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RESEARCH ARTICLE

Phenotypic characterization and genetic diversity studies of finger millet (*Eleusine coracana* (L.) Gaertn) germplasms

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Abstract

Eleusine coracana (L.) Gaertn, also known as ragi, is one of the most important millet crops, cultivated across many parts of India. It is well known for its climate resilience and drought tolerance capacity. In the recent years, finger millet is gaining popularity due to its nutritional status and as a measure of crop diversification for small and marginalized farmers. This study was undertaken with the objective to identify various traits that could potentially help in yield enhancement directly or indirectly. During the Kharif, 2022 the experiment was undertaken in a randomized block design (RBD) with three replications. Eight significantly important traits like days to 50 % flowering, days to maturity, plant height, ear length, number of fingers per ear, number of ears per plant, test weight and yield per plant were recorded. Higher mean performance across the majority of traits under study was exhibited by genotypes like Mut-4, G30-GN-2-2, VR-849 and VR-822. Correlation analysis showed a strong and positive association between the number of ears per plant and grain yield, indicating that selecting plants with more ears could potentially increase yield. Path coefficient study showed that the number of ears per plant had the highest direct positive effect on grain yield, followed by the number of days till 50 % flowering. The Mahalanobis D^2 analysis, grouped the genotypes into five groups; the maximum genetic divergence was found in clusters IV and V ($D^2 = 219.92$). This suggests a potential opportunity to select parents with diverse genetic backgrounds for future hybridisation attempts. This study provides valuable findings to improve yield potential of finger millet and enhance crop improvement programmes selection of suitable parents.

Keywords: character association; characterization; Mahanalobis D^2 statistics; path analysis

Introduction

A majority of millet crops are widely found to be cultivated in arid and semi-arid regions of Asia and Africa. *Eleusine coracana* (L.) Gaertn, often referred to locally as Ragi in India and Mandia in Odisha, belongs to the Poaceae family and is thought to have evolved from its wild parent *Eleusine africana*. Its domestication was mostly concentrated in the highlands of Ethiopia and Uganda (1). Finger millet, an allotetraploid plant (2n = 4x = 36, AABB), has exceptional resilience under harsh climatic circumstances like drought, deficient soils and unpredictable precipitation (1, 2). Because of its endurance, it is an essential crop for populations that practise subsistence farming throughout its production zones (2).

Finger millet is the fourth most important millet in the world; however, it is the third most grown millet in India, behind sorghum (jowar) and pearl millet (bajra). Among the top-producing Indian states are Karnataka, Tamil Nadu and Odisha. Finger millet continues to be underutilised in conventional agriculture, but its remarkable nutritional potential is drawing increased interest. Calcium (344 mg/100 g), phosphorus (238 mg/100 g), iron (3.9 mg/100 g), zinc (2.3-2.7 mg/100 g) and important sulfur-containing amino acids are among its most abundant nutrients, all of which are critical for human health (3). Finger millet maintains stable landraces over generations due to its high degree of self-pollination (less than 1 % outcrossing), which makes these landraces vital genetic resources for future crop improvement (3). The crop is essential to local food systems in Odisha, particularly in tribal and rainfed areas where it not only supplies a staple diet but is also ingrained in traditional customs and aids in the preservation of biodiversity (4). However, given contemporary issues like climate change, nutritional insecurity and the demand for sustainable farming methods, the genetic potential of these native finger millet germplasms is still mainly unrealized (5).

For conservation targeted breeding and crop improvement efforts, it is essential to investigate the genetic variety and variability found in germplasm collections. Based on observable agronomic variables, phenotypic characterization offers a useful method for evaluating variability because these traits are influenced by the genetic composition of the plant and can be used to successfully direct genotype selection (6). The objectives of this study are to quantify the degree and type of variability in important agronomic traits, analyse the relationships between yield and the characters that contribute to it using correlation and path coefficient analyses and use multivariate statistical tools like Mahalanobis D^2 statistics to investigate genetic divergence among the genotypes (6, 7). This would help to bring improvement in the further finger millet crop improvement programmes.

Materials and Methods

Plant accessions

During Kharif season of 2022, the present investigation was conducted at the EB-II section of the Department of Plant Breeding and Genetics, Odisha University of Agriculture & Technology, Bhubaneswar (20°52′ N, 82°52′ E). The experiment was carried out using 30 germplasms of finger millet germplasm sown in RBD with three replications. The germplasms were selected based on their local adaptation and agronomic performances. The germplasm under investigation has been presented in Table 1. The crop was grown in a well-drained, loamy soil with a spacing of 20 cm x 10 cm. The required agronomical packages of practices were followed during the experimental process to raise a good crop. The package of practices for optimal growth includes 2-3 ploughings, sowing during the Kharif season (June), application of 40:20:20 kg/ha N:P:K fertilizers, timely weeding at 20 and 40 days after sowing and protective irrigation during dry spells. Observations were recorded for eight quantitative traits like days to 50 % flowering, days to maturity, plant height (cm), ear length (cm), number of fingers per ear, number of ears per plant, 1000-seed weight (g) and grain yield per plant (g). These observations were subjected to statistical analysis.

Statistical analysis

The statistical significance of differences among treatments were evaluated, the collected data were subjected to two-way analysis of variance (ANOVA) (8). The mean effects of the treatments were compared using the Least Significant Difference (LSD) test at a 5 % probability level (using WINDOSTAT software version 9.30.).

Multivariate analysis

One of the significant steps in plant breeding and crop improvement is selection. And for selection to be effective, identification of traits that has significant and positive effective on yield is important. In this context, correlation analysis plays a crucial role in finger millet research by revealing the interrelationships among various traits associated with yield. Understanding these associations helps in the identification of germplasms that exhibit desirable traits for enhanced yield potential in finger millet. Such understandings are invaluable for researchers, allowing them to target specific traits that significantly contribute to yield and quality (8).

By differentiating the observed connections into direct and indirect effects, path coefficient analysis enhances correlation studies and provides an increased understanding of the causal links between traits (8). By identifying the traits that have the greatest direct impact on yield-related measures, this analytical method aids in breeding program selection. WINDOSTAT software version 9.30 was used in this work to conduct multivariate analysis, such as correlation and path coefficient calculations.

Genetic diversity analysis

Mahalanobis D^2 statistics, a reliable multivariate method for analysing genetic diversity and correlations among genotypes, were used to evaluate genetic divergence among the finger millet genotypes. The genotypes were grouped into discrete clusters using Tocher's clustering method, which made it easier to identify genetically varied groups (9). The amount of genetic variation within and between groups was measured using both intra-cluster and inter-cluster distances. WINDOSTAT version 9.30 was also used for this investigation.

Results

Analysis of variance

For every attribute assessed in this study, the genotypes showed highly significant genetic differences. The findings verified that each trait's observed variability was statistically significant (Table 2).

