EVALUATION OF GENETIC DIVERGENCE AMONG RABI SORGHUM (*SORGHUM BICOLOR* L. MOENCH) GERMPLASM THROUGH MULTIVARIATE TOOLS

S. Isha Parveen[1], Sk. Sameera[2]*, T. Bhagavatha Priya[3], M. Jyostna Kiranmai[4] and S. Balaji Nayak[5]
[1]Department of Genetics and Plant Breeding, Regional Agricultural Research Station
(Acharya N.G Ranga Agricultural University), Andhra Pradesh), Nandyal Andhra Pradesh, India
[2]Department of Genetics and Plant Breeding, Agricultural Research Station
(Acharya N.G Ranga Agricultural University, Andhra Pradesh), Nellore-524003, Andhra Pradesh, India
[3]Department of Agronomy, Agricultural Research Station
(Acharya N.G Ranga Agricultural University, Andhra Pradesh), Utukur , Andhra Pradesh, India
[4]Department of Agronomy, Regional Agricultural Research Station
(Acharya N.G Ranga Agricultural University, Andhra Pradesh), Nandyal, Andhra Pradesh, India
[5]Department of Soil Science and Agricultural Chemistry, Regional Agricultural Research Station
(Acharya N.G Ranga Agricultural University, Andhra Pradesh), Nandyal, Andhra Pradesh, India
*Corresponding author Email: s.sameera@angrau.ac.in
(Date of Receiving : 01-08-2024; Date of Acceptance : 03-10-2024)

ABSTRACT

Sorghum is an important nutricereal constituting staple diet of the major population in arid and semi-arid region of the country and tolerant to drought and heat. Precise information on the nature and degree of genetic diversity helps the plant breeder to select the parents for targeted hybridization. Principal components approach is very helpful and was analysed with 31 entries in deciding which agronomic traits of crop contributes most to yield the estimation of descriptive statistics of ten quantitative traits indicated the existence of diversity among the genotypes. In the present study, first three Eigen vectors which has eigen values greater than one and cumulatively explained about 73.9 per cent of the total variation among the ten quantitative traits in 31 genotypes of sorghum. Hence PC-I has eigen value 3.22 and accounted for 32.21 % of the variations. This represents an equivalent of five variables viz., final plant population, initial plant population, grain yield, lodging, plant height and indicated that were important contributing variables for the variation among the genotypes. The 31 genotypes were grouped into 5 clusters on the basis of average linkage and dendogram was cut at a distance of 1.50. The cluster 1 has all the genotypes except NJ 2702 (cluster 2), NJ 2710 (cluster 3), CSV 22R (cluster 4) and CSV 29R (cluster 5). The clustering pattern showed that there was significant genetic variability among the sorghum genotypes tested which indicated the presence of excellent opportunity to bring about improvement through hybridizing genotypes from different clusters and assembling desirable traits with higher heterotic potential.

Keywords : Clustering, diversity, Grain yield, Hybridization, Sorghum and Variation.

Introduction

Sorghum (*Sorghum bicolor* (L.) Moench) is the third most important cereal crop grown in the world. India contributes about 16% of the world's sorghum production. Sorghum is tolerant to drought and heat and also genetically suited to hot and dry agro-ecologies where it is difficult to grow other food grain crops. It is an important nutricereal constituting staple diet of the major population in arid and semi-arid

region of the country. It is also used for feed, fodder and for the production of alcoholic beverages. To expand the gain in sorghum productivity we need better breeding strategies that improve the productivity level and to boost the total production. House (1985) noted that cultivated sorghums are highly variable and suggested to enhance the productivity levels of sorghum, as the prior information on the nature and the magnitude of genetic diversity present in breeding material is a pre-requisite. Precise information on the nature and degree of genetic diversity helps the plant breeder to select the parents for targeted hybridization. It provides the raw material from which the desirable alleles for improved agronomic traits of interest can be selected and will be subsequently incorporated into elite lines. Jain and Patel (2016) reported that PCA is a reliable method in identifying few key traits contributing to the largest variation and in predicting the important traits influencing clustering of different cultivars. The purpose of principal component analysis is to reduce the volume of data. Principal components approach is very helpful in deciding which agronomic traits of crop contributes most to yield, subsequently, these agronomic traits must be emphasized in the breeding program. In-order to determine genetic variation, genotype classifications and genetic distance among them, the cluster analysis is done. Cluster analysis identifies and classifies individuals or variables on the basis of the similarity of the characteristics they possess. It seeks to minimize within-group variance and maximize between-group variance. It is also helpful for parental selection in the breeding programme and also for crop modeling. Therefore, the present study was done to evaluate the genetic diversity among sorghum genotypes specifically for grain and fodder yield to select the best genotypes that can be exploited in future sorghum breeding programmes.

