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EXPLORING GENETIC DIVERGENCE FOR YIELD AND YIELD-ASSOCIATED TRAITS IN WHITE FINGER MILLET USING PRINCIPAL COMPONENT ANALYSIS

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ABSTRACT

The presence of genetic diversity is a fundamental prerequisite for the success of any crop improvement programme, enabling the plant breeders to select divergent parents for hybridisation. To investigate this in white finger millet, an experiment was undertaken during *Kharif* 2022 with 52 white finger millet accessions and 8 checks for 16 yield-related and quality traits. The yield-related traits include days to 50 per cent flowering, plant height, number of fingers, finger length, finger width, number of tillers, panicle weight, days to maturity, grain yield per plot and test weight, and the quality traits examined were grain iron, zinc, calcium, magnesium, and phosphorus. Principal component analysis (PCA) was performed to assess the extent of diversity among accessions, and the first five principal components (PCs) were observed to have eigenvalues greater than one, which accounted for 75.85% of the total variability. The first principal component (PC1) contributed the maximum towards divergence (29.57%), followed by PC2 (20.04%), PC3 (14.21%), PC4 (7.54%) and PC5 (6.49%). The characters that contribute maximum towards genetic diversity were days to 50 per cent flowering, days to maturity, test weight, grain calcium, zinc, phosphorus and iron. Cluster analysis divided the total accessions into four clusters, and accessions from clusters I and III are promising for grain yield improvement, while those from cluster II are ideal for enhancing nutritional quality. Overall, the study concluded that the accessions studied were highly diverse for yield-related and quality traits, and careful selection of these accessions and traits will be beneficial for developing improved cultivars.

Keywords : Finger millet, Grain yield, PCA, Eigenvalue, Diversity.

Introduction

Finger millet (*Eleusine coracana* L. Gaertn.) is commonly called ragi and belongs to the family Poaceae. The cultivated finger millet is an allotetraploid ($2n = 4x = 36$), self-pollinated crop and originated from its wild relative, *E. indica*. In India, finger millet is cultivated in an area of approximately 1.21 million hectares with a production of 1.70 million tonnes (INDIA STAT 2022). Whereas in Telangana, it covers an area of 1000 hectares, yielding about 1650 tonnes (Directorate of Economics and Statistics, Telangana 2022). The main breeding efforts focus on improving grain and stover yield to enhance its economic potential. The grain colour of finger millet

varies from brown to reddish brown due to the presence of tannins and flavonoids (Vadivoo *et al.*, 1998), and white-grained finger millet is one among them. The white-grained finger millet is nutritionally on par with colour-grained finger millet and is desirable for its use, especially in bakery and other food products (Ravishankar, 2019). This is suitable for malting purposes as well as other end uses such as infant foods, weaning foods, and malted milk foods. Grains of finger millet are well known for their high nutritional profile, containing high amounts of iron, calcium, zinc, fibre, and essential amino acids (Upadhyaya *et al.*, 2011; Ambuko *et al.*, 2014). In addition to its nutritional benefits, it is a climate-

resilient and environmentally sustainable crop with prolonged storage qualities (Ayyangar and Rao, 1932).

Despite its tremendous potential, the cultivation of white-grained finger millet remains limited, with only a few cultivars released. It is crucial to assess genetic diversity within available germplasm lines to enhance their utilisation and breeding potential. Genetic diversity is the basis for the success of any breeding programme. Principal component analysis (PCA) is one of the most powerful statistical tools to assess the degree of diversity and relative contribution of different characters towards total variability. It reduces the dimensionality of complex datasets by identifying a smaller number of principal components that account for most of the total variation (Jackson, 1991) and for ranking accessions based on PC scores. With this background, the current experiment was carried out by using white finger millet accessions along with commercially available checks to assess genetic diversity.