Mean performances

The yield potentiality of the finger millet genotypes was evaluated by analysing their mean performances for characteristics enhancement. Mean performance evaluation helps to estimate the trait performance across genotypes and enabling the identification of superior lines. The mean performances of the traits under study have been presented in Fig. 1 & 2. The genotypes that showed the highest number of ears per plant, ranging from three to four ears per plant were G30-GN-2-2, Mut-4 and G26-GN-1-2. With numbers ranging from 7 to 9, genotypes G20-GG-2-4, VL 322 and VL 768 reported the highest number of fingers per ear. G30-GN-2-2 (22.31 g), Mut-4 (21.48 g) and

Table 1. List of genotypes of finger millet used in investigation

S. No.	Genotypes	S. No.	Genotypes
1	Mut-3	16	G39-GG-2-3
2	Mut-4	17	GPU-157
3	V3-VG-3	18	PR-202
4	V21-VE-3-7	19	P5-400
5	MR-33	20	RES-110
6	BM-107-2	21	RAU-8
7	BM-110-2	22	SRS-2
8	MG-1-3	23	VL-149
9	G5-GG-2-1	24	VL-322
10	G18-GG-2-2	25	VR-708
11	G20-GG-2-4	26	VR-768
12	G22-GE-3-2	27	VR-822
13	G24-GE-3-4	28	VR-849
14	G26-GN-1-2	29	Suvra
15	G30-GN-2-2	30	Nilanchala

Table 2. ANOVA for various quantitative traits for finger millet

S. No.	Sources	Replication	Treatment	Error
	Degree of freedom	**2**	**29**	**58**
1	Days to 50 % flowering	32.643	163.740**	36.665
2	Days to maturity	82.242	153.439**	59.529
3	Plant height (cm)	31.307	233.282**	75.999
4	Finger length (cm)	0.006	4.195**	0.365
5	Number of fingers per ear	0.060	2.622**	0.190
6	Number of ears per plant	0.108	1.571**	0.036
7	1000 seed weight (g)	0.015	0.112**	0.040
8	Grain yield per plant (g)	0.429	68.866**	0.837

** Significant at 1 % level

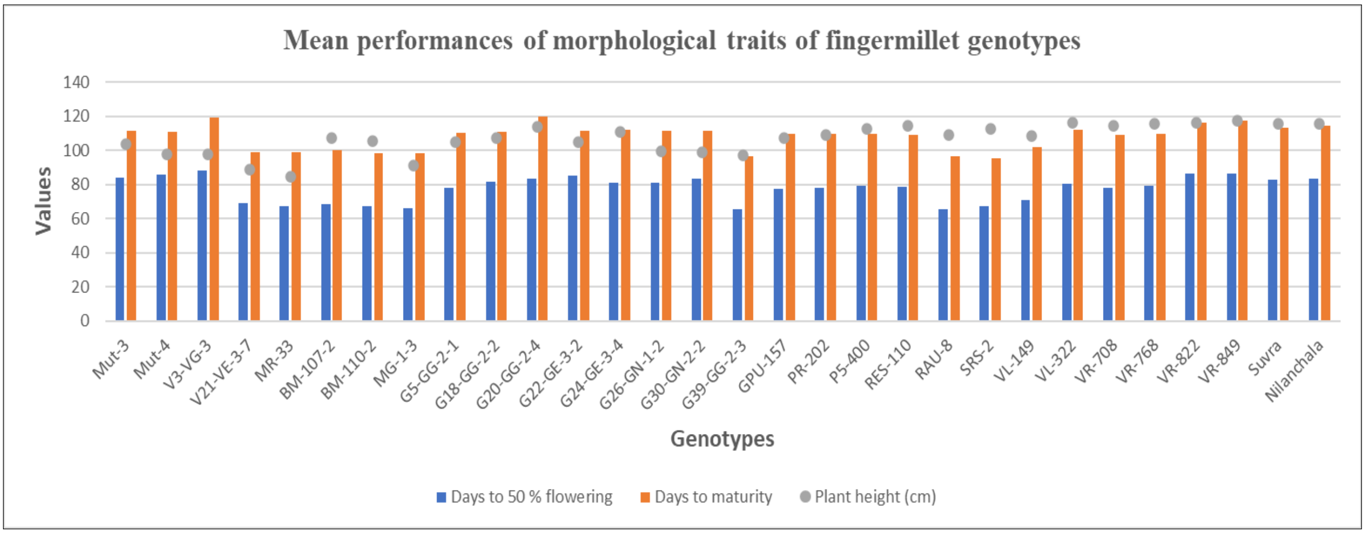

Fig. 1. Morphological characterization of traits in finger millet genotypes (days to 50 % flowering, days to maturity, plant height).

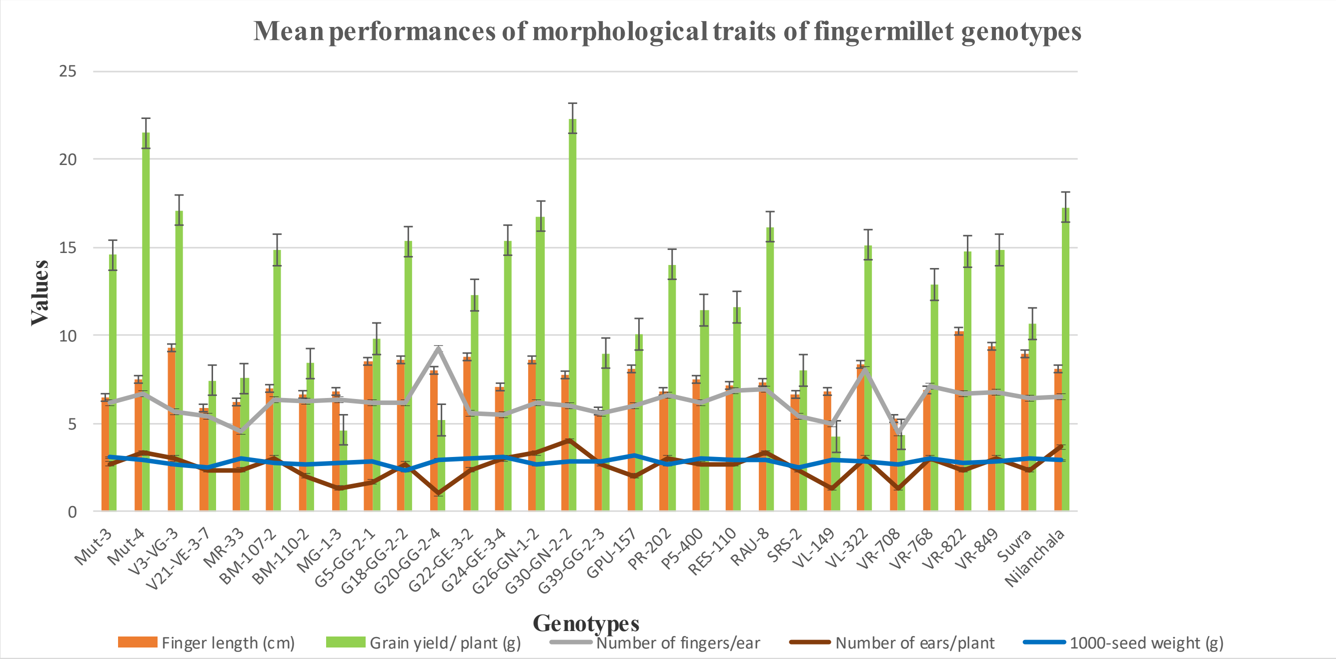

Fig. 2. Morphological characterization of traits in finger millet genotypes (finger length, grain yield per plant, number of fingers per ear, number of ears per plant, 1000-seed weight)

