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Elucidation of genetic diversity and principal component analysis in sorghum genotypes for yield and its contributing traits

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Abstract

A total of 112 sorghum lines consisting of grain and dual purpose sorghum was evaluated for six yield contributing characters by principal component analysis for identifying genetic diversity of germplasm and relationship among the individuals. For that, the observations were recorded on 50% flowering, plant height, earhead length, days to maturity, 100 seed weight and grain yield. Among the six traits the highest genetic variation was identified for grain yield with co-efficient of variation (CV) of 50.69% followed by plant height, 100 seed weight and earhead length. Days to maturity has shown the low variation with the CV of 2.69%. Principal component analysis was utilized to identify the variation and to evaluate the relative contribution of various traits for total variability. In the present research, component-I the contribution for 50% flowering and days to maturity which accounted 36.85% of the total variability. Plant height, grain yield and earhead length has contributed 27.61 of the total variability. PC 3 had the contribution for ear head length with 17.06% of the total variability. The total variation of 81.5% was explained by the first three axes for six quantitative characters. Hierarchical cluster analysis classified the 112 sorghum genotypes were clustered in to 3 distinct groups. Hence, the information on grain yield and its component trait were revealed the presence of diverse genotypes that can be utilized for evolving Sorghum varieties with higher grain yield.

Keywords: Sorghum, diversity and PCA

1. Introduction

Sorghum (*Sorghum bicolor* (L.) Monench) is predominant among cereals in the world and ranks fifth in production. It is widely cultivated for protein for many rural people in Asia and Africa and also malt production of non-alcoholic drinks, flour production, animal feed and fodder in semi arid tropics (Agarwal *et al*., 2004; Ajirlou *et al*., 2013; Vinoth *et al*., 2021) [1, 2, 14]. Sorghum is tolerant to high temperature and able to with stand drought conditions. It had highly tolerant to drought and used as fodder crop for semi arid areas compared to Corn (Tabosa *et al*., 1999) [13]. The selection of parents for crossing programme can be made by breeders after studying the genetic diversity available in a crop for introgression of genes by choosing distant parents. The distantly related parents can be chosen for producing improved hybrids that can tolerate biotic and abiotic stresses. For further genetic improvement of sorghum is basic need is to understand the architecture of the crop genotype (Jayaramachandran *et al*., 2011) [9]. Genetic diversity of the crop species is the gift of nature and arises due to geographical separation or due to genetic barriers to cross ability. The use of morphological characters is the most common approach utilized to estimate relationships between genotypes. A better understanding of genetic diversity in sorghum will facilitate crop improvement. Therefore there is a need to evaluate the available accessions for genetic diversity. The main objective of the present study was to assess the range of variation existing among the sorghum accessions and classify them in to clusters based on the similarity features for 6 quantitative characters through principal component Analysis (PCA) also to generate data on the performance of the sorghum genotypes for further evaluation.

2. Materials and Methods

A total of 112 sorghum accessions were collected from different sources and maintained Agricultural Research Station, Kovilpatti were used for this study. This experiment was conducted during rabi 2016 by adopting an augment design. The genotypes were raised in 4 m rows with the spacing of 45 x 15 cm and all the recommended agronomic practices were adopted. For evaluating the genetic variation, the following biometrical observations were recorded for six quantitative traits *viz.*, days to 50% flowering, plant height, earhead length, days to maturity, 100 seed weight and grain yield.

To identify the patterns of variation, the PCA was performed. The principal component with more than one eigen value was selected as proposed by Jeffers (1967) [10]. Clustering the genotypes into similar groups was performed using Ward's hierarchical algorithm based on squared Euclidean distances. The wards method of euclidiean distances was utilized in free diagram. Statistical analysis was accomplished using the software STAR 2.0.

