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RESEARCH PAPER

Genetic Diversity of Finger Millet Advanced Breeding Lines

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ABSTRACT

Finger millet is an important millet crop known for its three-fold security. The present study was undertaken to assess the associations among various traits and diversity amid 29 finger millet genotypes. All genotypes were evaluated for grain yield, yield components and disease traits at Agricultural Research Station, Vizianagaram, Andhra Pradesh. Association analysis of 14 traits revealed significant positive association between phenological traits and grain yield. It was also observed that longer ears tend to have higher grain yields. The variability of 14 traits was majorly captured by the first principal component where the phenological traits, disease traits and grain yield contributed higher percent compared to others. These traits can serve as reliable selection indices for improving yield potential and adaptability in finger millet breeding programs. Circle plot was also in agreement with association analysis that days to 50% flowering (DFF), days to maturity (DM), ear length (EL), and finger length (FL) were positively associated. Further, the biplot helped to view the grouping of various genotypes into clusters.

HIGHLIGHTS

- Associations were positively stronger for grain yield with finger length, finger number, and duration indicating possibility for simultaneous selection of these traits for higher yields
- Higher the disease score of blast and banded blight, lower the yields implying negative selection results in obtaining high yielding genotypes.
- In the Principal Component Analysis, first five PCs were able to capture 85% of the total variability as indicated by the steepness of the slope.
- Grouping of genotypes was based on maturity which can be viewed that early entries were distinctly placed away from late entries in the PC Biplot. It implies that same duration entries share some commonality.

Keywords: Finger millet, correlation, diversity, principal component analysis

Finger millet (*Eleusine coracana* L. Gaertn) is a vital minor millet crop grown predominantly in arid and semi-arid regions of India and Africa, known for its high nutritional value and resilience to abiotic stresses (Upadhyaya *et al.* 2006; Kumar *et al.* 2016: Maitra, 2020). It is a rich source of calcium, iron, dietary fibre, and essential amino acids, making it an important crop for nutritional security and climate-resilient agriculture (Devi *et al.* 2014; Banerjee and Maitra, 2020). However, despite its potential, finger millet productivity remains low due to limited genetic improvement and inadequate understanding of yield-contributing traits (Babu *et al.* 2013).

Understanding the interrelationship among quantitative traits is crucial for effective selection in breeding programs. Correlation analysis helps

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determine the degree and direction of association among yield and its component traits, facilitating the identification of traits with direct or indirect effects on grain yield (Panse and Sukhatme, 1985; Dewey and Lu, 1959). However, when multiple correlated traits are considered simultaneously, univariate approaches may not sufficiently explain the complex interrelationships among them. Principal Component Analysis (PCA) serves as an efficient multivariate technique to summarize the variability in large datasets and identify the most important traits contributing to genetic divergence (Jolliffe, 2002; Hair *et al.* 2010). In crop improvement studies, PCA has been effectively used to classify genotypes and determine trait contributions toward yield variation in cereals and millets (Singh *et al.* 2019; Kumari *et al.* 2021).

Hence, the present investigation was undertaken to study the association among yield and yield-related traits through correlation analysis and to identify the major traits contributing to variability using PCA in finger millet genotypes. The outcomes of this study will provide insights for the selection of superior genotypes and efficient utilization of genetic resources in finger millet breeding programs.

MATERIALS AND METHODS

Present investigation was undertaken at Agricultural Research Station, Viziangaram with 29 finger millet genotypes including check varieties (VR 929 and VL 376). Each genotype was sown in plots as 10 rows of 3m length. All the package of practices was followed except for disease control. Data was collected for 14 traits including disease traits. Standard protocol was followed for recording the data. Pearson phenotypic correlation analysis was performed. In addition, Principal Component Analysis (PCA) was also performed with agricolae package of PB perfect to assess the genetic diversity among genotypes and also to identify the major traits contributing to variability among finger millet genotypes.