Material and Methods

The present investigation was carried out during *Kharif* 2022 at ICAR-Indian Institute of Millets Research, Rajendranagar, Hyderabad, using a set of 52 white finger millet accessions and 8 checks (Fig 1). The experiment was laid out in a statistical design called an alpha lattice design with two replications. The plot size for each genotype is 1.35 square meters, with a spacing of 45 cm between rows and 15 cm between plants. All standard practices were followed to raise a healthy crop. Ten healthy, uniform, and representative plants were tagged in each genotype in each replication, and data was collected from those plants for days to 50 per cent flowering, plant height, finger length, finger width, number of fingers, number of tillers per plant, days to maturity, panicle weight, grain yield per plot and test weight. A random sample from each plot was collected to estimate the test weight (g) and nutritional parameters like grain iron (ppm), grain zinc (ppm), grain calcium (ppm), grain magnesium (ppm), grain phosphorus (mg/100g) and grain protein (%). The mean values of ten plants per genotype were subjected to Principal Component Analysis (PCA) using the method proposed by Pearson (1901) to identify the principal components contributing maximum towards genetic divergence. Further, hierarchical clustering using Ward's method was performed based on PCA-derived data in R software (version 4.2.3) using the hclust package.



Fig. 1: Experimental Plot of White Finger Millet Accessions

Results and Discussion

To select diverse parents for the hybridisation programme, the breeder must be aware of the characters and accessions contributing to maximum divergence. Principal Component Analysis (PCA) is a multivariate statistical approach that identifies the largest contributors to total variation, measuring diversity among accessions in terms of spatial distance. This approach is used to analyse data with many interconnected quantitative dependent variables by condensing the data into a smaller set of new variables without losing much of the original variability.

In the present study, data obtained from 16 characters of 52 white finger millet accessions, along with 8 checks, were subjected to PCA to reduce dimensionality by retaining maximum variability. Each data set corresponds to a single principal component. To simplify interpretation and avoid redundancy, data sets with less than 5% variance or Eigenvalues below one were excluded. This resulted in the selection of five principal components, which collectively account for 75.85% of the total variability. The first principal component was chosen in such a way that it corresponds more towards genetic variance, followed by subsequent components. Table 1 displays the principal components (eigenvalue greater than one), their respective eigenvalues, percentage variance, cumulative percentage variance and component loading of various characters. A scree plot (Fig. 2) provides a graphical representation of the eigenvalues, demonstrating the proportion of variance explained by each principal component.

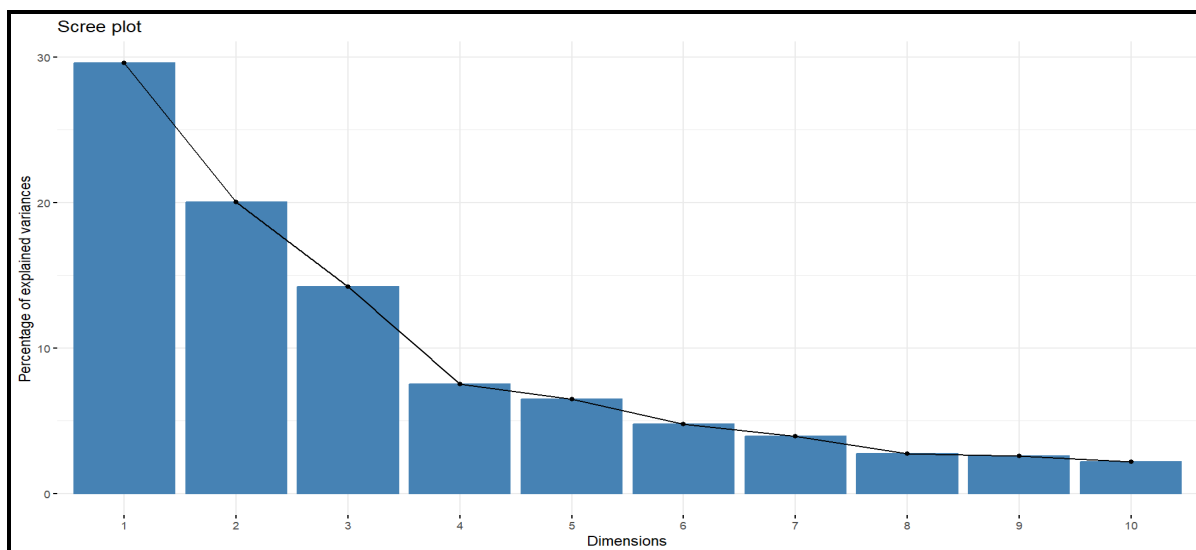
Table 1 : Eigenvalues and proportion of the total variance represented by the first five principal components