Nilanchala (17.27 g) had the highest grain yields per plant. Genotypes G39-GG-2-3 and RAU-8 showed the shortest periods of time to 50 % flowering and days to maturity, with both flowering at about 65 days and maturing at about 96 days. Mut-4, G30-GN-2-2, VR-849 and VR-822 were the lines that performed the best overall, with higher mean performance across the majority of traits under study.

Genetic variability and heritability analysis

For all characteristics, the phenotypic coefficient of variation (PCV) was marginally greater than the genotypic coefficient of variation (GCV), indicating a small environmental influence (Table 3). Significantly, both PCV and GCV were high for the number of ears per plant (PCV: 28.96 %, GCV: 27.99 %) and grain yield per plant (PCV: 39.61 %, GCV: 38.90 %), suggesting excellent genetic control

Table 3. Estimates of mean, range and genetic parameters for the quantitative traits for finger millet

S. No.	Traits	Mean	Range	CV (%)	GCV (%)	PCV (%)	h^2_{bs} (%)	GA	GAM
1	Days to 50 % flowering	77.74	65.33 - 88.33	7.79	8.37	11.43	53.60	9.82	12.63
2	Days to maturity	108.2	95.67 -119.67	7.13	5.17	8.81	34.46	6.77	6.25
3	Plant height (cm)	106.67	84.51 - 117.33	8.17	6.79	10.62	40.82	9.53	8.93
4	Ear length (cm)	7.53	5.23 - 10.2	8.02	15.00	17.01	77.78	2.05	27.25
5	Number of fingers per ear	6.22	4.47 - 9.2	7.01	14.48	16.09	81.04	1.67	26.86
6	Number of ears per plant	2.56	1 - 4	7.42	27.99	28.96	93.43	1.42	55.73
7	1000-seed weight (g)	2.82	2.29 - 3.13	7.14	5.48	9.00	37.05	0.19	6.87
8	Grain yield per plant (g)	12.24	4.22 - 22.31	7.47	38.90	39.61	96.44	9.63	78.70

(CV: Coefficients of variation; h^2_{bs}: Heritability broad sense; GA: Genetic advance at 5 %; GAM: Genetic advance over mean at 5 %)

and significant room for selection-based improvement. As a fraction of the mean, grain output per plant showed the highest heritability and genetic advancement, followed by finger length and the number of ears per plant. High genetic advancement and high heritability point to additive gene activity and successful selection for these qualities. In addition to showing significant GCV and PCV, traits like finger length and number of fingers per ear also showed strong heritability and genetic advancement, suggesting that they are suitable for genetic improvement. According to these results, there is a great deal of room for improvement in grain production and the main characteristics that contribute to it through focused breeding techniques.

Association between yield and related traits

The association between different characteristics under study and grain yield was evaluated using correlation analysis. According to the studies, phenotypic correlations may be impacted by environmental variation, while genotypic correlation coefficients were shown to be greater than phenotypic ones (Table 4). This suggests that trait connections were predominantly controlled by genetic variables. At both the phenotypic (0.865) and genotypic (0.916) levels, the highest significant positive association was found between the number of ears per plant and grain yield per plant, indicating that increasing the number of ears per plant could effectively increase grain yield. Days to 50 % blooming, days to maturity and finger length were among the other characteristics that shown strong positive correlations with grain output, underscoring their potential as indirect selection criteria in yield enhancement initiatives.

Days to 50 % blooming did not significantly correlate with 1000-seed weight, but it did show strong positive associations with days to maturity (0.567, 0.922), ear length (0.512, 0.812), fingers per ear (0.252, 0.348), number of ears per plant (0.218, 0.320) and plant height (0.212, 0.556). Furthermore, there was a positive correlation between the number of fingers per ear and days to maturity, plant height and ear length, suggesting dependency among important growth and yield factors. These results imply that in finger millet breeding projects, selection for yield-contributing traits including flowering time, finger length and number of ears per plant can be used to increase grain yield.

Path coefficient analysis

Grain yield per plant was used as the dependent variable in path coefficient analysis, which divided the correlation coefficients into direct and indirect effects and revealed the underlying relationships between yield and the traits that contribute to it at the genotypic and phenotypic levels (Fig. 3 & 4). The number of ears per plant had the largest direct influence on grain yield (0.7917 genotypic, 0.8047 phenotypic), followed by ear length, days to 50 % blooming, days to maturity and number of fingers per ear. Of the eight traits analysed, five had positive direct effects on grain output. Plant height and 1000-seed weight, on the other hand, showed detrimental direct effects on grain yield. Furthermore, traits such as days to maturity, ear length, number of fingers per ear, number of ears per plant and days to 50 % flowering exerted favourable indirect effects on grain yield, whereas plant height and 1000-seed weight contributed negative indirect effects. Through a number of characteristics such as days

Table 4. Phenotypic and genotypic correlation coefficients among eight quantitative traits of finger millet genotypes

Characters	Days to 50 % flowering	Days to maturity	Plant height	Ear length	Number of fingers per ear	Number of ears per plant	1000-seed weight	Grain yield per plant
Days to 50 % flowering^{p}	1	0.567**	0.212*	0.512**	0.252*	0.218*	0.139	0.433**
Days to 50 % flowering^{g}	1	0.922**	0.556**	0.812**	0.348**	0.320**	0.139	0.622**
Days to maturity^{p}		1	0.243*	0.473**	0.287**	0.132	0.125	0.314**
Days to maturity^{g}		1	0.701**	0.927**	0.546**	0.204	0.243*	0.539**
Plant height^{p}			1	0.272**	0.326**	0.022	0.186	0.077
Plant height^{g}			1	0.382**	0.550**	0.012	0.096	0.081
Ear length^{p}				1	0.321**	0.192	0.031	0.420**
Ear length^{g}				1	0.436**	0.217*	0.018	0.489**
Number of fingers per ear^{p}					1	0.076	0.144	0.197
Number of fingers per ear^{g}					1	0.096	0.153	0.234*
Number of ears per plant^{p}						1	0.020	0.865**
Number of ears per plant^{g}						1	0.013	0.916**
1000-seed weight^{p}							1	0.021
1000-seed weight^{g}							1	0.046
Grain yield per plant^{p}								1
Grain yield per plant^{g}								1

