

Genetic divergence studies for yield and quality traits in white and brown finger millet (*Eleusine coracana* (L).)

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Summary

The present study assessed the nature and magnitude of genetic variability for yield and quality-related traits in 64 finger millet genotypes for 25 parameters during *Kharif*, 2020-21 at Agricultural College Farm, Bapatla, Andhra Pradesh. In D² analysis, the maximum inter-cluster distance was observed between cluster IV, with white-seeded genotypes and cluster VI with brown-seeded genotypes indicating these clusters may give a high heterotic response and better segregants. The principal component analysis identified the maximum contributing variables *i.e.*, grain yield per plant, harvest index, fingers per earhead, test weight, peduncle length, seed protein content and seed calcium content in the first principal component. PCA scores of 64 genotypes indicated that genotypes IC0477628, IC0476988, IC0477206, VR1034, IC473950 and IC0477272 are diverse for yield and quality traits and hence hybridization between these genotypes is suggested for generating transgressive segregants.

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Introduction

Finger millet is a self-pollinated, allopolyploid crop, native to Africa with chromosome number $2n=4x=36$. The grain belongs to the Poaceae family, which originated in Ethiopia and the sub-family Chloridodeae. Different cultivars of finger millet grain are cultivated: brown, light brown and white (Devi *et al.*, 2014; Kumar *et al.*, 2016) grain colour used as the distinct means of cultivar differentiation. Finger millet is an essential crop in terms of its nutritional and pharmaceutical attributes. In India, finger millet occupies an area of 10.16 lakh hectares with a production of 13.85 lakh tonnes and a productivity of 1363 kg ha⁻¹. Among India's major finger millet-growing states, Karnataka is the leading state in area and production. In Andhra Pradesh, finger millet is grown in an area of 0.35 lakh hectares with a production of 0.44 lakh tones and productivity of 1277 kg ha⁻¹ (Agricultural Statistics at a Glance 2017-18).

Knowledge of the magnitude of variability present in any crop species for different traits is of utmost importance as it provides the basis for effective selection and segregants (Mahanthesha *et al.* 2017; Samdia & Haldhar 2019; Singh *et al.* 2022). A genetic divergence study is a prerequisite for assessing the genetic diversity among the genotypes and is a prime consideration in any crop improvement program. Through this study, diverse genotypes for yield and quality traits can be identified. In addition to that, hybridization between these diverse genotypes can be suggested for generating transgressive

segregants. In order to quantify the magnitude of genetic divergence among the population, two methods *i.e.*, Mahalanobis generalised distance using D² statistic and principal component analysis, are used. 'Mahalanobis D² statistics' is a powerful tool to measure the source of differentiation at intra-cluster and inter-cluster levels and thus helps select genetically divergent parents in a hybridization programme. The groups or clusters formed using Tocher's method in D² statistics are further confirmed by Principal Component Analysis (PCA). This analysis also highlights the importance of the largest contributor to the total variation at each axis of differentiation.

Materials and Methods

The present study was conducted for 64 finger millet genotypes (41 brown seeded and 23 white-seeded), including three checks during *Kharif*, 2020-21, at Agricultural College Farm, Bapatla, Andhra Pradesh. The experiment was carried out in an 8*8 square lattice design with two replications. The data was collected on five randomly selected plants per genotype for 25 parameters *viz.*, days to 50% flowering, days to maturity, plant height, flag leaf blade length, flag leaf blade width, Soil Plant Analysis Development Chlorophyll Meter Reading (SCMR) at 30 days, SCMR at 45 days, number of productive tillers per plant, number of fingers per earhead, finger length, finger width, earhead length, peduncle length, harvest index, test weight, seed protein content, seed calcium content, seed phosphorus content, seed iron content, seed zinc content, seed manganese content, seed copper content, tannin content, antioxidant activity and grain yield per plant. However, days to 50 per cent flowering and days to maturity were recorded on a plot basis. The data collected on different yield contributing characters were analysed using

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Mahalanobis D^2 analysis to determine the genetic divergence among the genotypes in terms of 'generalised group distance' (Mahalanobis 1928). The grouping of genotypes into different clusters was done using Tocher's method, as Rao (1952) described. Principal component analysis was carried out according to the procedure described by Banfield (1978).