3. Results and Discussion

First order statistical measures viz., mean, range and Coefficient of Variation (CV) % of all the six characters are presented in Table 1. Grain yield recorded the maximum variation of 50.69%, followed by plant height (CV=17.97%), 100 grain weight (CV= 17.81%) and ear head length (CV= 15.4%). Variation for days to maturity was lowest with the CV 2.69%. The genotype TKSV 1006 has taken a longer period of 93 days for 50% flowering while TKSV 1004 has taken a shorter duration than the rest of the genotypes to complete 50% flowering. The overall mean for days to 50% flowering was 74 days with a coefficient of variation of 4.34%. The average plant height of 112 sorghum accessions was 134.08 cm with a CV of 17.97%. The genotype TKSV 1156 was the tallest recorded 200 cm in height whereas the genotype TKSV 1011 (86 cm) was found to be short in stature. The mean plant height of 112 sorghum lines was 134.08 cm.

Table 1: Characteristic means and variation for six biometric characters in 112 sorghum accessions

Characters	Days to 50% flowering	Plant height	Earhead length	Days to maturity	100 grain weight (g)	Grain yield/plant (g)
Mean	73.95	134.08	21.10	118.95	3.20	38.62
Minimum Value	68.00	86.00	14.00	113.00	1.90	6.00
Maximum value	93.00	200.00	30.00	138.00	5.00	90.00
Range	25.00	114.00	16.00	25.00	3.10	84.00
CV%	4.34	17.97	15.40	2.69	17.81	50.69
SD	3.21	24.10	3.25	3.21	0.57	19.58

The trait ear head length had recorded an overall mean of 21.10 cm. The accessions TKSV 1156 was found with the longest ear head of 30.0 cm and the genotype TKSV 1017 exhibited short ear head (14.0 cm). The genotype TKSV 1006 was found to be a late maturing type (138 days) and early maturity was observed in TKSV 1047 (113 days). Over all mean 100 grain weight was 3.2 g. Maximum 100 grain weight was recorded by TKSV 115 (5.0 g), while TKSV 1004 had the minimum (1.9 g).

The mean grain yield of 112 genotypes was found to 38.62 g/plant. The line TKSV 1162 registered a maximum grain yield of 90 g per plant, while the lowest was recorded by TKSV 0808 (6.0 g). The lines expressing diverse phenotypes of grain yield may be used for developing mapping population to identify quantitative trait loci. Among all the traits investigated, plant height and grain yield recorded high mean, wide range and high standard deviation. The statistical analysis of six quantitative traits highlighted the presence of genetic diversity in the accessions.

A scree plot is a line plot of the Eigen values that explained the percentage of variation associated with each principal component in descending order. In accordance with Chatfield and Collins (1980) [5], data were considered in each component with an eigen value of more than 1 because it determines a minimum of 10.0% of the variation so that lesser number of components are considered. Sharma (2001) [12] recorded that Principal Component Analysis described the significance of the cluster that contributes the maximum variability to the total divergence at each axis of differentiation. It was supplemented by Fentry (2004) [6] that PCA further reduces a large set of components to a smaller set of variables and the first component can be expected to account for a large amount of the total variance. Scree plot of the PCA (fig 1) described the first three Eigen values in connection to the total variation in the dataset. The distribution of the six quantitative characters in first two components is described in loading plot (fig 2). The Biplot clearly described the traits plant height, grain yield, ear head length, days to 50% flowering and days to maturity had contributed low variability towards genetic variation.

The principal component approach is constructive in deciding which agronomic traits of crop contribute most to yield, subsequently these agronomic traits should be emphasized in the breeding programme (Jain *et al.*, 2013) [8]. The first three principal components with Eigen values more than 1 contributed about 81.51% of the total variability among the 112 sorghum accessions evaluated for different quantitative traits (Table 2). The remaining three principal components contributed only 18.49% towards the total diversity among the accessions studied. Thus only the first three PCs were considered. In the present study, quantitative traits which contributed more to the first principal component (PC 1) accounted for 36.85% of the total variation. The second and third principal component (PC) explained 27.61% and 17.06% respectively. The first PCA (PC 1) was related to days to 50% flowering and days to maturity. The second and third principal component (PC) explained 27.61% and 17.06% respectively. The important quantitative traits due to variations among the accessions mainly for days to 505 flowering and days to maturity having positive factor loading value while the remaining traits contributed negatively. The second principal component (PC 2) was related to diversity among sorghum genotypes due to plant height, grain yield and earhead length. Similarly, PC 3 expressed positive loading values for variations among Sorghum genotypes resulting from earhead length while negative contributions were shown by the remaining traits. Principal component analysis revealed that out of six components derived, first three explained most of the total variations present in sorghum accessions and aided in identifying important characters that contributed to the maximum divergence. These results are in accordance with the observations made in previous studies of workers (Agarwal *et al*., 2004, Akatwijuka *et al*., 2016) [1, 3].