* Significant at 5 % level; ** Significant at 1 % level; ^{p}: Phenotypic correlation, ^{g}: Genotypic correlation

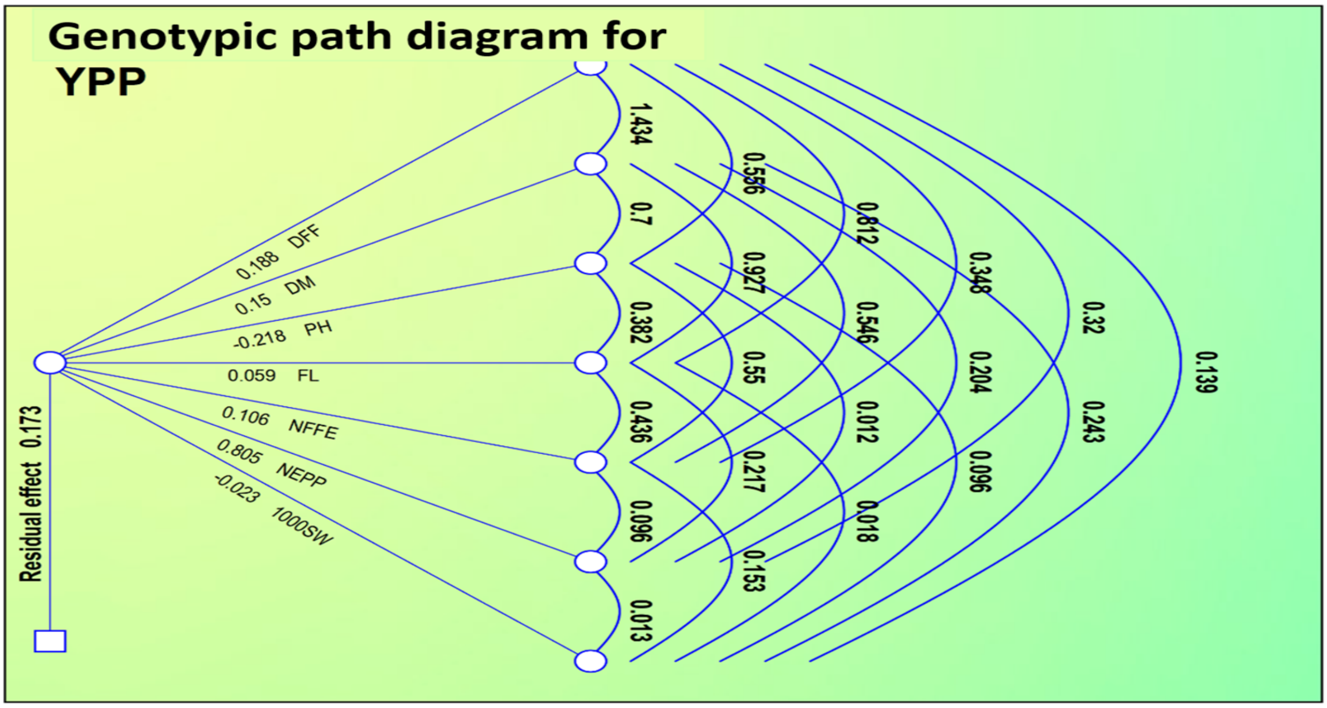

Fig. 3. Genotypic path diagram in finger millet germplasms for eight quantitative morphological traits.

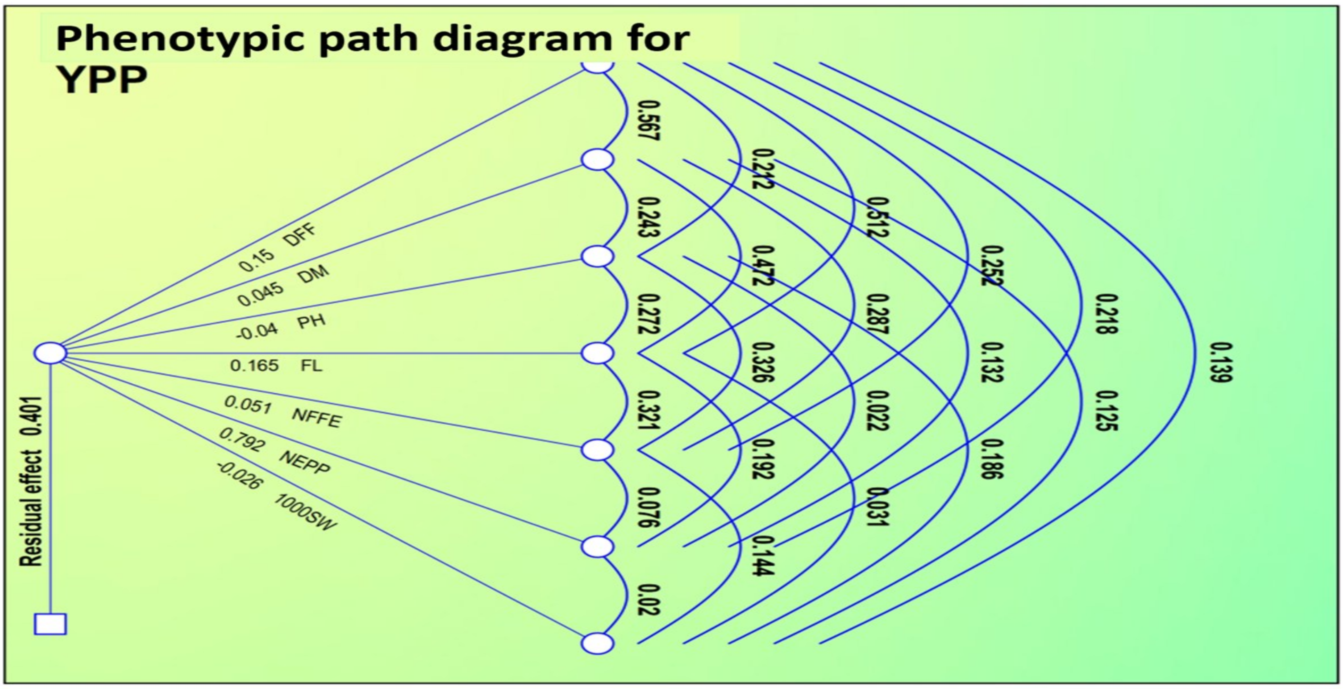

Fig. 4. Phenotypic path diagram in finger millet germplasms for eight quantitative morphological traits.

to flowering, ear length and number of ears per plant, days to maturity also had a favourable indirect impact on grain output. The most important trait for increasing grain yield, according to these findings is the number of ears per plant. Other traits like flowering time and ear length also play a significant role through direct and indirect pathways, helping to guide targeted selection in breeding programs.