Material and Methods

The plant material comprised of 31 elite entries of sorghum including three checks viz., NTJ 5, CSV 22R and CSV 29R pooled under Millets scheme, Regional Agricultural Research Station (RARS), Nandyal, Andhra Pradesh. The trial was grown in randomized block design with two replications during rabi 2020 at RARS, Nandyal (latitude of 15.46° N. longitude of 78.47° E and elevation of 203 M above the Mean Sea Level). The soil of the field was clayey in texture with pH value of 8.0 to 8.3 having good physical and chemical properties (Organic Carbon= 0.34, EC dsm-

= 0.23, N= 180 kg/ha, P_2O_5 = 42.4 kg/ha and K_2O= 312 kg/ha). The experimental unit was a four-row plot of 4.0 m long with row to row and plant to plant distance maintained at 0.45 and 0.15 meters respectively. NPK 80:60:40 fertilizers were applied as half basal dose of nitrogen and full dose of phosphorus and potassium at the time of sowing and half nitrogen applied at knee height stage of the crop. All other recommended agronomical practices were followed to raise a good crop during the season. Data were taken on initial plant population, final plant population, days to 50 % flowering, days to maturity, lodging, plant height (cm), panicle length (cm), grain yield (kg/ha), dry fodder yield (q/ha) and hundred seed weight (gms). The data was subjected to correlation analysis, principal component analysis (PCA) and cluster analysis using IBM statistical packages for social sciences (SPSS) of version 20. Cluster analysis was performed using Average linkage hierarchical clustering while dendrogram was constructed based on Euclidean distances and transformed values by standardizing Z scores.

Results and Discussion

The estimation of descriptive statistics of ten quantitative traits indicated the existence of diversity among the genotypes. Among all the traits investigated, dry fodder yield, grain yield, plant height, initial plant population, final plant population and days to maturity recorded higher variation in mean, range, variance and standard deviation (Table 1).

Knowledge of relationship among yield components is essential for the formulation of breeding programme aimed at achieving the desired combinations of various components of yield. The estimates of correlation coefficients among the different characters indicate the extent and direction of association. The correlation coefficients provide a reliable measure of association among the characters and help to differentiate the vital associations useful in breeding from those of the non-vital ones (Falconer, 1981). In simple terms, correlation is the measure of strength of linear relationship in between the characters. In the present investigation, grain yield recorded highly significant positive correlation with initial plant population and final plant population whereas lodging and plant height has shown significant negative correlation with grain yield at 6% and 9% LOS respectively. Fodder yield recorded highly significant positive correlation with plant height, days to 50% flowering, days to maturity and lodging (Table

2). Such strong positive correlations recorded among the genotypes, suggest that they are heritable and genetically controlled traits which could be transmitted into desired genotypes. The finding of present study was agreed with the Jain *et al.* (2011), Jain and Patel (2012). All the other yield contributing traits were also positively correlated with each other indicated that selection may be done in positive direction based on these traits towards crop improvement program.

The genetic diversity in 31 sorghum genotypes including three checks NTJ 5, CSV 22R and CSV 29R were observed for the seed and fodder yield and their component traits for the selection of high yielding genotypes for further release and further breeding programmes. The PCA grouped the ten quantitative traits in to ten components which accounted for the entire (100%) variability among the studied genotypes. According to Chatfied and Collins (1980), components with an eigen value of < 1 should be eliminated so that fewer components are dealt with. Furthermore, Hair *et al.* (1998) suggested that, eigen values greater than one is considered significant and component loading greater than 0.3 were considered to be meaningful. To estimate this, a scree plot is used. A scree plot is a simple line segment plot that shows the fraction of total variance in the data and it is a plot, in descending order of magnitude, of the eigen values of a correlation matrix. In the present study the Scree plot of the factors shows that the first three eigen values correspond to the whole percentage of the variance in the dataset (Fig. 1). In the present study, first three Eigen vectors which has eigen values greater than one and cumulatively explained about 73.9 per cent of the total variation among the ten quantitative traits in 31 genotypes of sorghum (Table 3). Hence PC-I has eigen value 3.22 and accounted for 32.21 % of the variations. This represents an equivalent of five variables viz., final plant population, initial plant population, grain yield, lodging, plant height and indicated that were important contributing variables for the variation among the genotypes. Genotypes with high PC 1 score therefore would have high level variability of these quantitative traits. Chozin (2007), Mujaju and Chakuya (2008) and Ali *et al.* (2011) reported important contribution of the first PCs in total variability while studying different traits. The second and third PC explained 2.58 and 1.60 eigen values and contributing 25.82% and 15.95% variations, respectively. The second PCA was related to days to 50% flowering, days to maturity, fodder yield, plant height and lodging. In the third PC variation was composed of panicle length, plant height,