RESULTS AND DISCUSSION

Correlation Analysis

The correlation matrix (Fig. 1) revealed significant associations among yield and its component traits in finger millet. Grain yield (GY) showed a positive and significant correlation with days to 50% flowering (DFF, r = 0.32**), days to maturity (DM, r = 0.23*), ear length (EL, r = 0.22*), finger length (FL, r = 0.22*), and number of fingers per ear (NFE, r = 0.32*). These findings suggest that genotypes exhibiting longer fingers, higher finger number, and optimum flowering duration tend to produce higher grain yield. Similar positive correlations of grain yield with flowering and panicle traits were reported by Singh *et al.* (2019), Kumari *et al.* (2021), and Shanmugasundaram *et al.* (2020).

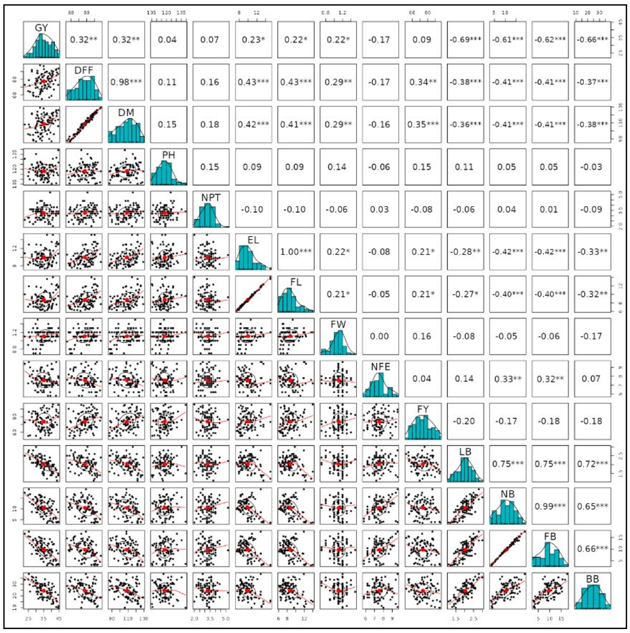

Fig. 1: Correlations among various traits in finger millet

Days to 50% flowering (DFF) and days to maturity (DM) were highly correlated (r = 0.98***), indicating that late-flowering genotypes also matured later. This strong relationship is consistent with earlier studies (Babu *et al.* 2013; Patel *et al.* 2018) and suggests that these phenological traits are genetically linked. Maturity was also significantly and positively correlated with ear length (EL, r = 0.42*), finger length (FL, r = 0.41*), finger width (FL, r = 0.29*), and fodder yield (NFE, r = 0.35*). Similarly, late duration entries had produced higher biomass as per Anuradha *et al.* (2020).

Negative significant correlations were observed between GY and disease traits such as leaf blast (LB, r = –0.69***), neck blast (NB, r = –0.62**), finger blast (FB, r = –0.62***) and banded blight (BB, r = –0.66***). These negative associations are obvious that with the incidence of higher disease reduces grain yield. Similar relationships have been documented in finger millet by Anuradha *et al.* (2020), while Upadhyaya *et al.* (2006) and Devi *et al.* (2014) noticed negative relationship of grain yield with yield components like finger width, leaf width and others. Days maturity also showed negative significance with disease traits indicating that late maturing entries are free from diseases either because of disease escape or due to inherent resistance of the genotypes.

Ear length (EL) and finger length (FL) exhibited significant positive intercorrelation (r = 0.21*), indicating that longer ears generally possess longer fingers which is a desirable combination for improving yield potential. A significant association was also observed between number of fingers per ear (NFE) and GY, emphasizing the contribution of reproductive structures to yield formation.

Principal Component Analysis

Although correlation analysis identifies pairwise associations, PCA further partitions total variability into principal components, highlighting the most influential traits contributing to diversity. Thus, integrating correlation and PCA helps breeders prioritize key traits for simultaneous selection and genetic improvement. The first two principal components (PCs) together explained 61.22% of the total variability, with PC1 accounting major portion of 44.57% and PC2 of 16.6% (Table 1). In addition, the scree plot (Fig. 2) implies that five PCs were able to capture major portion of the total variability as indicated by the steepness of the slope.

