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ASSESSMENT OF GENETIC DIVERSITY BY USING PRINCIPAL COMPONENT ANALYSIS IN FINGER MILLET (*Eluesine coracana L.* Gaertn)

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ABSTRACT

An experiment was conducted with 15 Finger millet genotypes to assess the heritable diversity among the parent lines during Kharif 2015. First three principal components exhibited more than one eigen values and accounted for 77.20 percent of total variation, comprised of 40.87 (PC 1), 21.88 (PC 2), 14.45 (PC 3) and 11.68 (PC 4). DHFM 4-9 and PR 202 scored maximum in PCA 1 and PCA 2, respectively. On the basis of Ward's linkage cluster analysis, four clusters were formed to identify relative genetic closeness among test genotypes. Cluster II harboured maximum of five genotypes fallowed by Cluster I with four genotypes, Cluster III and Cluster IV with three genotypes each. Combined analysis of principal components showed scattered position of genotypes across the plot which indicated that accessions have sufficient genetic diversity. Genotypes PR 202, DHFM 4-9, VL 380 and VR 708 had maximum distance from other genotypes were found to be more divergent and can be utilized for future breeding programmes. In principal component analysis, first three principal components with eigen value more than one contributed 77.00% towards the total variability. PC1 contributed maximum towards the total variability (40.874), where Characters viz., days to maturity, days to 50% flowering, straw yield per plot and number of fingers per ear showed maximum lodging values towards total divergence in PC 1.

Key words : *Genetic diveristy, vector, cluster, finger millet.*

Finger millet (*Eleusine coracana* (L.) Gaertn.) is one of the most important small millets grown in eastern and southern Africa. It serves as a subsistence and food security crop that is especially important for its nutritive and cultural value. Finger millet nutritionally superior to rice and wheat, which provides proteins, minerals and vitamins to the poorest of the poor community, where the need for such ingredients is the high. It is an important food crop in traditional low input cereal-based farming systems in Africa, and is of particular importance in upland areas of and It is an important food crop in traditional low input cereal-based farming systems in Africa, and is of particular importance in upland areas of eastern Africa, where it commands a high market price compared with other cereals Finger millet has also a high-yielding potential though yields are variable (compared to other cereals) but are generally good and needs improvement.

In any crop, germplasm resource not only serves as a valuable source of useful genes but also provides scope for building up a basic population of wide genetic variability. Bringing improvement over existing crop varieties is a continuous process in plant breeding. To achieve this objective, the breeder has to identify diverse parents having high genetic variability for combining desirable characters. Therefore, knowledge of sound genetic diversity is essential for undertaking any recombination breeding program. In earlier days, geographical diversity was considered as a measure of genetic diversity but recently it is observed that genetic materials from same eco geographic origin also possess diverse genetic makeup and it is not uncommon that the genetic materials of different eco geographic origin possess similar genetic architecture due to free and easy material transfer facilities. The usefulness of multivariate analysis for the study of morphologically complex individual and for measuring the degree of divergence between biological populations has been shown in different fields of research. Multivariate statistical techniques which simultaneously analyze multiple measurements on each individual under investigation are widely used in analysis of genetic diversity irrespective of whether it is morphological, biochemical or molecular marker-based and subsequently, classification of germplasm collections. Among the multivariate techniques, principal component analysis (PCA) and cluster analysis had been shown to be very useful in selecting genotypes for breeding program that meet the objective of a plant breeder (1). PCA may be used to reveal patterns and eliminate redundancy in data sets (2) as morphological and physiological variations routinely occur in crop species. Cluster analysis is commonly used to study genetic diversity and for forming core subset for grouping accessions with similar characteristic into one homogenous category. Clustering is also used to summarize information on relationships between objects by grouping similar units so that the relationship may be easily understood and communicated. Multivariate analysis has been used frequently for genetic diversity

Table-1: Eigen values, proportion of total variance represented by first four principal components, cumulative per cent variance and component loading of different characters in Finger millet (*Eluesine coracana* L. Gaertn).