S. No.	Components	PC 1	PC 2	PC 3	PC 4	PC 5
1.	Eigen Value	4.73	3.21	2.27	1.21	1.04
2.	% Variance	29.57	20.04	14.21	7.54	6.49
3.	Cumulative % variance	29.57	49.61	63.81	71.36	77.85

The first five principal components had eigenvalues greater than one and explained substantial genetic variance among the accessions studied. PC1 contributed the highest proportion (29.57%) to the total variability, followed by PC2 (20.04%), PC3 (14.21%), PC4 (7.54%), and PC5 (6.49%). Principal components with eigen values less than one were considered to be non-significant and excluded from interpretation.

Therefore, it was concluded that the first 5 principal components, which together accounted for 75.85% of the variability, were sufficient to describe the essential features of the data set.

The first principal component (PC1) is the most influential, contributed maximum toward divergence (29.57%) and was positively associated with days to 50 per cent flowering (0.336), grain phosphorus (0.324), grain zinc (0.320), grain calcium (0.308), days to maturity (0.290), number of fingers (0.183), grain magnesium (0.146), grain iron (0.61) and grain protein (0.001). On the other hand, test weight (-0.344), grain yield plot⁻¹ (-0.291), plant height (-0.257), number of tillers per plant (-0.253), finger length (-0.204), panicle weight (-0.203) and finger width (-0.157) were negatively loaded.

**Fig. 2** : Scree plot showing the eigenvalues of principal components

The second principal component (PC2) contributed 20.04% of total variance and positively associated with characters viz., grain iron (0.443), protein (0.429), finger length (0.308), grain zinc (0.304), grain calcium (0.263), grain phosphorus (0.245), grain magnesium (0.226), plant height (0.178), number of tillers per plant (0.147), finger width (0.047) and grain yield plot⁻¹ (0.012) and negatively loading for days to maturity (-0.302), days to 50% flowering (-0.266), number of fingers (-0.144), test weight (-0.110) and panicle weight (-0.023).

The third principal component (PC3) was characterized by 14.21% of total variability with positive loading for panicle weight (0.509), grain yield plot⁻¹ (0.440), number of fingers (0.375), number of tillers per plant (0.302), plant height (0.234), grain zinc (0.189), days to 50 per cent flowering (0.175), days to maturity (0.172), grain iron (0.167), grain magnesium

(0.143) and grain phosphorus (0.009), whereas grain protein (-0.203), finger width (-0.195), test weight (-0.184), finger length (-0.040) and grain calcium (-0.019) were negatively loaded.

The fourth principal component (PC4) described 7.54% of total variability and exhibited significant positive loading for finger length (0.382), number of fingers (0.371), plant height (0.178), test weight (0.050), grain iron (0.039), number of tillers per plant (0.038) and grain calcium (0.036) and negatively loading for finger width (0.640), grain magnesium (-0.333), panicle weight (-0.257), grain yield plot⁻¹ (-0.226), days to maturity (-0.096), days to 50 per cent flowering (-0.047), grain protein (-0.041) and grain zinc (-0.013).