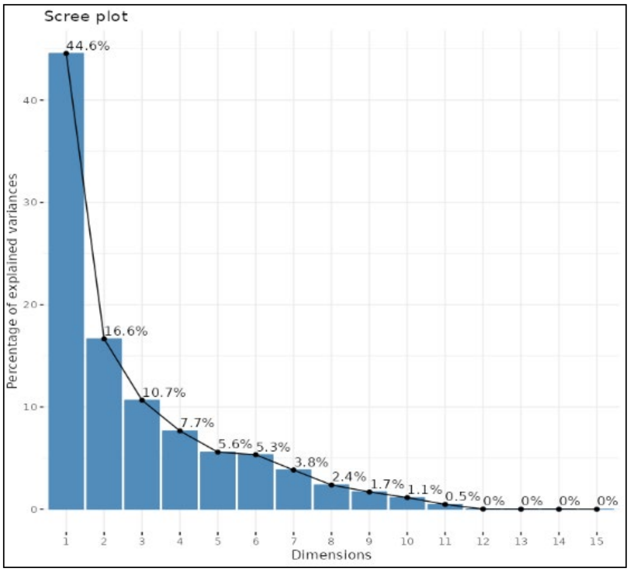

Fig. 2: Scree plot of principal components in finger millet

However, we can say that a substantial portion of phenotypic variation among genotypes can be captured using two principal components, which is in agreement with earlier reports in finger millet and other millets (Singh *et al.* 2019; Kumari *et al.* 2021; Shanmugasundaram *et al.* 2020).

Contribution of Variables to PC1 and PC2

In PC1, the traits contributing most to variability were days to maturity (DM), days to 50% flowering (DFF), Flag leaf length (FLL), finger blast (FB), neck blast (NB), grain yield (GY), leaf blast (LB), banded blight (BB) and ear length (EL), each contributing more than 7% to the total variation (Fig. 3). These traits largely represent duration,

