17.17	13.08	58.02	20.52
Stem diameter (cm)	18.48	13.96	57.11	21.74
Leaf length (cm)	10.43	6.38	37.35	8.03
Leaf width (cm)	14.76	9.93	45.24	13.75
Flag leaf length (cm)	19.06	13.01	46.59	18.29
Flag leaf breadth (cm)	18.61	13.30	51.12	19.59
Flag leaf area (cm2)	25.63	23.22	82.02	43.31
Chlorophyll index	15.41	14.65	90.40	28.70
Number of leaves	14.66	11.25	58.89	17.79
Number of nodes	14.61	11.18	58.60	17.63
Panicle length (cm)	19.50	11.65	35.72	14.35
Panicle length of branches (cm)	30.20	28.13	86.77	53.99
Days to 50 percent flowering	9.40	8.08	73.74	14.29
Days to maturity	6.57	4.37	44.16	5.98
Dry fodder yield per plant (g)	14.73	12.95	77.30	23.45
Hundred seed weight (g)	21.08	15.94	57.14	24.82
Grain yield per plant (g)	48.76	45.46	86.94	87.33

yield per plant (87.33 per cent). Moderate genetic advance as percent of mean was recorded by leaf width (13.75 per cent), flag leaf length (18.29 per cent), flag leaf breadth (19.59 per cent), number of leaves (17.79 per cent), number of nodes (17.63 per cent), panicle length (14.35 per cent) and days to 50 per cent flowering (14.29 per cent). Leaf length (8.03 per cent) and days to maturity (5.98 per cent) registered low genetic advance as percent of mean.

High heritability coupled with high genetic advance was observed for flag leaf area, chlorophyll index, panicle length of branches, dry fodder yield per plant and grain yield per plant. These findings were reported by Kalpande *et al.* (2018), Swamy *et al.* (2018), Ghorade *et al.* (2015) and Jimmy *et al.* (2017) for grain yield per plant.

Diversity analysis

Diversity analysis and Principal component analysis was performed using seventeen yield contributing traits. A total of four main clusters were formed using diversity analysis (Fig. 1) of which, the maximum number of accessions was found in cluster I (39 accessions) as reported by Sinha and Kumaravadivel (2015) and Desmae *et al.* (2016), followed by cluster II and III with 30 accessions. The least number of accessions was reported in cluster IV (9). The germplasms in cluster I had highest mean value whereas the germplasms in cluster IV showed poor mean performance for most of the traits. Thus, it is recommended that the accessions from cluster I and cluster IV can be used for hybridization programme.

Principal component analysis

The main aim of principal component analysis is to reduce the volume of data. It identifies a few or minimum traits that account for majority of diversity observed. Thus, these traits can be emphasized in the breeding programme.

The Principal component analysis (PCA) was performed for seventeen yield contributing traits (Table 2). The PCA extracted seven components which had eigen value of above one. These seven components had eigen value of 3.48, 2.67, 1.91, 1.60, 1.40, 1.14, 1.01, respectively. These components had contributed 20.45 per cent, 15.73 per cent, 11.25 per cent, 9.41 per cent, 8.25 per cent, 6.68 per cent and 5.94 per cent of variance to the total variance. Together they contributed 77.72 per cent of total variance.

The traits days to 50 per cent flowering and days to maturity were associated with principal component 1 (PC 1). Plant height, stem diameter, number of leaves, number of nodes and dry fodder yield per plant were associated with principal component 2 (PC 2). Leaf width, flag leaf