Results and Discussions

Diversity Analysis

Univariate analysis of variation implied the significant difference for all 25 traits studied under the present investigation. The 61 genotypes and checks were grouped into eight clusters using Tocher's method (Rao 1952), which were highly divergent, non-overlapping and distinct (Table 1). The genotypes within a cluster had smaller D^2 values than those belonging to different clusters. Cluster II has a maximum number of genotypes *i.e.* 22, while Cluster IV (VR1034), Cluster VI (IC0477628) and Cluster VIII (IC0477206) were monogenotypic. The tree-like structure called dendrogram was constructed based on clustering by Tocher's method (Figure 1). It was observed that genotypes from diverse geographical areas were distributed in the same cluster (Cluster I, II, III), signifying that clustering pattern of genotypes was independent of their geographical location indicating absence of parallelism between genetic diversity and geographical diversity in the present investigation. The highest intracluster distance was exhibited by cluster V (858.84), indicating diversification among the cluster genotypes (Table 2). Cluster IV, Cluster VI and Cluster VIII have zero intra-cluster distance as they are mono-

genotypic clusters. It was observed that white and brown seeded genotypes separately formed clusters. Clusters I, III, V, VI, VII and VIII exclusively consisted of brown-seeded genotypes, while Clusters II, IV exclusively consisted of white-seeded genotypes. The maximum intercluster distance was observed between Cluster IV and VI (23312.79), followed by Cluster II and VI (22593.78), indicating wide difference in the performance of white and brown seeded genotypes, especially in terms of nutritional and quality aspects and hence hybridization between genotypes from Cluster IV and VI as well as between Cluster II and VI will be useful to obtain maximum hybrid vigour and may result in transgressive segregants. The Cluster mean values for the 25 characters studied were presented in Table 3. The cluster means signifies the mean performance of all the genotypes present in a cluster. Among clusters of brown-seeded genotypes, mono-genotypic Cluster VI showed the highest cluster mean for grain yield, tannin content and antioxidant activity and hence this brown-seeded genotype from this cluster (IC0477628) can be used to develop high-yielding varieties with high tannin and antioxidant activity that can further prevent excessive oxidation, chronic disease and ageing. Among clusters of white seeded genotypes, Cluster IV which is solitary and consists of white seeded genotype (VR1034), has the highest cluster mean for grain yield hence this cluster can be used in breeding programmes for yield improvement. Among the characters studied, grain yield contributed (12.25 %) maximum towards genetic divergence.

Table 1. Clustering pattern by Tocher's method in 64 genotypes of finger millet (*Eleusine coracana* (L.))

Cluster Number	Number of genotypes	Name of genotype(s)	Source
I	11	IC0476903, IC0476860, Sri Chaitanya, IC0476797, IC0477680, IC0476922, IC0477211-X, IC0477184, IC0477010, IC0476709 and IC0477654	ICRISAT, ARS Vizianagaram
II	22	IC474207, IC473983, IC473948, IC474206, IC474433, IC474226, IC473950, IC473989, IC473994, IC474065, IC474231, IC474220, IC474221, VR950, VR1038, Hima, VR1024, VR942, VR1023, VR939, VR1029, VR1016	IIMR, ARS Vizianagaram
III	14	IC0477198, IC0587945, IC0476988, IC0477014, IC0506461, IC0477484, IC0477035, IC0476831, IC0477493, IC0477842, IC0477261, IC0477599, IC0477752 and Vakula	ICRISAT, ARS Perumalapalle
IV	1	VR1034	ARS Vizianagaram
V	10	IC0476946, IC0476586, IC0477385, IC0477467, IC0476588, IC0478036, IC0476560, IC0477004, IC0587948 and IC0476467	ICRISAT
VI	1	IC0477628	ICRISAT
VII	4	IC0477469-X, IC0587970, IC0506462, IC0477272	ICRISAT
VIII	1	IC0477206	ICRISAT