Table 2: Eigen value and percent of total variation and component matrix for the principal component axes

Principal component	PC1	PC2	PC3
Eigen value	2.211	1.656	1.024
% of variance	36.900	27.600	17.000
Cumulative variance	36.900	64.500	81.500
Days to 50% flowering	0.635	-0.155	-0.249
Plant height	-0.037	0.613	-0.152
Earhead length	0.293	0.442	0.417
Days to maturity	0.635	-0.155	-0.249
1000 grain weight	-0.266	0.100	-0.811
Grain yield	0.191	0.609	-0.144

The scree plot of 112 sorghum genotypes on the basis of first two principal components explained the percentage of variation associated with each principal component by drawing a graph between the eigen values and principal components (fig 3) Eigen values gradually declined from PC 1 to PC 6. The distribution of 112 Sorghum genotypes accounted by different variables from component 1 and 2 was in different groups, which clearly showed the presence of diversity among the accessions of grain sorghum (fig. 2 & fig. 3). The genotypes from the same geographical locations were scattered in various clusters. Ashwini karadi and Kajjidoni. 2019 [4] reported significance of first four principal components in the total variability of different agro morphological traits in sorghum. Kavithamani *et al*., 2019 [11] also reported three Principal components explained about 66.35% of the variability.

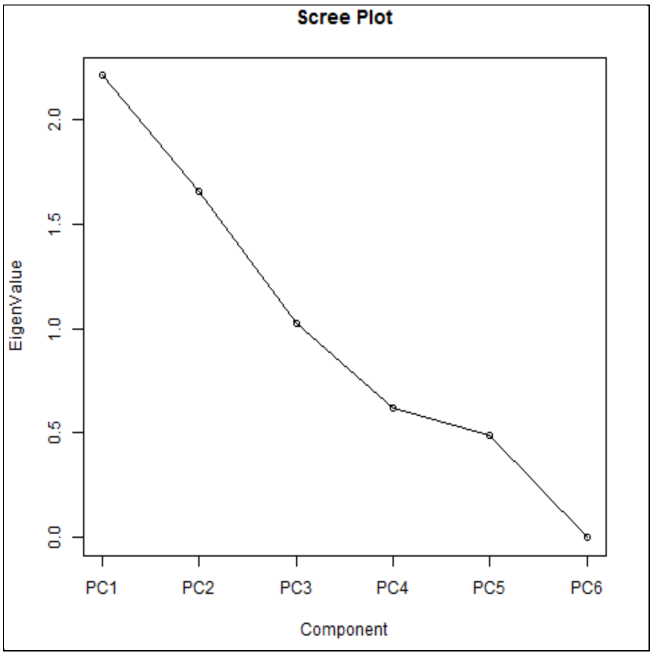

Fig 1: Scree plot showing eigen value and principal components

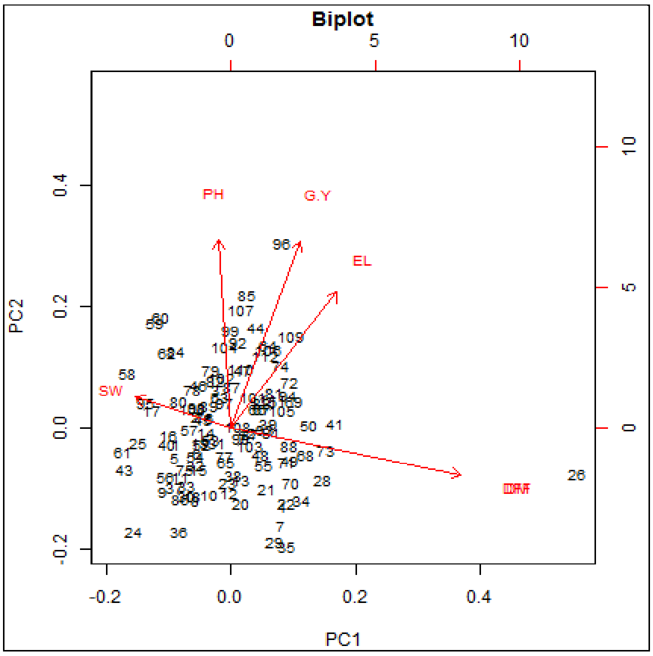

Fig 2: Loading plot of biometric characters on the basis of factor analysis across first two components