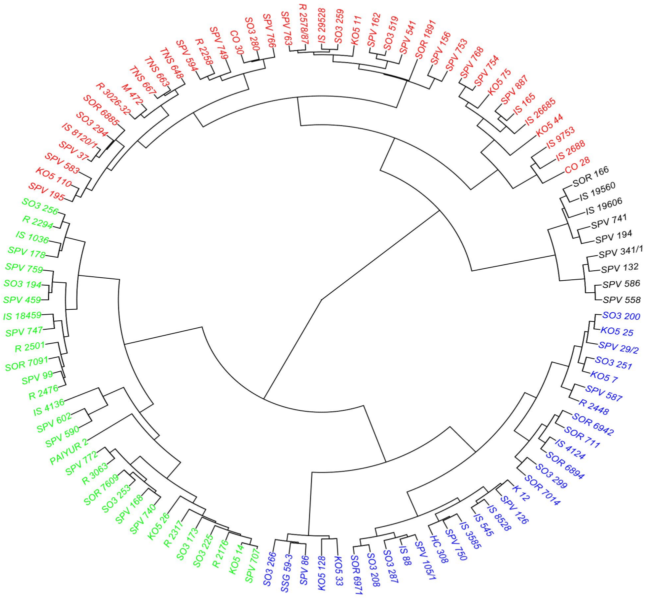

Fig. 1 : Dendrogram displaying the 108 accessions in various groups.

Table 2 : Eigen vectors and scores for first seven components retained from PCA of yield and yield contributing traits.

Variables	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**
Plant height (cm)	-0.204	0.247	-0.208	0.239	-0.226	0.060	-0.421
Stem diameter (cm)	-0.262	0.293	0.096	0.196	0.073	0.102	0.146
Leaf length (cm)	-0.293	0.105	0.093	0.138	-0.168	-0.244	-0.472
Leaf width (cm)	-0.150	-0.017	0.382	0.254	0.132	-0.450	-0.064
Flag leaf length (cm)	-0.359	-0.289	0.116	-0.218	-0.100	0.074	-0.139
Flag leaf breadth (cm)	-0.346	-0.267	0.293	-0.161	0.041	0.039	0.048
Flag leaf area (cm2)	-0.333	-0.299	0.263	-0.255	-0.104	0.120	-0.058
Chlorophyll index	0.092	0.038	0.300	-0.025	-0.510	0.089	0.378
Number of leaves	-0.319	0.408	-0.023	-0.081	0.123	0.206	0.072
Number of nodes	-0.319	0.408	-0.030	-0.081	0.121	0.204	0.081
Panicle length (cm)	-0.069	-0.226	-0.004	0.593	-0.101	-0.082	0.047
Panicle length of branches (cm)	-0.018	-0.043	-0.172	0.124	-0.677	0.227	-0.031
Days to 50 percent flowering	0.296	0.169	0.478	0.054	0.019	0.156	-0.223
Days to maturity	0.296	0.181	0.458	0.038	-0.006	0.177	-0.285
Dry fodder yield per plant (g)	-0.143	0.231	0.215	0.176	-0.135	-0.249	0.502
Hundred seed weight (g)	-0.027	-0.147	0.121	0.277	0.161	0.638	0.036
Grain yield per plant (g)	-0.096	-0.273	-0.061	0.436	0.269	0.171	0.087

breadth, flag leaf area, chlorophyll index, days to 50 per cent flowering, and days to maturity were associated with principal component 3 (PC 3). The traits like plant height, leaf width, panicle length, hundred seed weight and grain yield per plant were associated with principal component 4 (PC 4).

The traits hundred seed weight and grain yield per plant were associated with principal component 5 (PC 5). Number of leaves, number of nodes, panicle length of branches, hundred seed weight was associated with principal component 6 (PC 6). The traits chlorophyll index and dry fodder yield per plant were associated with principal component 7 (PC 7).

The traits *viz.*, days to 50 per cent flowering, days to maturity and hundred seed weight exhibited extensive variation in the population screened and hence it can be used as selection indices for yield improvement in sorghum. This was in similar trend with Desmae *et al.* (2016).

Conclusion

Hence, the traits like grain yield per plant, flag leaf area and panicle length of branches were found to have high phenotypic and genotypic coefficient of variation. Thus, selection for these traits will be effective. To know whether these traits are heritable and fixed, heritability and genetic advance was performed. Based on the above discussion, the traits *viz.*, flag leaf area, panicle length of branches, chlorophyll index, dry fodder yield per plant and grain yield per plant indicates additive gene action and also has high genetic gain. Thus, these traits can be used as selection criteria for yield improvement. As diversity analysis is performed based on mean data, the accessions from cluster I and IV will have extreme values and hence can be used as a parent for hybridization programme.

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