	PC 1	PC 2	PC 3	PC 4
Eigene Value (Root)	3.270	1.750	1.156	0.935
Expression of percentage variance	40.874	21.880	14.453	11.681
Expression of cumulative variance	40.874	62.754	77.207	88.888
Plant Height (cm)	0.280	0.290	0.093	0.715
Number of productive tillers/plant	-0.066	0.206	0.714	-0.454
Number of fingers/ Ear	-0.353	-0.181	0.481	0.443
Main Ear Length (cm)	0.251	-0.498	0.387	-0.026
Days to 50% Flowering	0.527	0.019	0.194	0.111
Days to Maturity	0.536	0.057	0.131	-0.045
Straw Yield/ Plot (kg)	-0.375	0.400	0.215	0.191
Grain Yield/ Plot (kg)	-0.156	-0.655	-0.013	0.187

Table-2 : PCA scores of 15 genotypes of Finger millet (*Eluesine coracana* L. Gaertn).

Genotype	PCA 1 X-Vector	PCA 2 Y-Vector	PCA 3 Z-Vector
KMR 214	51.546	2.591	23.006
VR 1081	53.871	-1.208	23.328
VL 386	45.121	-1.303	23.996
DHFM 9-5	55.774	3.719	26.165
VL 352	42.274	2.057	21.790
GPU 67	56.546	3.414	24.289
VL 501	46.724	-2.297	21.153
GPU 45	52.771	3.089	24.270
VL 380	43.911	-3.467	22.880
VR 936	59.704	3.592	24.537
SCN 6	59.826	-1.728	27.455
VR 708	39.537	2.485	20.262
PR 202	53.799	5.684	25.040
DHFM 4-9	62.198	0.434	26.749
GPU 28	42.027	0.937	20.645

analysis in many crops such as finger millet (3) and rice (4). The important objective of any plant scientist is to identify an optimum number of plant traits which are sufficient to explain the maximum variability in the crop growth from sowing to harvest. This study was undertaken to run a classification analysis on the fingermillet genotypes by means of descriptive statistic and to understand the association of various characters, PCA and cluster analysis which would enable breeders to classify the available germplasm into distinct groups on the basis of their genetic diversity.

MATERIALS AND METHODS

The experiment was undertaken with fifteen genotypes obtained from All India Coordinated Research Project on Small millets, ICAR, GKVK campus, Bengaluru evaluated under rainfed conditions during *Kharif*, 2015 Agriculture and Research Station, Vizianagaram, Andhra Pradesh. Sowing was completed by just onset of monsoon by direct seeding in agronomically standardized geometry with 22.5 cm × 10 cm spacing in three replications. The fertilizer dose of 60:40:30kg NPK/ha (50% N in + Full P and K at the time of sowing) was applied at the time of sowing seed and seeds were sown by hand dibbling. The remaining 50% N was applied after three weeks of sowing. Standard pest management measures were taken during the crop growth period as and when required. Observations were recorded on five plants for eight quantitative characters viz., plant height, number of tillers per plant, number of fingers per ear, main ear length, days to 50% flowering, days to maturity, straw yield per plot and grain yield. The principal component analysis was computed using the software statistical package for the social sciences (SPSS) 16.0 package (5). As suggested by (6), principal components with eigen values less than one was considered. Clustering pattern of genotypes recorded by using Ward minimum variance dendrogram.

RESULTS AND DISCUSSION

The breeders are interested to evaluate morphological markers based genetic diversity because they are inexpensive, rapid and simple to score. Further, study of these traits needs neither sophisticated methods nor complicated equipments and these traits can be inherited without specific biochemical and molecular techniques (7). The principal component analysis is a technique which identifies plant traits that contribute most of the observed variation within a group of genotypes. This tool has a practical application in the selection of best genotypes for breeding purpose. The results of PCA revealed that the first three components with eigen value of greater than one contributed about 77.20% of total variability in 15 genotypes involving all the eight quantitative traits studied (Table-1).

The importance of traits towards the PC could be seen from the corresponding eigen values. The first principal component accounted for 40.87% of the total

Table-3 : Grouping of fifteen genotypes of Finger millet (*Eluesine coracana* L. Gaertn) in different Clusters.