The fifth principal component (PC5) contributed 6.49% of the total variability. The characters viz., plant

height (0.457), finger length (0.380), finger width (0.369), magnesium (0.324), test weight (0.255), days to maturity (0.231), number of fingers (0.180), phosphorus content (0.147), days to 50% flowering (0.099) and grain iron (0.005) loaded positively, whereas grain protein (0.353), panicle weight (-0.167),

number of tillers per plant (-0.156), grain yield plot⁻¹ (-0.138) and grain zinc (-0.117) were negatively loaded. Table 2 displayed the detailed character loading of five principal components across 52 white finger millet accessions and 8 checks.

Table 2 : Character loadings of five principal components across 52 white finger millet accessions and 8 checks

S. No.	Characters	PC 1	PC 2	PC 3	PC 4	PC 5
1	Days to 50 per cent flowering	0.336	-0.266	0.175	-0.047	0.099
2	Plant height (cm)	-0.257	0.178	0.234	0.178	0.457
3	Finger length (cm)	-0.204	0.308	-0.040	0.382	0.380
4	Finger width (cm)	-0.157	0.047	-0.195	-0.640	0.369
5	Number of tillers per plant	-0.253	0.147	0.302	0.038	-0.156
6	Number of fingers	0.183	-0.144	0.375	0.371	0.180
7	Days to maturity	0.290	-0.302	0.172	-0.096	0.231
8	Panicle weight (g)	-0.203	-0.023	0.509	-0.257	-0.167
9	Grain yield plot ⁻¹ (g)	-0.291	0.012	0.440	-0.226	-0.138
10	Test weight (g)	-0.344	-0.110	-0.184	0.050	0.255
11	Grain iron (ppm)	0.061	0.443	0.167	0.039	0.005
12	Grain zinc (ppm)	0.320	0.304	0.189	-0.013	-0.117
13	Grain calcium (ppm)	0.308	0.263	-0.019	0.036	0.115
14	Grain magnesium (ppm)	0.146	0.226	0.143	-0.333	0.324
15	Grain phosphorus (mg/100 g)	0.324	0.245	0.009	-0.163	0.147
16	Grain protein (%)	0.001	0.429	-0.203	-0.041	-0.353

The PCA scores for yield-related and quality traits in 52 white finger millet accessions and 8 checks were plotted on a two-dimensional scatter diagram to visualise the distribution of accessions based on their diversity. This graphical representation highlights the key traits contributing most to genetic variation and effectively illustrates the extent of diversity among the accessions.

Dim1 (29.6%) and Dim2 (20%) represent the first two principal components, which together explain the maximum amount of variation in the dataset. The lines radiating from the centre of the biplot indicate the variables included in the study. The length of the line indicates the magnitude of its contribution towards the diversity. The longer line indicates the maximum contribution, and the shorter line indicates the lower contribution towards diversity. From the PCA biplot (Fig. 3), the characters that contribute more towards diversity were days to 50 per cent flowering, days to maturity, test weight, grain calcium, grain zinc, grain phosphorus and grain iron and the characters that contribute less towards diversity are number of fingers, finger length, plant height, grain yield plot⁻¹, number of tillers per plant, grain magnesium, finger width and panicle weight.

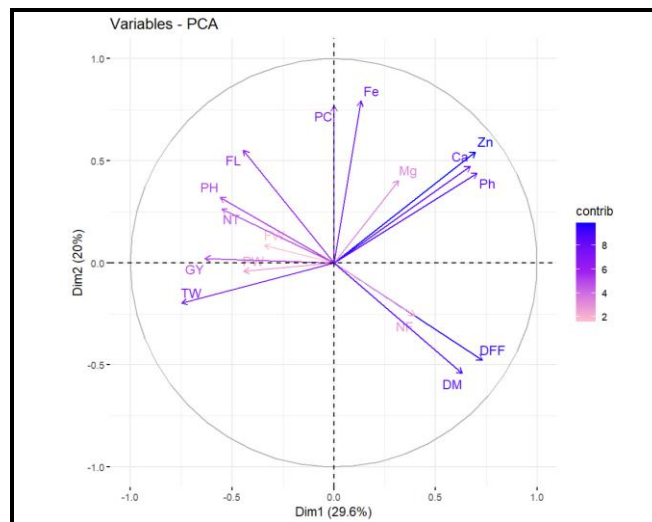


Fig 3. Two-dimensional graph showing the contribution of characters towards divergence in 52 white finger millet accessions and 8 checks based on PCA scores