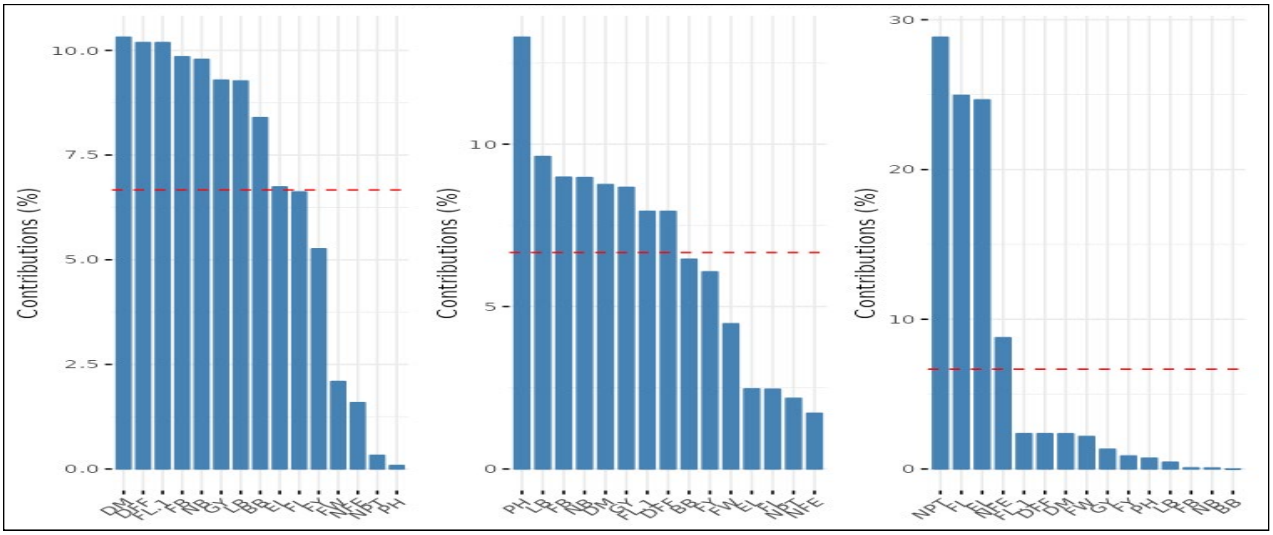

Fig. 3: Contribution of traits variability to PC1, PC2 and PC3

Table 1: Eigenvalues and Eigenvectors

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14
Eigen values and Variance %														
Eigen Value	6.68	2.5	1.6	1.15	0.84	0.8	0.58	0.36	0.25	0.17	0.07	0	0	0
Variance %	44.57	16.65	10.66	7.66	5.59	5.33	3.83	2.37	1.69	1.14	0.47	0.02	0.01	0
Cumulative Variance %	44.57	61.22	71.88	79.54	85.12	90.46	94.29	96.66	98.36	99.5	99.97	99.99	100	100
Eigenvectors														
GY	-0.3	0.29	-0.11	-0.2	0.07	-0.1	0.03	0.25	-0.09	-0.32	0.76	-0.03	0.02	0.02
DFF	-0.32	-0.28	-0.15	0.05	-0.23	0.14	-0.05	0.17	0.2	0.02	0.01	0.37	0.01	-0.13
DM	-0.32	-0.3	-0.15	0.03	-0.19	0.1	-0.01	0.12	0.18	0.04	-0.03	-0.79	0	0.25
PH	-0.03	-0.36	-0.09	0.23	0.53	-0.57	0.34	0.21	0.17	-0.06	-0.04	0.03	0	-0.02
NPT	-0.06	-0.15	-0.54	-0.2	0.4	0.47	0.32	-0.28	-0.3	0	-0.03	0.03	-0.01	0.01
EL	-0.26	-0.16	0.5	0.14	0.14	0.2	0.1	-0.04	-0.25	-0.08	0.01	-0.01	0.71	-0.04
FL	-0.26	-0.16	0.5	0.14	0.11	0.21	0.12	0	-0.24	-0.1	0.03	0.02	-0.7	0.05
FW	-0.14	-0.21	0.15	-0.52	0.44	-0.05	-0.62	-0.14	0.19	0.02	-0.03	0.02	-0.02	0
NFE	0.13	-0.13	0.3	-0.63	-0.21	-0.01	0.57	-0.07	0.32	0.03	0.05	0.02	0.01	0
FLL	-0.32	-0.28	-0.15	0.05	-0.23	0.14	-0.05	0.17	0.2	0.02	0.01	0.37	0.01	-0.13
FY	-0.23	-0.25	-0.09	-0.1	-0.35	-0.53	-0.03	-0.5	-0.45	0.02	0.05	0.04	-0.02	0
LB	0.3	-0.31	0.07	0.15	0.03	0.09	-0.06	-0.04	-0.03	0.65	0.59	-0.01	0	0
NB	0.31	-0.3	-0.03	-0.16	-0.1	0.03	-0.1	0.34	-0.31	-0.23	-0.02	-0.23	-0.03	-0.67
FB	0.31	-0.3	-0.03	-0.14	-0.1	0.02	-0.1	0.37	-0.29	-0.21	-0.04	0.2	0.06	0.68
BB	0.29	-0.25	0	0.27	-0.06	0.14	-0.08	-0.46	0.34	-0.59	0.25	-0.01	0	0.02

grain yield and disease components, indicating that PC1 differentiates genotypes based on yield potential and disease potential. Similar findings were reported by Babu *et al.* (2013) and Patel *et al.* (2018), who observed that phenological duration and finger characteristics, are key contributors to genetic divergence in finger millet.

PC2, which explained 16.6% of the total variation, was mainly influenced by plant height (PH), leaf blast (LB), finger blast (FB), neck blast (NB), days to maturity (DM), grain yield (GY), Flag leaf length (FLL) and days to 50% flowering (DFF). These traits were similar to that of PC1 except for inclusion of plant height as major contributing factor of more than 10%.

PC3 was influenced by number of productive tillers (NPT), finger length (FL), ear length (EL) and number of fingers per ear (NFE) accounting to more than 20%. These traits were associated with reproductive efficiency and biomass production, indicating their importance in discriminating genotypes with different tillering and reproductive capacities.