Genetic diversity analysis

The Mahalanobis D^2 statistics, divided the thirty finger millet genotypes into five distinct clusters (Table 5, Fig. 5). The greatest number of genotypes (i.e., 18 genotypes) was found in cluster I, which was followed by cluster III (8 genotypes), cluster IV (2 genotypes) and clusters II and V, each of which had one genotype. Cluster III had the highest level of genetic variability (16.28) and cluster IV the lowest (5.23), with intra-cluster distances ranging from 0 to 16.28. There was no intra-cluster variability in Clusters II or V. Clusters IV and V had the highest inter-cluster divergence (219.92), indicating significant genetic dissimilarity, while clusters II and III had the lowest difference (21.34) (Fig. 6).

Significant trait variation has been identified between clusters based on cluster means (Table 6). For breeding high-yielding genotypes, Cluster VI showed promise since it had the greatest values for days to 50 % blooming, ears per plant and grain yield. The early maturity qualities displayed by Cluster III genotypes made them appropriate for short-duration cultivars. The largest finger length was found in cluster II, while the highest number of fingers per ear, plant height and 1000-seed weight were found in cluster V, which also exhibited poor yield-related traits.

Table 5. Clustering patters of the finger millet genotypes

Cluster	Number of genotypes	Name of genotypes
I	18	P5-400, RES-110, VR-768, PR-202, Mut-3, BM-107-2, G24-GE-3-4, G18-GG-2-2, G22-GE-3-2, VR-849, VL-322, Suvra, VR-822, G26-GN-1-2, V3-VG-3, RAU-8, Nilanchala, GPU-157
II	1	G5-GG-2-1
III	8	BM-110-2, SRS-2, V21-VE-3-7, G39-GG-2-3, MR-33, MG-1-3, VL-149, VR-708
IV	2	Mut-4, G30-GN-2-2
V	1	G20-GG-2-4

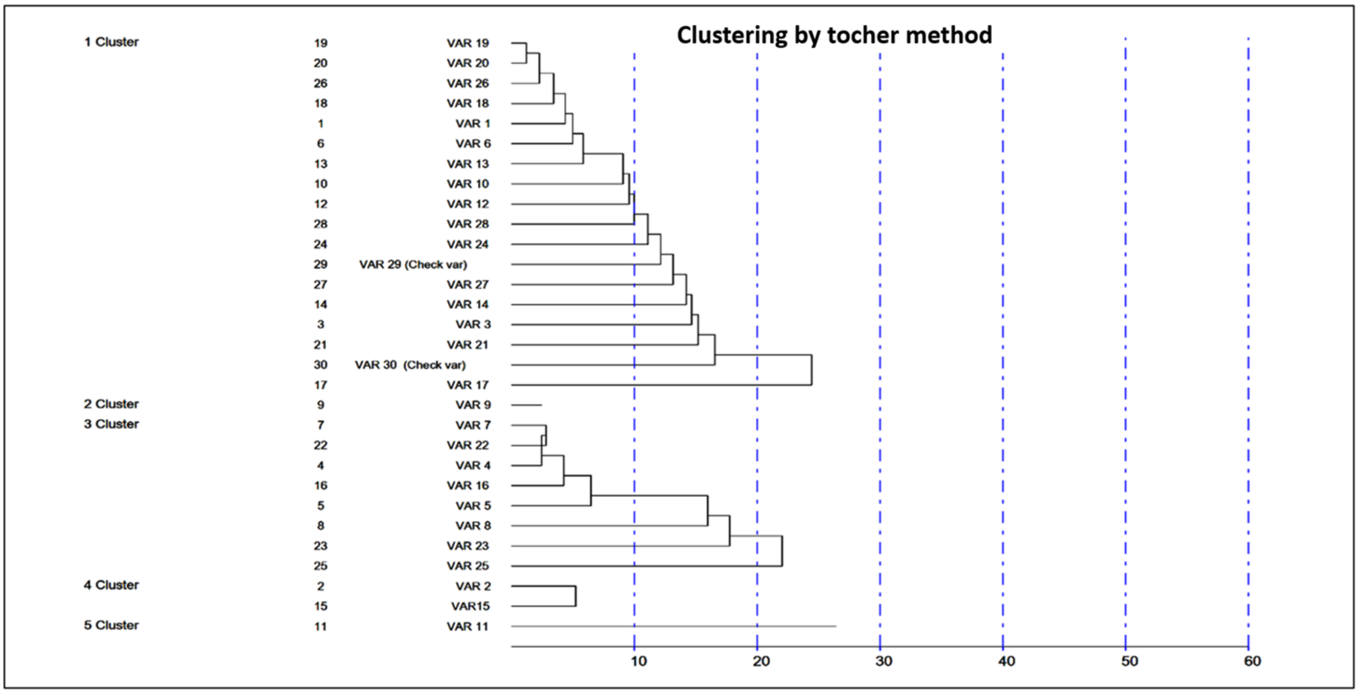

Fig. 5. Dendrogram of thirty genotypes of *E. coracana* (L.) using Tocher's method.