DFF = Days to 50 per cent flowering, **FL** = Finger length, **FW** = Finger width, **PH** = Plant height, **NT** = Number of tillers per plant, **PW** = Panicle weight, **NF** = Number of fingers, **DM** = Days to maturity, **GY** = Grain yield plot⁻¹, **TW** = Test weight, **Zn** = Grain zinc, **Fe** = Grain iron, **Mg** = Grain magnesium, **Ca** = Grain calcium, **P** = Grain phosphorus, **Pro** = Grain protein

A two-dimensional PCA scatter plot (Fig. 4) was generated to illustrate the diversity among the 52 accessions and 8 checks. Ward's hierarchical clustering grouped these accessions into four clusters. The first cluster contained the maximum number of accessions

35, followed by the second cluster with 18 accessions, the third cluster with six accessions, and the fourth cluster with only one genotype. Each number on the plot represents a genotype, and lines radiating from the origin represent the characters studied.

Cluster I comprised 35 accessions characterised by moderate to high grain yield per plot, high grain iron content, and low to moderate levels of grain calcium, zinc, phosphorus, and protein. The accessions IC0473972-1, IC0473983, IC0474037, IC0474225, and E-319 exhibited the highest grain yield per plot. Cluster II consisted of 17 accessions with moderate grain yield and low to moderate nutritional content. Notable accessions in this cluster were IC0475624, IC0065595-2, IC0473970, IC0474233, and IC0474228. Cluster III comprised 17 accessions with almost all check varieties. Accessions IC0473948 and IC0621996 were grouped in this cluster, showing similar characteristics to the checks. Cluster IV was represented by only one genotype, *i.e.* IC0473957, which recorded the highest grain yield plot⁻¹ along with high grain iron, grain zinc, grain calcium, grain magnesium, grain phosphorus and grain protein content.

The clustering results revealed that the white finger millet accessions studied in the present experiment were highly divergent, indicating their potential utility in breeding programmes. For improving grain yield, Cluster I and III accessions could be selected, while Cluster II accessions may serve as valuable sources for enhancing nutritional quality. A backcross breeding strategy could be employed to incorporate desirable traits into high-yielding varieties.

The PCA-based diversity studies revealed that the characters days to 50 per cent flowering, days to maturity, test weight, grain calcium, grain zinc, grain phosphorus and grain iron content contributed more towards diversity. The results were in accordance with Anantharaju and Meenakshiganesan (2008), Ulaganathan and Nirmalakumari (2015), Kaluthanthri and Dasanayaka (2016), Patel *et al.* (2017), Patil *et al.* (2017), Damtie *et al.* (2019), Suman *et al.* (2019) and Ladumor *et al.* (2021) for days to 50 per cent flowering and days to maturity and Devaliya *et al.* (2017) for iron content.