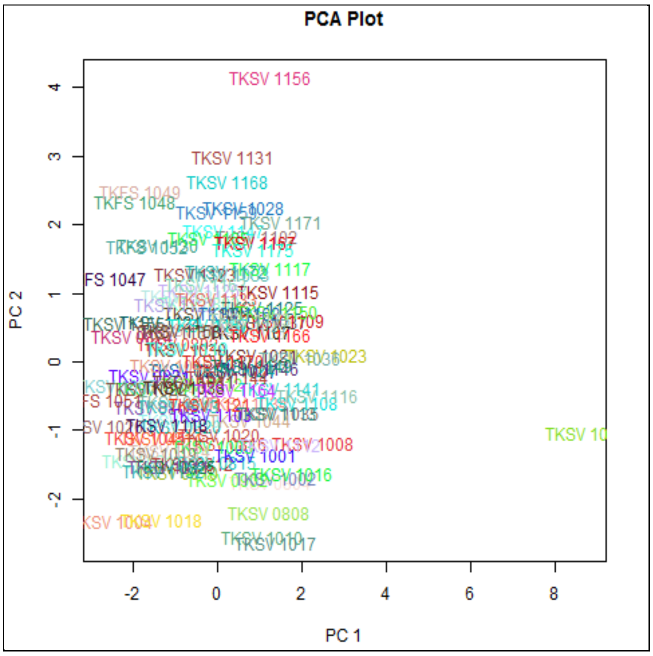

Fig 3: Distribution of genotypes across first two components two components based on PCA

The hierarchical clustering using agglomerative type adopted the Euclidean distance matrix using the method of wards linkage and the dendrogram obtained is depicted as fig 4. The 112 sorghum genotypes were clustered in to three groups. The first cluster (C I) with 68 genotypes is a major cluster with a large number of genotypes, while comparatively fewer genotypes were grouped in C II and C III. The pattern of clustering observed in the genotypes of grain sorghum revealed the presence of wide variability among them. Greater genetic divergence was recorded among sorghum genotypes and also the diversity was found within each region and was scattered with geographical origin utilizing Sudanese sorghum landraces (Grenier *et al*., 2004) [7].