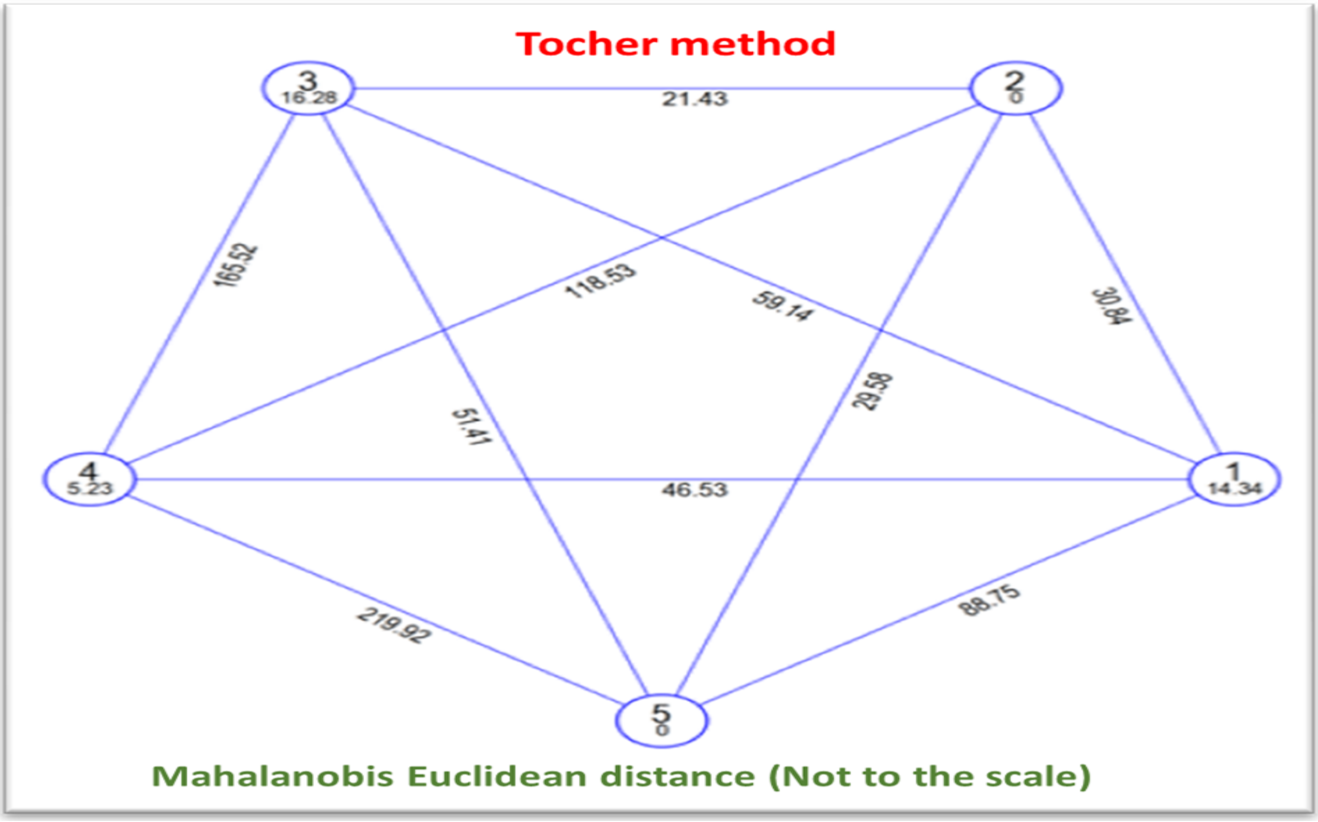

Fig. 6. Intra and inter-cluster distance of thirty maize inbred lines based on Mahalanobis Euclidean distance.

Table 6. Mean performance of the five clusters

Clusters	Days to 50 % flowering	Days to maturity	Plant height (cm)	Finger length (cm)	Number of fingers per ear	Number of ears per plant	1000-seed weight (g)	Grain yield per plant (g)
I	80.5	110.91	110.1	8.02	6.42	2.83	2.85	14.17
II	78.33	110.33	104.91	8.53	6.13	1.67	2.79	9.81
III	69	99.67	100.33	6.23	5.38	1.96	2.72	6.69
IV	84.67	111.17	98.44	7.63	6.34	3.67	2.86	21.9
V	83.67	119.67	113.88	7.97	9.2	1	2.92	5.16

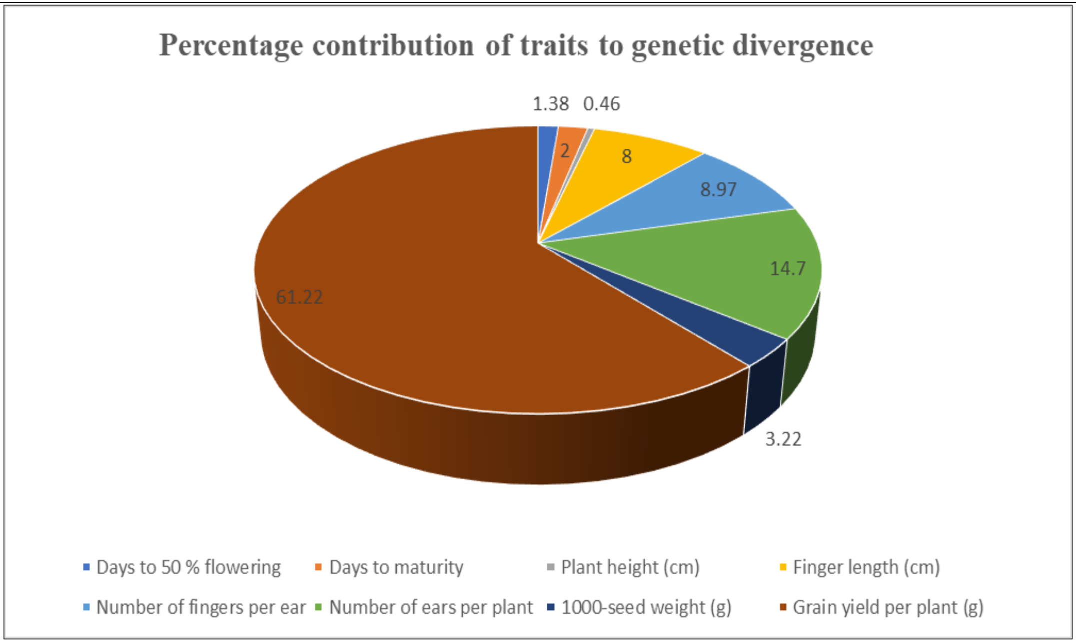

Fig. 7. Percent contribution of eight morpho-agronomic traits to genetic divergence.

Plant height showed a negligible contribution (0.46 %) to genetic divergence, while grain yield per plant (61.22 %) was the most important factor, followed by the number of ears per plant (14.7 %) and finger length (8.97 %) (Fig. 7). To increase productivity, breeding efforts should prioritise both yield components and finger related traits due to the polygenic nature of yield and its sensitivity to environmental factors.

Discussion

The present research highlights the possibility for focused crop development by offering important insights into the genetic variability, phenotypic correlations and diversity across finger millet genotypes gathered from Odisha. For every attribute under study, there was notable variation across the genotypes, which reflected their various regional adaptations and origins (10). Key characteristics include flowering time, maturity, plant height, ear length, fingers per ear, ears per plant, 1000-seed weight and grain production varied significantly across finger millet genotypes, according to mean performance analysis (11). The genotypes with the most ears per plant were G30-GN-2-2, Mut-4 and G26-GN-1-2, whereas the genotypes with the most fingers per ear were G20-GG-2-4, VL 322 and VL 768. Mut-4, Nilanchala and G30-GN-2-2 had the highest grain yields (11). G39-GG-2-3 and RAU-8 showed early flowering and maturity, while Mut-4, G30-GN-2-2, VR-849 and VR-822 were the best-performing lines in general (12).

Strong genetic control with little environmental influence was indicated by the high GCV and PCV for grain production per plant and number of ears per plant (12, 13). For grain yield per plant, number of ears per plant, number of fingers per ear and finger length, broad-sense heritability and high genetic advancement as a percentage of the mean were observed. This suggests that these traits are largely controlled by additive gene effects and are subject to selection (14, 15). The effectiveness of selection is presumably limited by non-additive gene activity in traits with high heritability but moderate genetic advancement (16).

Stronger genetic than environmental influences were highlighted by the fact that genotypic correlations outnumbered phenotypic correlations (17, 18). The number of ears per plant, days to 50 % flowering, days to maturity and finger length - all exhibited a strong positive genotypic correlation with grain yield, highlighting their potential as indirect selection criteria for yield enhancement (19). The number of ears per plant had the strongest positive and significant genotypic correlation with yield, suggesting that it could be a crucial characteristic in selection programs aimed at increasing output (20, 21). The number of ears per plant had the largest positive direct effect on grain yield, according to path coefficient analysis. Days to 50 % blooming, finger length, number of fingers per ear and days to maturity were next in line and these traits also had significant indirect effects (13, 22). In order to maximise breeding results, it is necessary to take indirect factors into account and use constrained selection models, as evidenced by the negative direct effects observed for plant height and 1000-seed weight (23).