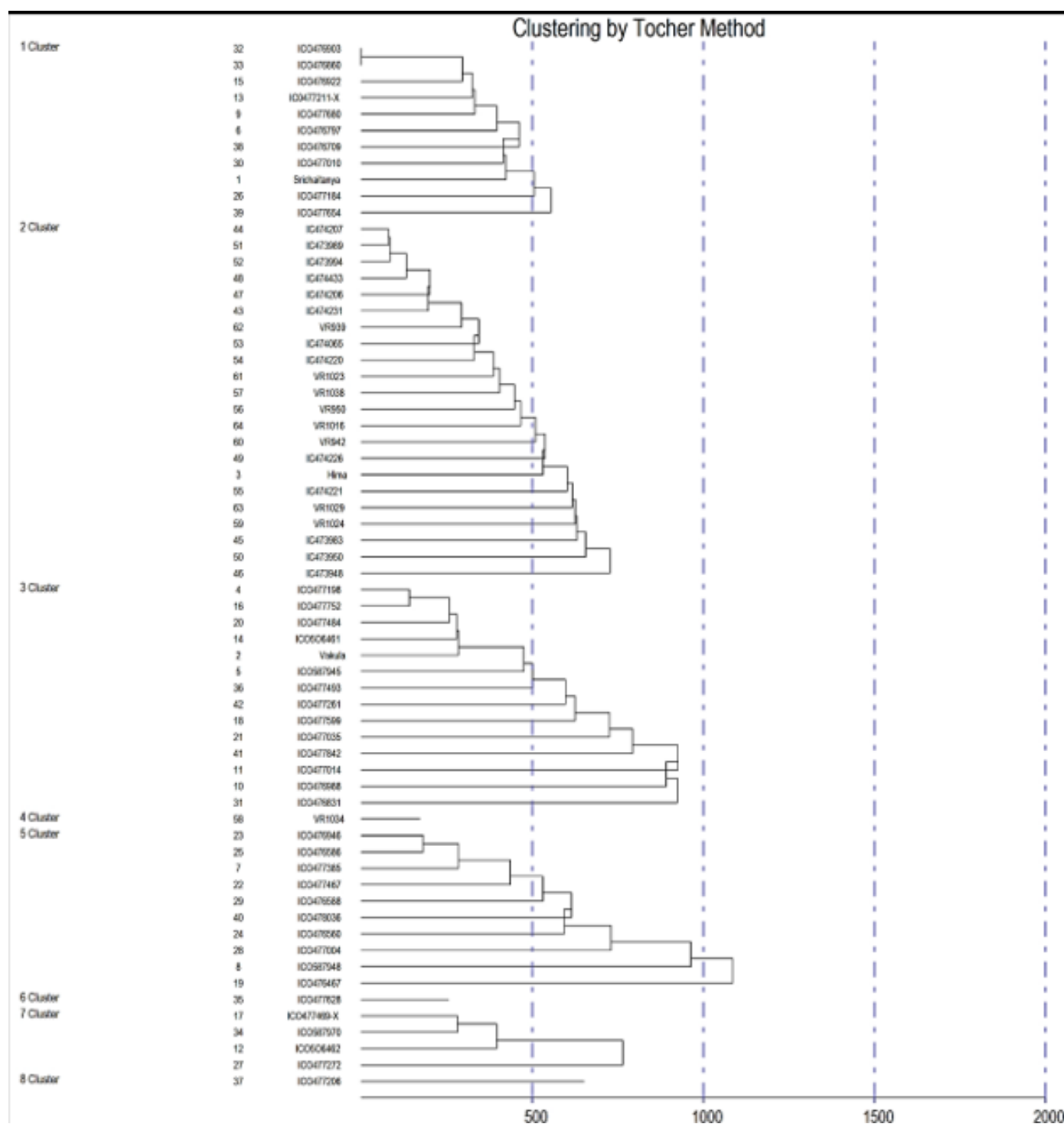


Figure 1. Dendrogram showing relationship based on Mahalanobis' D^2 values in eight clusters among 64 genotypes of finger millet (*Eleusine coracana* (L.))

Table 2. Average intra and inter-cluster distances (D^2 values) among eight clusters in 64 genotypes of finger millet (*Eleusine coracana* (L.))

Cluster No.	I	II	III	IV	V	VI	VII	VIII
I	504.34	20817.79	1310.85	22616.30	3803.94	1203.30	2087.05	4633.18
II		562.21	17035.20	834.85	9672.86	22593.78	13348.40	7456.64
III			789.48	18180.90	2069.92	1054.35	2387.45	3797.85
IV				0	10538.33	23312.79	14543.39	9252.30
V					858.84	3883.25	2541.02	1671.91
VI						0	3493.56	6688.81
VII							754.55	1955.15
VIII								0

Note: Bold and diagonal values indicate intra-cluster D^2 distance

Table 3. Cluster means of eight clusters estimated by Tocher's method in 64 genotypes of finger millet (*Eleusine coracana* (L.)

