



## Assessment of Genetic Diversity in Sorghum (*Sorghum bicolor* (L.) Moench) Genotypes using Principal Components and Cluster Analysis

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### Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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### ABSTRACT

**Aims:** Understanding and using the genetic variation in sorghum genotypes is crucial for enhancing the crop because sorghum is a significant grain yield crop in worldwide. Selective breeding will be made possible by a thorough understanding of the genetic diversity among the genotypes. So, it will soon be possible to profile the genetic diversity of sorghum. In the current study, the genetic diversity of 28 sorghum genotypes was examined using 10 quantitative characters.

**Study Design:** Randomized block design (RBD) with four replications.

**Place and Duration of Study:** Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India. Between February 2022 and May 2022.

**Methodology:** The descriptive statistical analysis, analysis of variance (ANOVA) and correlation analysis were carried out for each of the 10 quantitative characters. Using principal component analysis (PCA), the proportion of each trait's contribution to overall genetic variation was looked at. Plotting the first two Principal components in opposition to one another allowed the identification of patterns of variability among genotypes and characteristics. Using the Ward's linkage approach, hierarchical clustering was carried out on the Euclidean distance matrix.

**Results:** Descriptive statistics and analysis of variance (ANOVA) shows the significant genetic variability inherent in the sorghum genotype at 1% level of significance. Correlation revealed the connection between panicle width and 1000 seed weight to grain yield per plant was quite favorable and significant. The Scree plot of the variables gives that the first three Principal components (PC), which have eigenvalues greater than one, collectively explained about 74.15% of the total variation. By Biplot, ICSB 541, ICSV 15013, ICSB 52, ICSB 24001 and Macia show higher value of Panicle width, 1000 Seed weight and Grain yield per plant. B35 has considerably longer and wider leaves. By Cluster analysis, cluster II is important which had the greatest mean values for panicle width, 1000 seed weight and Grain yield per plant. Cluster II and III had the maximum intercluster distance (4.43).

**Conclusion:** Based on the quantitative character data, the genotypes ICSB 541 and ICSV 15013 were shown to be superior for earliness and high yield for grain yield in this study. Therefore, in order to produce better types, these genotypes should be utilized in subsequent breeding programmes.

*Keywords: Pearson coefficient; biplot; ward's linkage; dendrogram.*

## 1. INTRODUCTION

Sorghum (*Sorghum bicolor* (L.). Moench), a C4 cereal grass that is a member of the Gramineae family, is widely utilized as a crop for food, feed, fiber, and bioenergy. Sorghum is similar to maize in terms of its close composition, amino acid concentration, and nutritional value. Sorghum typically contains a little lower gross, digestible, and metabolizable energy, though, because to its decreased fat content [1]. The top sorghum-producing nations, according to the Food and Agriculture Organization (FAO), have been the United States, Nigeria, India, Mexico, and Argentina [2].

The USDA estimates that the world's sorghum acreage will be 40.97 million hectares (101.23 million acres) and its production will be 59.76 million tonnes in 2020–21. The corresponding estimates for India were 4.80 million hectares (11.86 lakh acres) and 4.40 million tonnes. India is sixth in the world in terms of output and third in terms of sorghum area. As of the 12th of August 2020, India's acreage planted with jowar in 2020–21 was 14.53 lakh hectares, down from 14.56 lakh hectares in 2019–20. Rajasthan led all other states in area and production with 5.75 lakh ha, followed by Maharashtra with 2.67 lakh ha, Uttar Pradesh with 2.08 lakh ha, Madhya Pradesh with 1.38 lakh ha, and Tamil Nadu with 0.74 lakh ha [3].

Due to its neutral flavor and color, low allergenicity, and capacity to grow in drought-like circumstances, sorghum is considered as an alluring raw material for wheat and gluten free products. After maize, rice, wheat, and barley, sorghum is the fifth-most significant cereal crop in the world (FAO/UN, 2012). Sorghum can

withstand heat and drought and is genetically adapted to hot, dry agro-ecologies where it is challenging to cultivate other food grains. Better breeding techniques that increase productivity and increase overall production are required to further the progress in sorghum productivity [4].

Leland R. House (1985) pointed out that cultivated sorghums are widely heterogeneous and advised that prior knowledge of the kind and degree of genetic variety available in breeding material is a prerequisite to improving the production efficiency of sorghum [5]. Plant breeders can choose the parents for selective hybridization with the use of specific information on the type and level of genetic variability. It offers the starting points from which it is possible to choose desirable alleles for enhanced agronomic qualities of interest, which are then included into elite lines.