hundred seed weight, fodder yield and initial plant population. Overall, the PCA analysis under this study shows that phenotypic markers are useful in genotypes of sorghum and able to identify few key traits that accounted for the largest variability. The present study supported by earlier workers also (Ali *et al.*, 2011 and Akatwijuka *et al.*, 2016).

Kaiser-Meyer-Olkin (KMO) Measure gives information about the adequacy of the data and the barlett test of sphericity shows the suitability of the model. If the KMO value is more than 0.8, then the data can be used for further analysis. In the table 4, as the KMO value is more than 0.5, the data is said to be moderate. Barlett test should be always significant to confirm the suitability of model.

According to Chahal and Gosal (2002), characters with largest absolute value closer to unity within the first principal component influence the clustering more than those with lower absolute value closer to zero. Therefore, in the present study, differentiation of the genotypes into different clusters was because of relatively high contribution of few characters rather than small contribution from each character. The thirty-one genotypes were grouped into five clusters on the basis of average linkage and dendogram was cut at a distance of 1.50 are presented in Fig. 2. The cluster analysis sequestrates genotypes into clusters which exhibit high homogeneity within a cluster and high heterogeneity between clusters. The cluster 1 has all the genotypes except NJ 2702 (cluster 2), NJ 2710 (cluster 3), CSV 22R (cluster 4) and CSV 29R (cluster 5). Distribution pattern of all the genotypes into five clusters showed the presence of considerable genetics diversity among the genotypes for most of the traits under consideration. The clustering pattern showed that there was significant genetic variability among the sorghum genotypes tested that indicated the presence of excellent opportunity to bring about improvement through hybridizing genotypes from different clusters and assemble desirable traits with higher heterotic potential. Thus, the PC analysis, cluster analysis and correlation coefficient in this present set of the experiment provided facilitation in the classification of genotypes and identification of the subset of genotypes having quantitative difference between yield and yield parameters. Various useful correlations and aforementioned information extracted from cluster and PC analysis will be helpful in designing breeding programmes to obtain high yielding genotypes in sorghum for seed as well as fodder yield.

Table 1: Descriptive statistics for ten quantitative traits in 31 genotypes of sorghum

	Mean	Min-Max	Range	Variance	Standard deviation
Initial Plant Population	145.15	123-162.5	39.5	97.90	9.89
Final Plant Population	136.37	112-155	43.0	143.86	11.99
Days to 50% flowering	70.71	59-83	24.0	33.95	5.83
Days to maturity	111.08	103-119	16.0	16.46	4.06
Lodging	0.89	0-15	15.0	10.23	3.20
Plant height	169.21	118-310.5	192.5	1890.96	43.49
Panicle length	21.13	13.4-26.4	13.0	9.32	3.05
Grain yield	4371.9	2888-5592.5	2704.5	701653.54	837.65
Fodder yield	7253.6	4166.5-15625	11458.5	6983989.54	2642.72
100 seed weight	2.81	2.2-3.8	1.6	0.13	0.36

Table 2 : Pearson phenotypic correlation coefficient between ten quantitative traits in sorghum