Character	Cluster number							
	I	II	III	IV	V	VI	VII	VIII
Days to 50% flowering	61.41	73.27	61.14	52.00	57.35	60.50	59.00	72.50
Days to maturity	91.00	101.36	90.86	83.00	87.55	89.00	89.00	100.50
Plant height (cm)	90.24	91.35	94.61	105.85	86.79	96.70	91.25	78.15
Flag leaf blade length (cm)	28.04	32.81	30.86	37.75	30.14	37.65	28.15	33.20
Flag leaf blade width (cm)	0.96	1.13	1.03	1.24	1.00	1.17	0.97	1.00
SCMR at 30 days	39.42	41.24	38.87	42.50	41.16	39.90	44.11	30.80
SCMR at 45 days	44.82	44.86	43.05	44.80	45.21	46.00	48.09	39.20
Productive tillers per plant	3.09	2.99	3.32	4.90	3.00	4.80	4.11	2.20
Fingers per earhead	9.14	8.54	8.85	12.75	7.59	12.75	10.90	4.85
Finger length (cm)	6.84	6.40	7.09	9.30	6.15	9.20	8.20	4.20
Finger width (cm)	1.11	1.03	1.18	1.55	0.97	1.70	1.49	0.60
Earheadlength (cm)	8.51	7.84	8.81	12.50	7.37	12.50	10.96	5.45
Peduncle length (cm)	13.63	14.07	13.77	18.55	13.36	19.25	10.21	11.40
Harvest index (%)	30.55	29.18	31.14	38.50	27.05	38.50	36.25	20.50
Test weight (g)	2.71	2.59	2.73	3.20	2.43	3.20	3.01	1.80
Seed protein content (%)	7.15	10.78	5.74	10.15	5.77	7.20	6.03	3.75
Seed calcium content (mg/100g)	395.29	560.54	375.46	527.25	346.36	328.50	400.09	495.00
Seed phosphorus content (g/100g)	0.20	0.28	0.19	0.25	0.21	0.23	0.18	0.23
Seed iron content (mg/100g)	3.96	5.59	3.29	5.15	3.93	3.95	3.33	4.05
Seed zinc content (mg/100g)	2.01	3.27	1.85	3.05	2.21	1.55	1.63	1.55
Seed copper content (mg/100g)	1.61	2.37	1.49	2.25	1.47	1.15	1.93	1.25
Seed manganese content (mg/100g)	1.93	3.05	1.04	2.55	1.33	0.65	2.10	1.85
Tannin content(CE%)	2.88	0.04	2.45	0.04	0.94	2.95	1.63	0.32
Antioxidant activity (% DPPH Activity)	94.88	19.51	87.73	15.55	69.62	98.15	76.68	62.22
Grain yield per plant (g)	22.13	20.02	22.58	34.45	17.55	34.45	29.34	10.20