Multivariate approaches are commonly used in the statistical technique of categorization because they are widely used to summarize and describe the inherent disagreement between genotypes. The two most crucial multivariate analysis techniques are Principal Component Analysis (PCA) and Cluster analysis [6]. PCA is particularly useful in identifying the crop agronomic traits that contribute most to yield; as a result, the breeding programme should place more emphasis on these agronomic traits [7]. Using cluster analysis, it is possible to categorize different genotypes of things based on how similar their attributes appear. It intends to boost between-group variance while limiting within-group variance. Additionally, it is useful for crop modelling and parental selection in breeding programmes [8].

The main goal of this study was to identify the range of variation among genotypes of sorghum in general, group them according to similarities in the quantitative character traits under investigation, and produce data on their performance for plant breeders to use in further assessing the genotype in question.

## 2. MATERIALS AND METHODS

Twenty-eight sorghum genotypes were received from the International Crop Research Institute for Semi-Arid Tropics (ICRISAT), India, which were raised at TNAU in Coimbatore, Tamil Nadu, in a Randomized block design (RBD) with four replications for one season (February 2022). Each genotype was raised in a single solid row that was 2 meters long with row spacing 45 cm. Throughout the whole crop time, all of the advised agronomic packages of operations, including irrigation, fertilizer applications, and crop protection management, were Done. Six plants were randomly selected for each replication, and observations were made on ten quantitative traits. The traits measured were plant height (PH) in cm, number of leaves per plant (NOL), leaf length (LL) in cm, leaf width (LW) in cm, panicle length (PL) in cm, panicle width (PW) in cm, 1000 seeds weight (SW) in grams, grain yield per plant (GYPP) in grams, days to 50% flowering (DFL), and days to maturity (DMY).

The genetic diversity among the genotypes was evaluated statistically using the mean values. Because of different qualities were evaluated on very different scales, the data were first adjusted to zero mean and constant variance before analysis. For each of the ten quantitative data points, the descriptive statistical analysis, analysis of variance (ANOVA), and correlation analysis was performed [9]. The percentage of each trait's contribution to overall genetic variation was examined using principal component (PCA) analysis. The patterns of variability among genotypes and features were identified by plotting the first two Principal components against one another. Using the Ward's linkage approach, hierarchical clustering was carried out on the Euclidean distance matrix [10]. The RStudio programme, version 4.1.1, was used to conduct these analyses.

## 3. RESULTS AND DISCUSSION

### 3.1 Descriptive Statistics

The morphological heterogeneity among the sorghum genotypes was revealed by the

descriptive statistics for ten quantitative features given in Table 1, which opens the door for improvement through hybridization and selection. The coefficient of variation (CV) for panicle width (20.27%), leaf width (22.51%), plant height (23.15%) were all rather high, indicating vulnerability to environmental fluctuation impacting their expression to some extent. The increased grain yield per plant (73.1 g) was attained by ICSB 541. B 35 clearly shows a taller plant (320 cm) than the others. The early maturing genotype is ICSV 15013, and the late maturing genotype is ICSR 89016.

### 3.2 Analysis of Variance (ANOVA)

The analysis of variance (ANOVA) for the Randomized block design (RBD) for all 10 quantitative features is given in Table 2, showing the significant genetic variability inherent in the sorghum genotype and not significant within Genotype (Replication).

### 3.3 Correlation Analysis

Ten quantitative features were utilized to characterize the 28 sorghum Genotype, and their correlation coefficients are shown in Table 3 with significant values. The connection between panicle width and 1000 seed weight to grain yield per plant was quite favorable and significant [11]. Days to 50% flowering and Days to maturity was negatively and significantly correlated with Grain yield per plant that shows early maturing has more grain yield. These findings make it clear that these characteristics are related to grain yield and have an association with one another. As a result, selection for any of these traits that contribute to grain production will ultimately result in an increase in all of the other traits. The results of this study were in agreement with those of Jain [12] and [13].