Cluster No.	Total of genotypes	Name of the genotypes
Cluster I	4	KMR 214, GPU 45, PR 202, VR 1081
Cluster II	5	DHFM 9-5, GPU 67, VR 936, SCN 6, DHFM 4-9
Cluster III	3	VL 386, VL 380, VL 501
Cluster IV	3	VL 352, GPU 28, VR 708

Table-4 : Average Cluster distances among fifteen genotypes of Finger millet (Eluesine coracana L. Gaertn)

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	94.129	246.248	358.663	638.013
Cluster II		121.806	884.953	1407.174
Cluster III			80.193	210.648
Cluster IV				45.163

Table-5 : Cluster mean values for eight character Finger millet (*Eluesine coracana* L. Gaertn)

	Plant Height (cm)	Number of productive Tillers per plant	Number of fingers/ Ear	Main Ear Length (cm)	Days to 50% Flowering	Days to Maturity	Straw Yield/ Plot (kg)	Grain Yield/ Plot (kg)
Cluster I	113.200	2.283	6.467	8.225	85.417	115.000	4.751	1.497
Cluster II	109.667	2.173	6.733	9.947	97.067	126.667	4.489	1.439
Cluster III	103.133	2.044	8.511	9.578	72.889	97.222	4.189	2.148
Cluster IV	101.311	2.222	7.489	7.500	63.444	90.444	4.574	1.253

variation in the population. Plant days to maturity (0.536) contributed more to the variation followed by, days to 50% flowering (0.527) and straw yield per plot (-0.375) had the highest loadings in PC1 indicating their significant importance for these components. These traits had the largest participation in the divergence and carried the largest portion of its variability. All other characters contributed negative to the first component. The second principal component (PC 2) described 21.88 per cent of total variance. Characters *viz*., grain yield per plot (-0.655) followed by main ear length -0.498) and straw yield per plot (0.400) explained the maximum variance in this component. The third principal component (PC 3) was characterized by 14.45 per cent contribution towards the total variability. Characters *viz*., number of tillers per plant (0.0.714), number of fingers per ear (0.0.481) and main ear length (0.387) showed maximum loading values in this principal component. The fourth principal component (PC 4) was recorded 11.68 per cent contribution towards the total variability. Characters *viz*., plant height (0.715), number of productive tillers per plant (-0.454) followed by number of fingers per ear (0.443) explained the maximum variance in this principal component. These results are in accordance with (8,9,10,11).

The PCA scores for 15 finger millet genotypes in the first three principal components were computed and were considered as three axes as X, Y and Z and squared distance of each genotype from these three axes were calculated and presented in Table-2. The genotypes identified on extreme positive side on both the axis were considered to be the better genotypes *i.e*. genotypes (14) DHFM 4-9 (62.198), (11) SCN 6 (59.826) and (10) VR 936 (59.704) along PCA I axis and genotypes *viz*., (13) PR 202 5.684) and (4) DHFM 9-5 (-5.216) along PCA II axis. In 3D plot, genotypes (14) DHFM 4-9, (11) SCN 6 (59.826), (10) VR 936, (13) PR 202 5.684) and (4) DHFM 9-5 were found to be away from the center. These genotypes might be used in hybridization programmes. These three PCA scores for 15 genotypes were plotted in graph to get two dimensional and three dimensional scatter diagrams (Fig.-1 and Fig.-2). Based on Ward minimum variance dendrogram, the clustering pattern revealed that out of four clusters, Cluster II consists of maximum of five genotypes fallowed by Cluster I with four genotypes, Cluster III and IV are with three genotypes each indicating the distinctness from other genotypes for most of the characters studied (Table-3).