	Initial PP	Final Plant population	Days to 50% flowering	Days to Maturity	Lodging	Plant height	Panicle length	Grain Yield	Fodder Yield	100 Seed Weight
Initial plant population	1									
Final plant population	0.939** **0.000**	1								
Days to 50% flowering	-0.050 **0.790**	-0.072 **0.699**	1							
Days to maturity	0.109 **0.558**	0.199 **0.283**	0.725** **0.000**	1						
Lodging	-0.339 **0.062**	-0.487** **0.005**	0.283 **0.123**	0.110 **0.556**	1					
Plant height	-0.017 **0.927**	-0.124 **0.507**	0.393* **0.029**	0.276 **0.134**	0.532** **0.002**	1				
Panicle length	-0.124 **0.507**	-0.019 **0.918**	-0.054 **0.773**	0.113 **0.544**	0.057 **0.761**	-0.435* **0.014**	1			
Grain Yield	0.590** **0.000**	0.673** **0.000**	0.033 **0.862**	0.210 **0.256**	-0.338 **0.063**	-0.304 **0.097**	0.093 **0.619**	1		
Fodder Yield	0.010 **0.958**	-0.044 **0.813**	0.582** **0.001**	0.501** **0.004**	0.477** **0.007**	0.851** **0.000**	-0.267 **0.146**	-0.190 **0.306**	1	
100 Seed Weight	0.223 **0.229**	0.239 **0.195**	-0.272 **0.139**	-0.132 **0.478**	-0.036 **0.849**	0.062 **0.741**	-0.086 **0.647**	-0.057 **0.759**	0.179 **0.335**	1

**. Correlation is significant at the 0.01 level (2-tailed).   *. Correlation is significant at the 0.05 level (2-tailed).

Table 3: Eigen vectors and variance of ten quantitative traits in genotypes of sorghum

	PC 1	PC 2	PC 3
Initial Plant Population	0.891	0.032	.272
Final Plant Population	0.961	0.017	.154
Days to 50% flowering	-0.036	0.893	-0.135
Days to maturity	0.230	0.845	-0.191
Lodging	-0.583	0.428	0.179
Plant height	-0.269	0.611	0.651
Panicle length	0.003	-0.036	-0.667
Grain yield	0.804	0.076	-0.245
Fodder yield	-0.150	0.767	0.537
100 seed weight	0.173	-0.246	0.624
Eigenvalue	3.22	2.58	1.60
Proportion %variance	32.21	25.82	15.95
Cumulative %variance	32.21	58.03	73.98

Table 4: KMO and Bartlett's Test

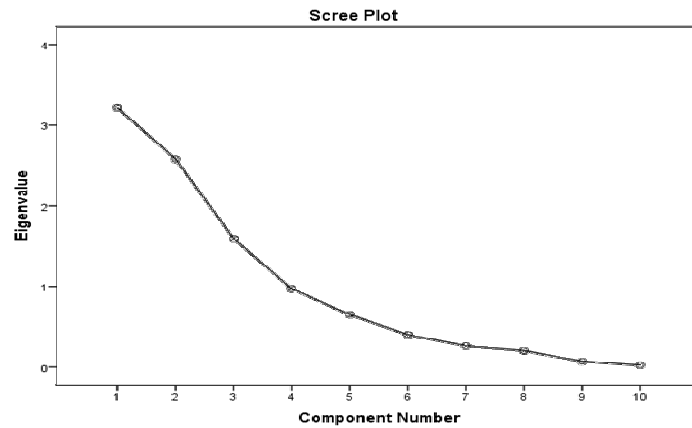| KMO and Bartlett's Test		
Kaiser-Meyer-Olkin Measure of Sampling Adequacy.		0.532
Bartlett's Test of Sphericity	Approx. Chi-Square	205.171
	df	45
	Sig.	0.000