### 3.4 Principal Component Analysis

PCA is crucial in the analysis of multivariate data reduction techniques and aids in the selection of principal components that account for the most variation. The number of variables being analyzed and the number of components being extracted are equal. One can anticipate that a significant portion of the total variation will be accounted by the first component. Variation is getting reduced in succeeding principal components (PC). Eigenvalues greater than 1 that account for at least 10% of variation were taken into consideration, as advised by Brejda et al. [14]. The Scree plot of the variables in the

**Table 1. Descriptive statistics of sorghum Genotypes for Quantitative characters**

	PH	NOL	LL	LW	PL	PW	SW	GYPP	DFL	DMY
Minimum	129.4	9	54.7	4.9	18.4	2.8	33.5	38.2	47	91
Maximum	320.0	14	89.2	11.8	34.7	5.9	46.3	73.7	58	111
Range	190.7	5	34.5	7.0	16.3	3.1	12.8	35.5	11	20
Mean	191.7	10.9	70.2	8.0	27.4	4.0	39.4	51.3	52.1	99.8
Standard Deviation	44.38	1.21	9.79	1.80	4.06	0.81	3.54	7.55	2.77	5.63
Coefficient of Variation	23.15	11.12	13.95	22.51	14.84	20.27	9.01	14.72	5.33	5.64

PH - Plant height, NOL - Number of leaves per plant, LL - Leaf length, LW - Leaf width, PL - Panicle length, PW - Panicle width, SW - 1000 seeds weight, GYPP - Grain yield per plant, DFL - Days to 50% flowering, DMY - Days to maturity

**Table 2. ANOVA (Mean Squares) for Quantitative characters of Sorghum Genotypes**

Source of variation	df	PH	NOL	LL	LW	PL	PW	SW	GYPP	DFL	DMY
Genotype	27	7876.79**	6.18**	383.63**	13.01**	66.11**	2.63**	49.64**	228.28**	30.37**	131.79**
Replication	3	126.99 <sup>NS</sup>	0.06 <sup>NS</sup>	17.15 <sup>NS</sup>	0.25 <sup>NS</sup>	2.47 <sup>NS</sup>	0.06 <sup>NS</sup>	5.32 <sup>NS</sup>	8.74 <sup>NS</sup>	9.52 <sup>NS</sup>	33.51 <sup>NS</sup>
Error	81	57.89	0.28	8.41	0.11	1.36	0.03	2.76	5.05	4.93	17.76
Total	111										

\*\*  $P < 0.01$ , \*  $P < 0.05$ , <sup>NS</sup> – Not significant, PH - Plant height, NOL - Number of leaves per plant, LL - Leaf length, LW - Leaf width, PL - Panicle length, PW - Panicle width, SW - 1000 seeds weight, GYPP - Grain yield per plant, DFL - Days to 50% flowering, DMY - Days to maturity

**Table 3. Pearson correlation coefficient between ten quantitative traits in sorghum Genotypes**

	PH	NOL	LL	LW	PL	PW	SW	GYPP	DFL	DMY
PH	1.00									
NOL	0.12	1.00								
LL	0.43*	0.45*	1.00							
LW	0.33	0.3	0.81	1.00						
PL	-0.29	0.3	0.38	0.23	1.00					
PW	-0.01	-0.08	0.22	0.42*	-0.09	1.00				
SW	-0.07	-0.09	-0.23	-0.1	-0.24	0.44*	1.00			
GYPP	-0.24	-0.06	-0.31	-0.09	-0.24	0.43*	0.77*	1.00		
DFL	-0.02	0.07	0.14	0.06	0.14	-0.49*	-0.73*	-0.62*	1.00	
DMY	0.08	0.07	0.25	0.13	0.24	-0.45*	-0.65*	-0.6*	0.91*	1.00

\*\*  $P < 0.01$ , \*  $P < 0.05$ , <sup>NS</sup> – Not significant, PH - Plant height, NOL - Number of leaves per plant, LL - Leaf length, LW - Leaf width, PL - Panicle length, PW - Panicle width, SW - 1000 seeds weight, GYPP - Grain yield per plant, DFL - Days to 50% flowering, DMY - Days to maturity