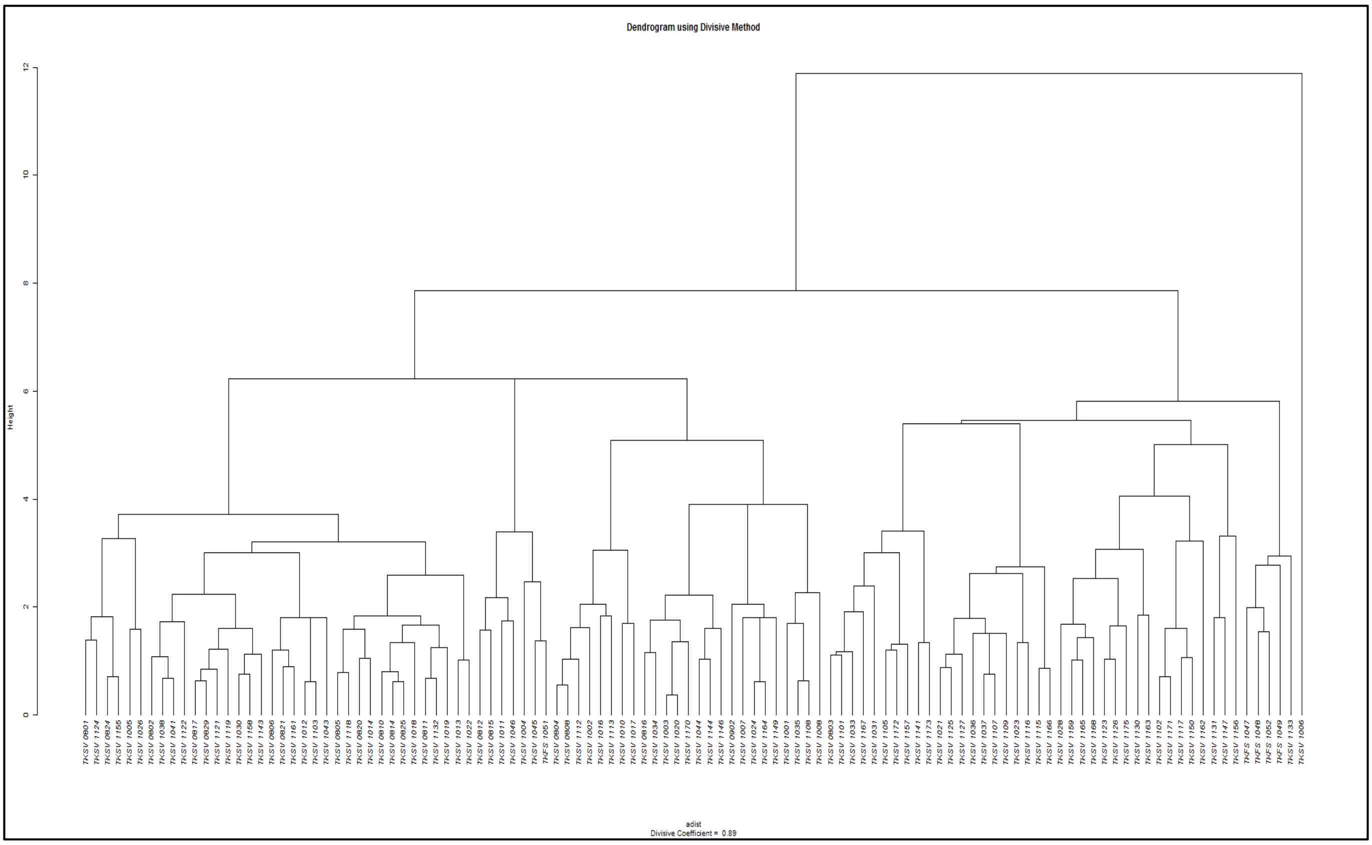

Fig 4: Dendrogram generated by Agglomerative clustering method

Characteristic average of three cluster groups of 112 sorghum genotypes is given in Table 3. The first cluster showed the maximum average for the trait 100 seed weight (3.29 g). The second cluster had the highest average value for grain yield (53.79) and plant height (154.81). The third cluster was with the highest average for the trait days to 50% flowering (93.0), earhead length (28.0) and days to maturity (138.0). On the basis of average of three clusters the significant cluster I had the maximum average for 100 grain weight. Thus the genotypes that come under these clusters may be utilized in the crossing programme as parents. Efficient exploitation of this diversity is helpful in identifying potential sorghum lines for hybrid breeding programme. Crossing between genotypes from diverse clusters will provide segregating sorghum progeny for yield thereby, leading to the development of high yielding sorghum varieties with higher grain yield.

Table 3: Average of three clusters based on Principal Component Analysis

Traits	I	II	III
Days to 50% flowering	73.56	74.12	93.00
Plant height	121.14	154.81	122.00
Earhead length	19.79	23.00	28.00
Days to maturity	118.56	119.12	138.00
100 grain weight	3.29	3.08	2.20
Grain yield	28.87	53.79	50.00

4. Conclusion

In order to identify the genetic diversity of the germplasm and the relationships between the individuals, a total of 112 sorghum lines, including grain and dual-purpose sorghum, were examined for six yield-contributing traits by principal component analysis. Grain yield had the most genetic variance among the six variables, with a co-efficient of variation (CV) of 50.69%. The first three axes for six quantitative parameters explained a total variation of 81.5%. The 112 sorghum genotypes were divided into 3 different groups by hierarchical cluster analysis. The presence of several genotypes that can be used to develop Sorghum varieties with better grain yield was thus disclosed by information on grain yield and its component characteristic.

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