Note: Bold values are maximum values

Principal component analysis in genetic divergence

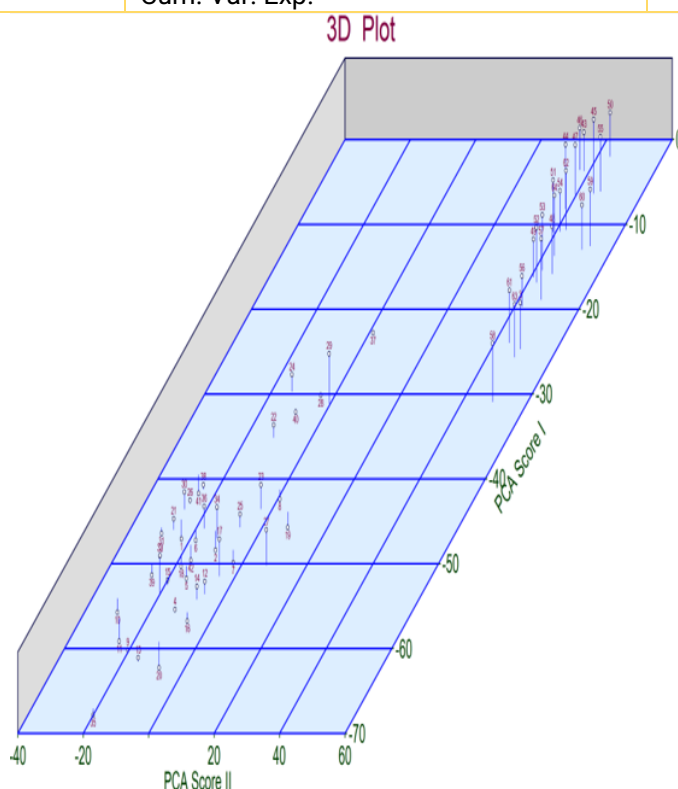
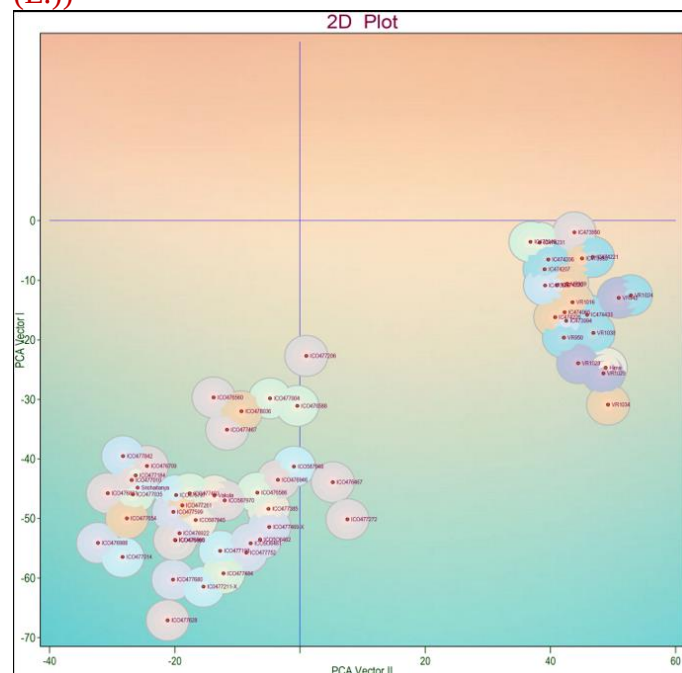
Principal component analysis or canonical vector analysis is a sort of multivariate analysis where canonical vectors or roots represent the different axis of differentiation and the amount of variation accounted for by each of such axes, respectively (Rao 1952). It is called principal component analysis as it reflects the importance of the largest contributor to the total variation at each axes of differentiation. It measures divergence between varieties regarding spatial distance rather than quantifying it as D^2 does. It gives group constellations as varietal distribution in a two-way pictorial graph fixing the relative position of each variety. Principal components (eigenvalue greater than one), eigenvalues (Latent Root), per cent variability, cumulative per cent variability and component loading of different characters were presented in Table 4.

In the present investigation, the first six principal components with eigenvalues of more than one contributed 83.28 per cent towards the total variability, indicating that the essential features of the data set had

been exhibited in the first six principal components. The results implied that the first principal component with an eigenvalue of 7.49 contributed maximum towards variability (29.97%). The analysis identified the maximum contributing variables *i.e.* as grain yield per plant, harvest index, fingers per earhead, test weight, peduncle length, seed protein content and seed calcium content in the first principal component. It is important to study the variance as the relative contribution to the signs (indicative of direction) in principal component analysis. These PCA scores of 64 genotypes were plotted in a graph to get 2D and 3D scatter diagrams. From the diagram, it was observed that genotypes IC0477628, IC0476988, IC0477206, VR1034, IC473950 and IC0477272 are diverse for yield and quality traits and hence hybridization between these genotypes can be suggested for generating transgressive segregants. Meanwhile, simultaneous selection for yield and quality traits may not be possible and balanced selection criteria should be followed depending on the objective.

Table 4. Canonical vectors for 25 characters in 64 genotypes of finger millet (*Eleusine coracana* (L.))