**Table 4. Eigenvalue, Eigenvectors and variance of 10 quantitative traits in genotypes of sorghum**

	<b>PC1</b>	<b>PC2</b>	<b>PC3</b>	<b>PC4</b>	<b>PC5</b>	<b>PC6</b>	<b>PC7</b>	<b>PC8</b>	<b>PC9</b>	<b>PC10</b>
PH	0.099	-0.272	0.671	-0.301	0.195	-0.306	0.207	-0.399	-0.156	0.132
NOL	0.136	-0.307	-0.278	-0.71	-0.348	0.359	0.195	-0.01	-0.115	-0.067
LL	0.239	-0.541	0.008	0.031	0.073	-0.113	-0.071	0.252	0.741	0.116
LW	0.138	-0.557	0.039	0.266	-0.157	-0.032	-0.517	0.123	-0.524	-0.122
PL	0.201	-0.155	-0.67	0.034	0.415	-0.384	0.161	-0.297	-0.178	0.143
PW	-0.265	-0.378	0.002	0.512	-0.099	0.375	0.575	-0.205	-0.026	0.038
SW	-0.444	-0.108	-0.033	-0.104	-0.187	-0.525	0.315	0.57	-0.174	0.119
GYPP	-0.431	-0.06	-0.144	-0.024	-0.495	-0.283	-0.307	-0.551	0.251	0.063
DFL	0.447	0.183	0.027	0.167	-0.442	-0.025	0.075	0.025	-0.093	0.726
DMY	0.449	0.113	0.023	0.179	-0.392	-0.345	0.302	-0.059	0.062	-0.618
eigenvalue	3.703	2.388	1.324	0.915	0.623	0.429	0.256	0.184	0.120	0.057
Variability %	37.031	23.885	13.242	9.146	6.232	4.295	2.563	1.844	1.195	0.568
Cumulative %	37.031	60.915	74.157	83.303	89.535	93.830	96.392	98.237	99.432	100.000

*PH - Plant height, NOL - Number of leaves per plant, LL - Leaf length, LW - Leaf width, PL - Panicle length, PW - Panicle width, SW - 1000 seeds weight, GYPP - Grain yield per plant, DFL - Days to 50% flowering, DMY - Days to maturity*

current study shown in Table 4, reveals that the first three Eigenvectors, which have eigenvalues greater than one, collectively explained about 74.15% of the total variation among the 10 quantitative characters in 28 genotypes of sorghum.

Since PC1 accounted for 37.03 percent of the variances, its eigenvalue is 3.7. This is the equivalent of four different variables, namely 1000 seeds weight, Grain yield per plant, Days to maturity and Day to 50% flowering and it shows that these were significant contributing factors for the variance across genotypes. As a result, genotypes with high PC1 scores would show considerable levels of variation in these quantitative traits. When examining several features, Mujaju [15] discovered a significant contribution from the first PCs to overall variability. The PC2 and PC3 with 2.3 and 1.3 eigenvalues and contributing 23.88% and 13.24% variations, respectively. PC2 is associated with leaf length and leaf width, while PC3 variation was completely fabricated of plant height and number of leaves.

The genotypes with quantitative variable that could be explained by the first two dimensions were separated by the biplot. As a result, a breeder may easily estimate the gap between genotypes and choose the best genotypes based on the many characteristics that are condensed

into the two main principal components and assessed simultaneously. Jain [12] also employed biplot analysis to estimate the genetic diversity in sorghum; in this case, a high level of genetic diversity was seen since the genotypes stayed dispersed across the four quadrants according to [13]. The genotype's arrow direction and location could be used to predict how well a genotype performed for any trait according to [16].

Genotypes ICSB 541, ICSV 15013, ICSB 52, ICSB 24001 and Macia present in left bottom quadrant show higher value of panicle width, 1000 seed weight and grain yield per plant. B35 has considerably longer and wider leaves. Genotypes present in top right quadrant are late maturing, as their Days to maturity and Days to 50% flowering are high. Similarly, genotypes present in left bottom quadrant are early maturing, as they are present opposite to top right quadrant.

The results illustrate that PC analysis can be useful in assessing sorghum genotypes and able to highlight important features that accounted for the greatest variability. The current study is backed up by other studies as well, including Akatwijuka et al. [17]. Both Sinha and Kumaravadivel [18] and Makanda [19] discovered considerable variations among many morphological features in sorghum.