The thirty genotypes were divided into five clusters by genetic divergence analysis using Mahalanobis D^2, with cluster I having the most genotypes (20), probably due to similar selection pressures (24, 25). While clusters IV and V displayed the greatest distance between clusters, cluster III displayed the highest intra-cluster variability, indicating that these would be the best parents for hybridisation in order to maximise heterosis and produce transgressive segregants (26, 27). Cluster means showed that while cluster III had genotypes that matured early, cluster VI was superior in terms of ears per plant and grain production, making it appropriate for creating high-yielding cultivars (24, 28). Genetic divergence was mostly caused by grain output per plant, which was followed by finger length and the number of ears per plant (29). In order to obtain consistent yield improvements throughout agroclimatic zones, breeding programs should concentrate not only on grain yield but also on the number of ears per plant and finger length, given the polygenic nature of production and its sensitivity to environmental factors (27, 30).

Strong genetic control is shown by the significant genotypic and phenotypic variation seen for important yield-related parameters including grain yield per plant and number of ears per plant, which makes them appropriate candidates for direct selection (28). These variables' significance as selection indices in breeding programs is suggested by their substantial positive correlations and direct impacts on yield, which have been verified by correlation and path coefficient analyses (19, 20). Furthermore, these qualities' high heritability and significant genetic advancement reinforce their usefulness in attaining effective genetic gain (17). Significant inter- and intra-cluster variability was found in the genetic divergence study using Mahalanobis D^2 statistics, particularly between clusters IV and V, which can be excellent parental sources for hybridisation to take advantage of heterosis and produce superior transgressive segregants (24, 27).

This study not only demonstrates the potential of using a variety of indigenous germplasms in future crop development efforts, but it also reinforces the basis for trait-based selection in finger millet breeding (31). However, supplementary molecular-level investigation would offer deeper insights into the underlying genetic architecture for an effective exploration of phenotypic variance characteristics (32, 33). To confirm the phenotypic findings and pinpoint particular alleles or QTLs linked to desired qualities, future research should use genomic methods such molecular markers or genome-wide association studies (GWAS) (34, 35). Furthermore, evaluating genotype × environment interactions and performance stability might be aided by multi-location studies conducted in various agroclimatic zones (36, 37). Closing this gap would improve precision breeding and aid in the creation of high-yielding, climate-resilient finger millet cultivars that are suited to local requirements.

Conclusion

From the above study, a significant amount of genetic variability was found in 30 finger millet genotypes, indicating the potential of these germplasms for crop development. Significant variation was observed among all the traits under study. The highest mean performance for number of fingers per ears were exhibited by germplasm G20-GG-2-4 while germplasm Mut-4 showed the highest mean performances for number of ears per plant and grain yield. The variation between GCV and PCV was minor suggesting environmental variation has a relatively smaller impact on these traits, which are mostly controlled by genetic factors. This fact was further reinforced by the fact that the genotypic correlation coefficients were consistently greater than their phenotypic correlation coefficients. While the correlation analysis suggested a very strong and positive significant association between number of ears per plant and grain yield thus, suggesting section based on number of ears per plant could potentially increase grain yield. The number of ears per plant had the most direct impact on grain yield, which further clarified the causal links between the traits. Through indirect channels, other characteristics like finger length, number of fingers per ear, days to 50 % flowering and days to maturity all made positive contributions, suggesting their secondary but helpful functions in increasing yield. The Mahalanobis D^2 analysis, grouped the genotypes into five groups; the maximum genetic divergence was found in clusters IV and V (D^2 = 219.92). The formation of transgressive segregants with better agronomic traits and heterotic combinations may arise from the hybridisation between distant clusters made possible by this variety. The development of high-yielding and nutrient-rich cultivars through improved finger millet breeding can significantly enhance food and nutritional security. In marginal and drought-prone locations, it supports sustainable agriculture by fostering resilience to climate stress. As a result, these are a vital tool for developing focused breeding plans meant to increase finger millet productivity and adaptability.

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Authors' contributions

Conceptualization was done by PM and TKM. Material preparation, conduct of experiment, data collection and analysis were performed by PM, GVMR and KRRR. The first draft of the manuscript was written by PM and checked by DL. Statistical analysis was done by SRP, MRM and KCP. The manuscript was reviewed, read and edited with significant contributions by DL and TKM. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

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References

1. D'Andrea C, Lyons D, Haile M, Butler A. Ethnoarchaeological approaches to the study of prehistoric agriculture in the highlands of Ethiopia. In: Marijke van der Veen, editor. The exploitation of plant resources in ancient Africa; 1999. p. 101-22. https://doi.org/10.1007/978-1-4757-6730-8_10
2. Ramashia SE, Anyasi TA, Gwata ET, Meddows-Taylor S, Jideani AI. Processing, nutritional composition and health benefits of finger millet in sub-Saharan Africa. Food Science and Technology. 2019;39:253-66. https://doi.org/10.1590/fst.25017
3. Bhatt A, Singh V, Shrotria PK, Baskheti DC. Coarse grains of Uttaranchal: ensuring sustainable food and nutritional security. Indian Farmer's Digest. 2003;7(1):34-8.
4. Singh P, Srivastava S. Nutrient composition of some new varieties of finger millet (*Eleusine coracana*). Journal of Community Mobilization and Sustainable Development. 2006;1(1-2):115-20.
5. ICAR. Indian Institute of Millets Research (IIMR) [Internet]. [cited