S. No.	Parameter	PC ₁	PC ₂	PC ₃	PC ₄	PC ₅	PC ₆
1	Days to 50 % flowering	0.18	0.20	0.09	0.41	0.26	0.03
2	Days to maturity	0.18	0.20	0.09	0.42	0.27	0.03
3	Plant height (cm)	-0.24	0.13	0.00	0.04	0.21	0.45
4	Flag leaf blade length(cm)	-0.30	0.19	0.27	-0.33	-0.09	0.22
5	Flag leaf blade width(cm)	0.04	0.18	0.13	-0.05	0.09	0.61
6	SCMR at 30 days	0.04	-0.07	-0.46	-0.04	-0.14	0.34
7	SCMR at 45 days	0.02	-0.17	-0.49	0.00	-0.10	-0.01
8	Productive tillers per plant	-0.09	0.11	-0.02	0.04	-0.24	-0.16
9	Fingers per earhead	-0.27	0.19	-0.13	0.21	-0.08	-0.05
10	Finger length(cm)	-0.13	0.24	0.19	0.03	0.00	-0.04
11	Finger width(cm)	-0.14	0.18	0.06	0.03	-0.06	-0.11
12	Earhead length(cm)	-0.29	0.14	0.05	-0.03	-0.13	0.03
13	Peduncle length(cm)	-0.32	0.10	-0.27	-0.24	0.43	0.03
14	Harvest Index (%)	-0.30	0.14	-0.12	-0.20	0.09	0.01
15	Test weight (g)	0.23	-0.10	0.45	-0.25	-0.16	0.01
16	Seed protein content (%)	0.21	0.26	-0.18	-0.08	-0.02	-0.18
17	Seed calcium content (mg/ 100 g)	0.23	0.26	-0.11	-0.14	-0.01	0.07
18	Seed phosphorus content (g/100g)	0.10	0.16	0.01	-0.13	-0.31	-0.03
19	Seed iron content (mg/100 g)	0.25	0.22	0.07	-0.06	0.02	-0.18
20	Seed zinc content (mg/100 g)	0.07	0.30	-0.14	-0.25	0.24	-0.22
21	Seed copper content (mg/100g)	0.06	0.18	-0.02	0.40	-0.36	0.04
22	Seed manganese content (mg/100g)	0.04	0.13	-0.13	0.05	-0.40	0.28
23	Tannin content (CE%)	-0.13	-0.30	0.08	0.12	0.14	0.07
24	Antioxidant Activity (%DPPH Activity)	-0.18	-0.34	0.05	0.11	0.06	0.05
25	Grain yield per plant(g)	-0.33	0.22	-0.05	0.16	0.01	-0.10
	Eigene Value (Root)	7.49	5.41	2.91	2.05	1.76	1.21
	% Var. Exp.	29.97	21.62	11.63	8.20	7.03	4.84
	Cum. Var. Exp.	29.97	51.59	63.22	71.42	78.45	83.29

**Figure 2 (a).** Three-dimensional (3D) graph showing relative positions based on PCA scores in**64 genotypes of finger millet (*Eleusine coracana* (L.))****Figure 2 (b).** Two-dimensional (2D) graph based on PCA scores showing relative positions of 64 genotypes in finger millet (*Eleusine coracana* (L.))

Conclusion

In the present investigation brown seeded genotypes, namely, IC0477628, IC0477211-X, IC0477272, and IC0477680, recorded high cluster mean for yield and yield contributing traits. White-seeded genotypes, namely, VR1034 and VR1029 are suitable for yield and yield contributing characters; hence these genotypes are identified for future crop improvement programmes. White-seeded genotypes, namely, VR1016, VR1023, VR939, VR942, IC474231, IC473948 and VR950, can be recommended in breeding programmes for biofortification as they recorded superiority for all nutritional traits studied compared to the brown-seeded genotypes. Brown-seeded genotypes, namely, IC0477680, IC0477628, IC0476988, IC0477014, and IC0477211-X recorded high tannin and antioxidant activity at par with check variety Sri Chaitanya and can be used to improve tannin and antioxidant activity to develop varieties with potential health benefits. Consumption of such nutrient-dense genotypes will improve nutritional status and sustain the production of finger millet, contributing to nutritional security.

The success rate of hybridization is very low in finger millet as the crop is self-pollinated as well as due to its practical difficulty of conducting hand emasculation. Identification of true hybrids is also difficult in finger millet. Therefore, to overcome these problems in finger millet, crossing between brown-seeded genotypes, IC0477628, IC0477272, IC0477680, IC0477211-X, IC0476988, IC0477014 and white-seeded genotypes, VR1034, VR1029, VR1016, VR1023, VR939, VR942, IC474231, IC473948 and VR950 is recommended for obtaining transgressive segregants for yield and quality traits. Further, it was observed that simultaneous selection for yield and quality traits might not be possible and balanced selection criteria should be followed depending on the objective.

Declarations of interests

All authors of this manuscript declare that they have no conflict of interest.

Data sharing

All relevant data are within the manuscript.

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