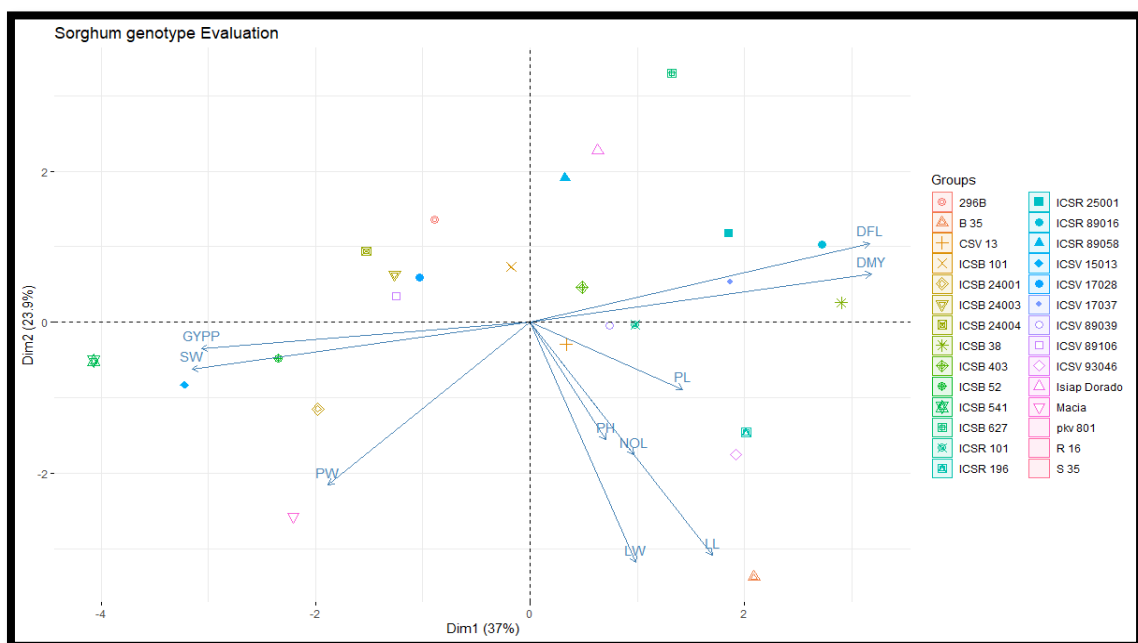


Fig. 1. Biplot of sorghum Genotypes based on ten quantitative traits

### 3.5 Cluster Analysis

The dendrogram of the hierarchical clustering algorithm, which used Ward's linkage approach on the Euclidean distance, is displayed in Fig. 3. Three clusters were formed by the 28 sorghum genotypes. Table 5 lists the genotype counts for each cluster, with clusters I and III having the most genotypes (12 genotypes each), and cluster II having the fewest (4 genotypes).

The cluster mean of the three cluster groups for 28 sorghum genotypes were presented in Table 6. Cluster II had the highest mean value for panicle width (4.37 cm), 1000 seed weight (42.13 g) and grain yield per plant (56.35 g) and also lowest mean value for days to maturity (94.58) and days to 50% flowering (49.50). Cluster III had highest mean value for plant height (247.62 cm), number of leaves (12.00), leaf length (87.12 cm), leaf width (10.86 cm) and panicle length (30.03 cm). Cluster I showed highest mean value

for Days to 50% flowering (54.25). As per the cluster means, the important cluster is cluster II which had the greatest mean values for panicle width, 1000 seed weight and Grain yield per plant. The genotypes associated with these clusters may therefore be used as the parental in a breeding programme according to [18].

Table 7 shows that the Cluster II and III had the maximum intercluster distance (4.43), and if those genotypes were used in a hybridization program, they might produce a wide range of variability in segregating generations. Cluster I and II had the smallest observed intercluster distance (3.16). Clusters II and III display the greatest (2.65) and smallest (1.72) intracluster distances, respectively. For the purpose of choosing the type of cluster for further selection and the parents of hybridization, the clusters that contributed the most to the divergence were given greater weight.