The investigation revealed that maximum inter cluster distance recorded for Cluster II and IV (1407.174) followed by Cluster II and III (884.953). Maximum intra cluster distance observed for Cluster II (121.806) followed by Cluster I (94.129), which suggested that the genotype within Cluster II (DHFM 9-5, GPU 67, VR 936, SCN 6 and DHFM 4-9) and Cluster I (KMR 214, GPU 45, PR 202 and VR 1081) were highly diverse. Inter cluster and intra cluster distances were presented in the table 4. Cluster means (Table-5) for different characters indicated that Plant height had a range of 113.20 cm in cluster I to 101.311 cm in cluster IV; number of tillers per plant was observed maximum as 2.28 in cluster I and

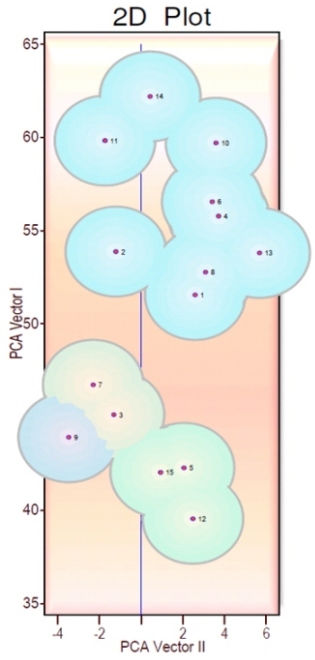

Fig.-1 : 2D plot showing scattering in 15 genotypes of finger millet (*Eluesine coracana* L. Gaertn)

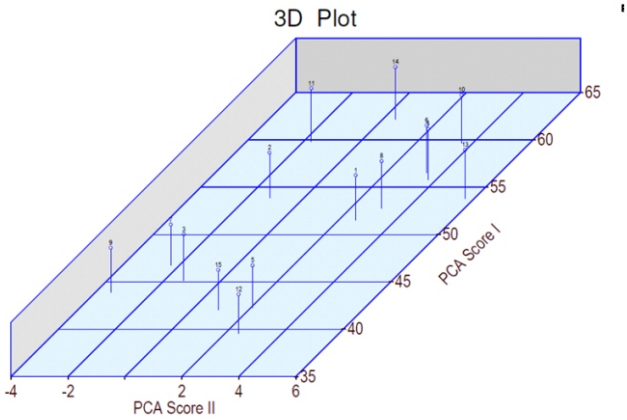

Fig.-2 : 3D plot showing scattering in 15 genotypes of finger millet (*Eluesine coracana* L. Gaertn)

minimum as 2.04 in cluster III; number of fingers per ear had a range of 8.51 in cluster III to 6.46 in cluster I; days to 50% flowering and days to maturity highest in cluster II (97.06 and 126.66) and lowest in cluster IV (63.44 and 90.44), Grain yield per plot had a range of 2.14 kg in Cluster III to 1.25 kg in Cluster IV. Relationship between all the genotypes studied is represented in dendrogram by using Wards minimum variance linkage method (fig. 3). Clustering pattern and cluster information represented in fig. 4. These findings were in accordance with findings of (9,10,11, and 12).

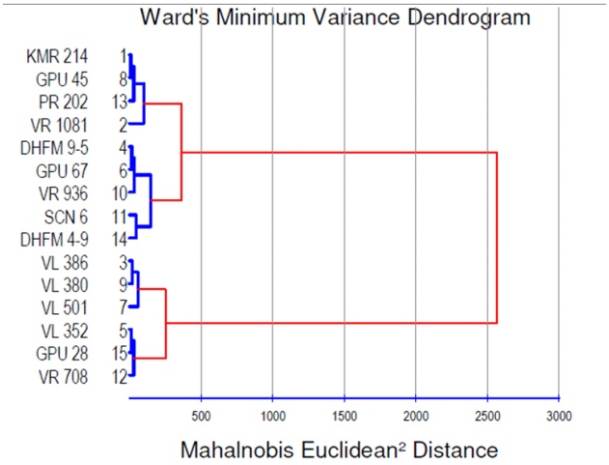

Fig.-3 : Dendrogram showing relationship among 15 finger millet (*Eluesine coracana* L. Gaertn) genotypes in four clusters.

Fig.-4 : Clustering pattern and cluster information of five characters in finger millet (Eluesine coracana L. Gaertn) investigated.

CONCLUSION

Based on PCA and clustering pattern by Ward minimum variance, the genotypes viz., DHFM 4-9, SCN 6, VR 936, PR 202 and DHFM 9-5 may be utilized in future breeding programmes for quality high grain yielding lines thereby increasing the productivity of the crop which gives higher returns to the farming community.

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