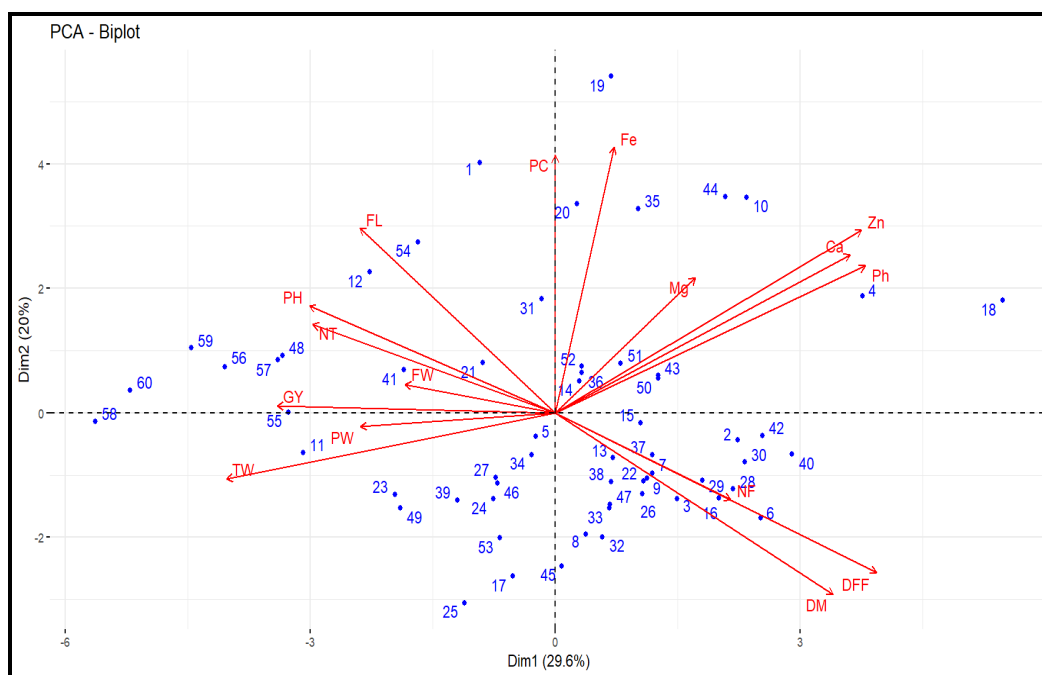


Fig. 4 : Two-dimensional graph showing the relative position of 52 white finger millet accessions and 8 checks based on PCA scores

1	IC0475624	11	IC0474356	21	IC0473970	31	IC0473990	41	IC0474228	51	E - 331
2	IC0473924	12	IC0065595-2	22	IC0473971	32	IC0473992	42	IC0474231	52	FR - 97
3	IC0473989	13	IC0065595-3	23	IC0473972-1	33	IC0473993	43	IC0474233	53	GN - 5 (WC)
4	IC0474038	14	IC0473996	24	IC0473972-3	34	IC0474037	44	IC0473950	54	KMR-340 (WC)
5	IC0474183	15	IC0473858	25	IC0473978	35	IC0474044	45	IC0474433	55	GPU-67 (CC)
6	IC0474207	16	IC0473874	26	IC0473973	36	IC0474045	46	IC0402775	56	VL - 376 (CC)
7	IC0474219	17	IC0473947	27	IC0473983	37	IC0474065	47	IC0621993	57	PR202 (CC)
8	IC0474222	18	IC0473948	28	IC0473984	38	IC0474206	48	IC0621996	58	CFMV - 1 (CC)
9	IC0474227	19	IC0473957	29	IC0473986	39	IC0474225	49	E - 319	59	CFMV - 2 (CC)
10	IC0474232	20	IC0473959	30	IC0473987	40	IC0474226	50	E - 325	60	CFMV - 3 (CC)

Conclusion

The principal component analysis (PCA) revealed a significant genetic diversity among the 52 white finger millet accessions and 8 checks, with days to 50 per cent flowering, days to maturity, test weight, grain zinc, grain calcium, grain phosphorus, and grain iron contributing the most to variability. Cluster analysis grouped the accessions into four distinct clusters, identifying potential high-yielding and nutritionally rich lines for breeding programs. These findings emphasise the potential of white finger millet germplasm for developing improved cultivars with enhanced yield and nutritional traits, contributing to sustainable agriculture and food security.

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