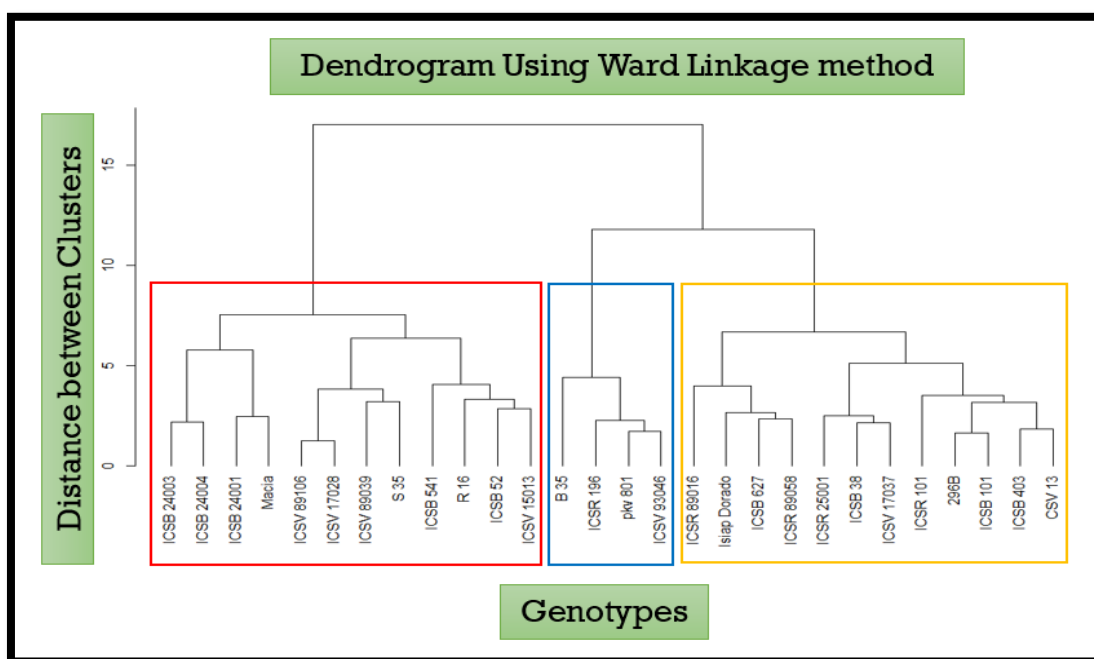


Fig. 2. Dendrogram of 28 sorghum genotypes based on ten quantitative traits

Table 5. Cluster means of three cluster groups of sorghum genotypes

Cluster	Number of Genotypes	Name of Genotypes
I	12	ICSB 24003, ICSB 24004, ICSB 24001, Macia, ICSV 89106, ICSV 7028, ICSV 89039, S 35, ICSB 541, R 16, ICSB 52, ICSV 15013
II	4	B 35, ICSR 196, pkv 801, ICSV 93046
III	12	ICSR 89016, isiap Dorado, ICSB 627, ICSR 89058, ICSR 25001, ICSB 38, ICSV 17037, ICSR 101, 296B, ICSB 101, ICSB 403, CSV 13

**Table 6. Characteristic means of three cluster groups of sorghum genotypes**

Cluster	PH	NOL	LL	LW	PL	PW	SW	GYPP	DFL	DMY
I	171.60	10.67	66.66	7.41	27.90	3.53	37.49	48.15	54.25	103.58
II	193.08	10.83	68.03	7.67	25.96	4.37	42.13	56.35	49.50	94.58
III	247.62	12.00	87.12	10.86	30.03	4.15	36.63	45.57	53.25	104.25

*PH - Plant height, NOL - Number of leaves per plant, LL - Leaf length, LW - Leaf width, PL - Panicle length, PW - Panicle width, SW - 1000 seeds weight, GYPP - Grain yield per plant, DFL - Days to 50% flowering, DMY - Days to maturity*

**Table 7. Intercluster and Intracluster distances among sorghum genotypes**

Intercluster Distance			
	Cluster I	Cluster II	Cluster III
Cluster I	0		
Cluster II	3.16	0	
Cluster III	3.65	4.43	0
Intracluster Distance			
	Cluster I	Cluster II	Cluster III
	2.21	2.65	1.72

#### 4. CONCLUSION

This study provides evidence that quantitative features can be used to assess the genetic diversity at an early stage. studies of correlation clearly demonstrated that variables such as panicle width and 1000 seed weight were considerably and positively associated with grain yield per plant, while days to 50% flowering and days to maturity were significantly and adversely connected. ANOVA demonstrates that significant differences between genotypes were discovered, and both PCA and cluster analysis can be useful in identifying genotypes that call for additional investigation. PCA suggested that ICSB 541, ICSV 15013, ICSB 52, ICSB 24001 and Macia had higher value of Panicle width, 1000 Seed weight, Grain yield per plant and early maturing whereas Cluster analysis identified B 35, ICSR 196, pkv 801 and ICSV 93046 genotypes with same specification as before. But PCA and cluster analysis agree on the majority of features. Therefore, choosing parents must be based on the greater intercluster distance and the better mean yield and its component performance. The genotypes ICSB 541 and ICSV 15013 were discovered to be superior for earliness and high yield for grain yield based on the quantitative character data. Therefore, these genotypes ought to be used in subsequent breeding programmes to create better kinds.

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#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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