2025 Jun 19]. Available from: https://www.millets.res.in/

6. Sharma N, Bandyopadhyay BB, Chand S, Pandey PK, Baskheti DC, Malik A, Chaudhary R. Determining selection criteria in finger millet (*Eleusine coracana*) genotypes using multivariate analysis. The Indian Journal of Agricultural Sciences. 2022;92(6):763-8. https://doi.org/10.56093/ijas.v92i6.118939
7. Nagaraja TE, Bhat S, Nandini C, Saritha HS, Parveen SG. A multivariate approach to assess the genetic diversity in finger millet [*Eleusine coracana* (L.) Gaertn.] germplasm accessions. EJPB. 2023;14(4):1317-29.
8. Eric MO, Pangirayi T, Paul S, Mwangi G, Abhishek R. Correlations, path coefficient analysis and heritability for quantitative traits in finger millet landraces. Philipp J Sci. 2016;145(2):197-208.
9. Shinde SR, Desai SV, Pawar RM. Genetic variability and character association in finger millet [*Eleusine coracana* (L.) Gaertn]. Int J Plant Sci. 2014;9(1):13-6.
10. Devaliya SD, Singh M, Intawala CG, Bhagora RN. Genetic variability studies in finger millet [*Eleusine coracana* (L.) Gaertn]. Int J Pure App Biosci. 2018;6(1):1007-11.
11. Madhavilatha L, Sudhakar P, Latha P, Shanthi Priya M, Hemanth Kumar M. Studies on genetic variability, correlation and path analysis for quantitative traits in finger millet. J Pharm Innov. 2021;10(6):709-12.
12. Suman A, Surin S, Ahmad E. Finger millet germplasm characterization and evaluation using principal component analysis. Int J Chem Stud. 2019;7(2):1002-5.
13. Mahanthesha M, Sujatha M, Meena AK, Pandravada SR. Correlation and path coefficient analysis in finger millet (*Eleusine coracana* (L.) Gaertn). J Pharmacogn Phytochem. 2018;7(4):3193-6.
14. Shet MN, Jagadeësha GY, Lokesh C, Gireesh, Gowda J. Genetic variability, association and path coefficient studies in two interspecific crosses of finger millet [*Eleusine coracana* (L.) Gaertn]. Int J Plant Sci. 2010;5(1):24-9.
15. Ganapathy S, Nirmalakumari A, Muthiah AR. Genetic variability and interrelationship analyses for economic traits in finger millet germplasm. World Agric Sci. 2011;7(2):185-8.
16. Haradari C, Ugalat J, Nagabhushan A. Study on character association, genetic variability and yield components of finger millet (*Eleusine coracana* L.). J Crop Weed. 2012;8(2):32-5.
17. Dhamdhere DH, Pandey PK, Shrotria PK. Genetic variability, heritability and genetic advance of yield components and mineral nutrients in finger millet (*Eleusine coracana* (L.) Gaertn). PJR. 2011;9(1):46-8.
18. Lule D, Tesfaye K, Fetene M, Santie de Villiers. Multivariate analysis for quantitative traits in finger millet (*Eleusine coracana* subsp. *coracana*) population collected from eastern and southeastern Africa: detection for patterns of genetic diversity. Int J Agric Res. 2012;7(6):303-14. https://doi.org/10.3923/ijar.2012.303.314
19. Vidhate NM, Sarode SB, Gomashe SS. Study of correlation and path analysis in finger millet [*Eleusine coracana* (L.) Gaertn]. Int J Chem Stud. 2020;8(4):118-22. https://doi.org/10.22271/chemi.2020.v8.i4b.9677
20. Chavan BR, Jawale LN, Shinde AV. Correlation and path analysis studies in finger millet for yield and yield contributing traits (*Eleusine coracana* L. Gaertn). Int J Chem Stud. 2020;8(1):2911-4. https://doi.org/10.22271/chemi.2020.v8.i1ar.8713
21. Keerthana K, Chitra S, Subramanian A, Elangovan M. Character association and path coefficient analysis in finger millet (*Eleusine coracana* (L.) Gaertn) genotypes under sodic condition. J Pharm Innov. 2019;8(6):556-9.
22. Anuradha N, Patro TSSK. Genetic variability of quantitative traits in finger millet genotypes. J Pharmacogn Phytochem. 2019;8(3):2664-7.
23. Jadhav R, Ratna Babu D, Lal Ahamed M, Srinivasa Rao V. Character association and path coefficient analysis for grain yield and yield components in finger millet (*Eleusine coracana* (L.) Gaertn). EJPB. 2015;6(2):535-9.
24. Negi S, Kumar V, Bhatt A. Genetic diversity among finger millet [*Eleusine coracana* (L.) Gaertn] genotypes for yield and its contributing traits. IJCMAS. 2017;6(8):3332-7. https://doi.org/10.20546/ijcmas.2017.608.397
25. Lule D, Tesfaye K, Fetene M, De Villers. Inheritance and association of quantitative traits in finger millet (*Eleusine coracana* subsp. *coracana*) landraces collected from eastern and southeastern Africa. International Journal of Genetics. 2012;2(2):12-21.
26. Sapkal SR, Bhavsar VV, Barhate KK, Kohakade SN. Correlation and path analysis for different characteristics in germplasm of finger millet (*Eleusine coracana* (L.) Gaertn.). IJCMAS. 2019;8(1):1020-7. https://doi.org/10.20546/ijcmas.2019.801.111
27. Suryanarayana L, Sekhar D, Tejeswara Rao K. Genetic divergence studies in finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes. J Pharmacogn Phytochem. 2019;8(4):3050-2.
28. Bedis MR, Patil HS, Patil VS, Jangale GD. Genetic divergence in finger millet (*Eleusine coracana* G.). Natl J Plant Improv. 2007;9(1):58-9.
29. Devaliya SD, Singh M, Intawala CG. Genetic divergence studies in finger millet (*Eleusine coracana* (L.) Gaertn.). IJCMAS. 2017;6(11):2017-22. https://doi.org/10.20546/ijcmas.2017.611.240
30. Patel S, Patil HE, Patel B. Genetic diversity analysis in finger millet (*Eleusine coracana* (L.) Gaertn.). JPP. 2020;12:2188-94.
31. Ashoka P, Raut D, Sudeepthi B, Gawande KN, Reddy GSV, Padhan SR, et al. Millet's role as a climate resilient staple for future food security: a review. Int J Environ Clim. 2023;13(11):4542-52. https://doi.org/10.9734/ijecc/2023/v13i113634
32. Krishnababu ME, Mandal O, Begum M, Saikanth DRK, Nandy R, Kaushal K, Mishra P. Exploring millet genetic diversity for improved crop resilience: a review. Int J Environ Clim Change. 2024;14(1):898-905. https://doi.org/10.9734/ijecc/2024/v14i13908
33. Mishra A, Mishra TK, Swain B, Priyadarsini A, Nanda S, Dwibedi SK, Dash M. Molecular heterosis for biomass and biofuel related traits in rice. Cereal Res Commun. 2024;52(3):919-36. https://doi.org/10.1007/s42976-023-00454-7
34. Mishra P, Nanda SR, Barpanda T, Dash M, Dash S, Choudhury S, et al. The complexity of kodo millet: genomic analysis and implications in crop improvement. Planta. 2025;261(1):1-20. https://doi.org/10.1007/s00425-024-04588-8
35. Mishra P, Padhan SR. Finger millet: a sustainable approach for nutritional security and its biofortification. In: Pradhan J, Sahoo JP, Samal KC, Dash M, editors. Millets and other potential crops. CRC Press; 2024. p. 27-43. https://doi.org/10.1201/9781003531937-9
36. Padhan SR, Jat SL, Mishra P, Darjee S, Saini S, Padhan SR, Ranjan S. Corn for biofuel: status, prospects and implications. In: Kausik P, editor. New prospects of maize, IntechOpen; 2024. p. 181-200. https://doi.org/10.5772/intechopen.112227
37. Chowdhury P, Mahi NA, Yeassin R, Chowdhury N, Farrok O. Biomass to biofuel: impacts and mitigation of environmental, health and socioeconomic challenges. Energy Convers Manage X. 2024;25:100889. https://doi.org/10.1016/j.ecmx.2025.100889

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