Fig. 1 : Scree plot of factor analysis of 31 genotypes of sorghum between Eigen values and the component number.
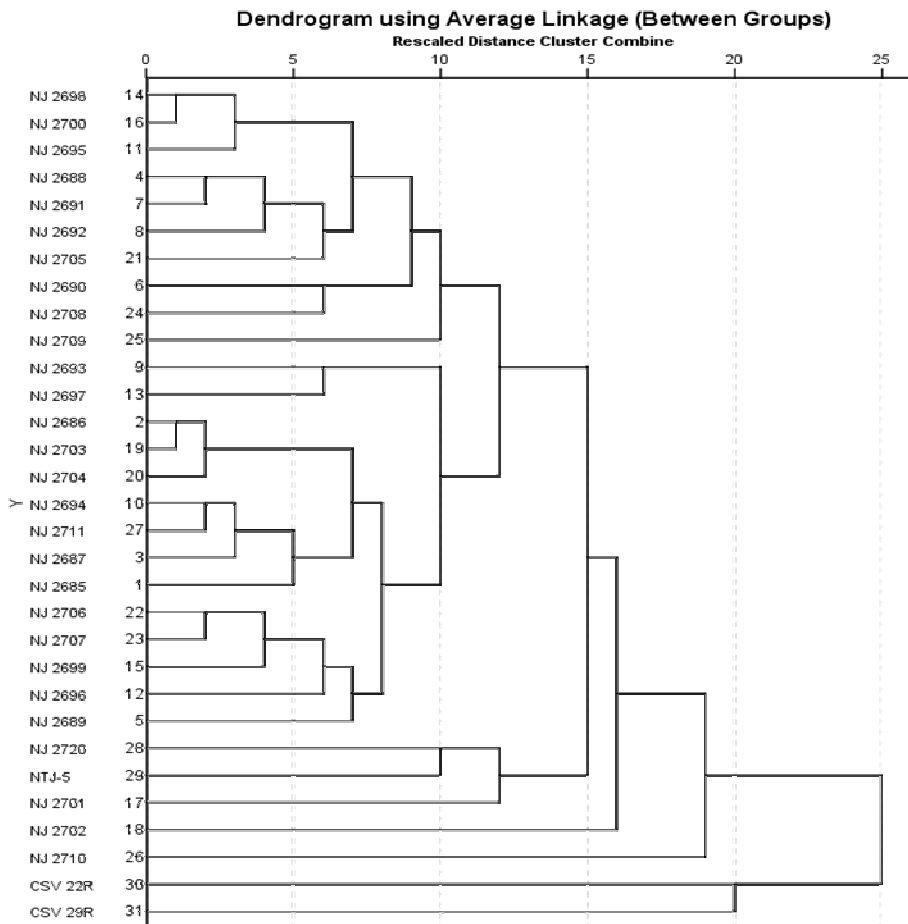

Fig. 2: The dendrogram of sorghum genotypes resulting from cluster analysis using average linkage (between groups) method.

Acknowledgement

I would like to extend my gratitude to the research team for their collaborative efforts in collection and analysis of data. Their expertise has greatly benefited the study. The authors sincerely acknowledge the Acharya NG Ranga Agricultural University for the support rendered in conduct of the research work.

References

Akatwijuka, R., Rubaihayo, P.R. and Odong, T.L. (2016). Genetic diversity among sorghum landraces of southwestern highlands of Uganda. *African Crop Sci. J.,* **24**, 179-190.

Ali, M.A., Jabran, K., Awan, S.I., Abbas, A., Ehsanullah, Z.M., Acet, T., Farooq, J. and Rehman, A. (2011). Morphophysiological diversity and its implications for improving drought tolerance in grain sorghum at different growth stages. *Australian J. Crop Sci.,* **5**, 311-320.

Chahal, G.S. and Gosal, S.S. (2002). Principles and Procedures of Plant Breeding, Biotechnology and Conventional Approaches. Narosa Publishing House, New Delhi.

Chatfield, C. and Collins, A. (1980). Introduction to multivariate analysis. Chapman and Hall.

Chozin, M. (2007). Characterization of sorghum accessions and choice of parents for hybridization. *J. Akta Agri. Edisi Khusus,* **2**, 227-232.

Falconer, D.S. (1981). Introduction to Quantitative Genetics. Second edition. Longman, New york.

Hair, J.F., Tatham, R.L., Andrson, R.E. and Black, W. (1998). Multivariate data analysis. 5th Edn. Prentice-Hall International Inc., London, U.K., ISBN-13, 978-0138948580.

House, L.R (1985). A Guide to Sorghum Breeding. 2nd edition. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, India. 206pp.

Jain, S.K. and Patel, P.R. (2012). Genetic variability in land races of forage Sorghum {*Sorghum bicolor* (L) Moench} collected from different geographical origin of India. *Int. J. Agri. Sci.,* **4**, 182-185

Jain, S.K. and Patel, P.R. (2016). Principal component and cluster analysis in sorghum (*Sorghum bicolor* (l.) Moench). *Forage Res.,* **42**, 90-95.

Jain, S.K., Elangovan, M. and Patel, P.R. (2011). Variation and association among fodder yield and other traits in germplasm of forage sorghum (*Sorghum bicolor* (L.).

Mujaju, C. and Chakuya, E. (2008). Morphological variation of sorghum landrace accessions on-farm in Semiarid areas of Zimbabwe. *Int. J. Botany,* **4**, 376-382.