Circle plot and Biplots

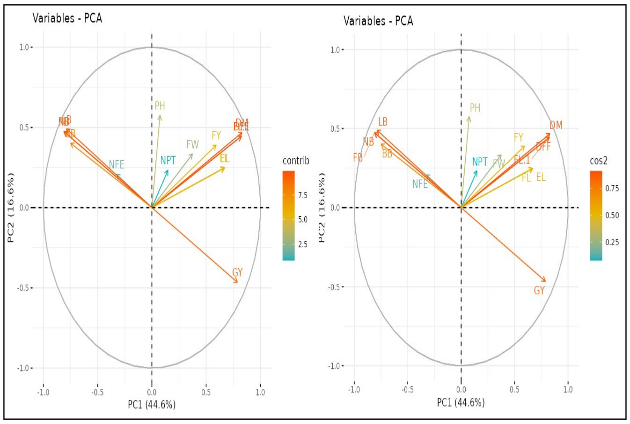

Fig. 4: Circle plot indicating the contribution of various traits towards divergence

The PCA circle plot (Fig. 4) provided a graphical representation of the relationships among various traits utilized for assessing diversity. Traits positioned close to each other such as days to 50% flowering (DFF), days to maturity (DM), ear length (EL), and finger length (FL) were positively associated, suggesting that genotypes with longer fingers tend to mature later. Conversely, grain yield (GY) appeared on the opposite side of leaf blast (LB), neck blast (NB), and banded blight (BB), indicating a negative association between yield and disease traits, consistent with the correlation analysis results (Fig. 1).

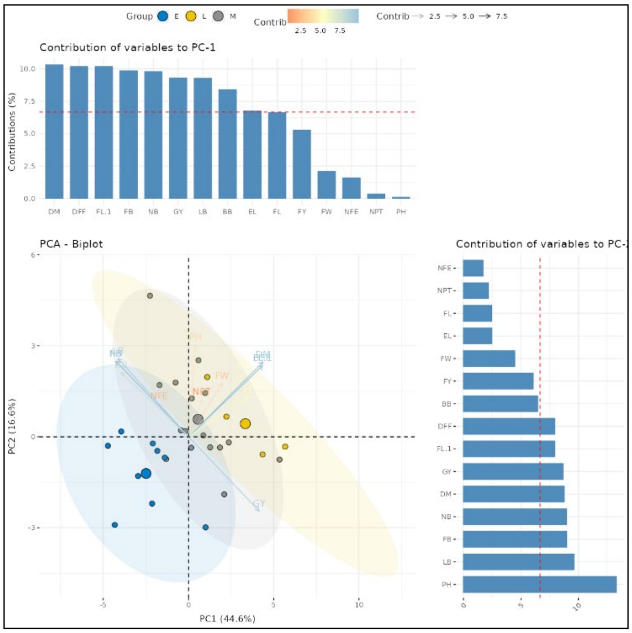

Fig. 5: Biplot showing diversity of finger millet genotypes

Another PCA biplot (Fig. 5) with inclusion of genotypes provided the relationships among traits and with genotypes. This plot also showed the relation among early (E), medium (M) and late (L) duration genotypes. It can be seen clearly that early maturing entries grouped on one side opposing the days to maturity and days to 50% flowering vectors while late maturing entries were on the same side of the vector whereas medium duration genotypes were scattered. It implies that same duration entries share some commonality. Genotypes located near the vector grain yield (GY), can be considered high yielders while those associated with number of productive tillers per plant (NPT) and plant height (PH) exhibited higher biomass accumulation but relatively lower yield efficiency. Genotypes away from disease traits such as LB, FB, NB and BB can be considered as resistant genotypes. These results corroborate earlier findings by Upadhyaya *et al.* (2006) and Devi *et al.* (2014), who highlighted the trade-off between vegetative growth and reproductive productivity in finger millet.

CONCLUSION

Association analysis revealed that longer ears, higher finger number, and optimum maturity duration are likely to give higher grain yield. Diversity analysis through PCA revealed that yield, phenological duration and disease traits were the most discriminating characteristics among the evaluated genotypes. These traits can serve as reliable selection indices for improving yield potential and adaptability in finger millet breeding programs.

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