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Research Note

Genetic diversity assessment in Indian finger millet (*Eleusine coracana* L.) germplasm *via* qualitative traits

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Abstract
The present research investigates the genetic diversity of finger millet (*Eleusine coracana* L.), a nutrient-rich crop vital for sustainable agriculture and food security. Sixteen qualitative traits, including growth habits, pigmentation, and grain attributes, were examined among 150 accessions, shedding light on the diversity within the germplasm. The study quantified and interpreted trait relationships using the Shannon-Weaver Diversity Index and Spearman's Rank Correlation. Principal Component Analysis (PCA) revealed the pivotal traits shaping genetic diversity. Most genotypes exhibited decumbent growth habit and diverse leaf sheath pubescence intensities. Round-shaped grains predominated with copper brown as a common color among grain traits. Pericarp persistence remained consistent among all genotypes. The Shannon-Weaver Diversity Index highlighted varying levels of diversity among traits, with 'ear head shape' exhibiting the highest diversity. Spearman's Rank Correlation exposed relationship between leaf sheath pubescence and seed shattering, emphasizing the importance of trait management in crop breeding. These results provide insights into genetic diversity within finger millet germplasm and its potential application in developing resilient and productive cultivars, addressing food security and sustainability challenges in agriculture.

Keywords: Finger millet, Genetic diversity, Qualitative traits, Spearman's rank correlation, PCA

Food security and safety are critical challenges in agriculture, with implications for human health, nutrition, and overall well-being. The increasing global population (9 billion by 2050), coupled with changing climatic conditions and environmental pressures, has intensified the need for sustainable agricultural practices that ensure an adequate and safe food supply (Pradhan *et al*., 2019). Crop diversification is essential for food security, given climate-related production constraints and global malnutrition issues. Monoculture (*viz.* wheat, rice, maize) reliance on calorie-rich crops necessitating heavy pesticide and fertilizer inputs contributes to these challenges, underscoring the need for diversified crops to enhance resilience and nutritional outcomes. The importance of millet under climate change and population explosion is multifaceted. Millets are resilient crops that thrive in harsh and variable climatic conditions (Singh *et al*., 2023; Wimalasiri *et al*., 2023). Furthermore, millet are rich in essential nutrients such as iron, zinc, and calcium and have a low glycemic index, making them suitable for managing and preventing conditions like diabetes and hyperlipidemia (Mihiretu *et al*., 2023; Anitha *et al*., 2021). In recognition of the benefits of millets for food security, nutrition, and climate resilience, the United Nations has declared 2023 as the International Year of Millets. This initiative aims to increase awareness about the health benefits of millets and promote their cultivation and consumption. By highlighting the importance of millets, the International Year of Millets seeks to address the challenges posed by climate change and population

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growth by promoting sustainable and nutritious food systems (He *et al*., 2022). Diversifying staple crops with millets, or Nutri-cereals, offers a path to nutritional security and sustainable agriculture. Despite these attributes, they remain underutilized globally, making them “orphan cereal crops” in the scientific community (Choudhary *et al*., 2023). Millet’s genetic diversity aids in developing resilient, high-yielding varieties by identifying traits for stress tolerance, yield improvement, and nutritional quality, supporting sustainable agriculture development (Wezel *et al*., 2013; Dwivedi *et al*., 2011).

Finger millet (*Eleusine coracana* (L.) Gaertn.) holds historical, cultural, and nutritional significance in Asia and Africa. It is an allotetraploid plant (2n = 4x = 36), primarily cultivated in arid and semi-arid regions of Central Africa and India. Its name derives from panicles resembling fingers. Globally, it ranks 4th among millets, belonging to the Poaceae family’s chloridoideae sub-family, and is the sole millet in the chlorideae tribe. Finger millet is adaptable and can thrive from sea level to 2400 m in the Himalayas, grown in over 25 African and Asian countries (Sood *et al*., 2019; Hittalmani *et al*., 2017). India leads in production, with 1.19 million hectares, 1.98 million tons, and 1661 kg per ha. Finger millet is a nutritionally rich and adaptable crop, suitable as a staple food and famine reserve due to its protein content (7.3 g/100 g^{-1}), dietary fiber (15–20%), and high calcium content (344 mg/100 g^{-1}), as well as its wide adaptability and extended shelf life under ambient conditions (Upadhyaya *et al.,* 2011; Patil *et al.,* 2022). India is the largest producer of finger millet, with more than 34,160 cultivable genotypes available worldwide, and India alone has 22,583 genotypes (Ramakrishnan *et al*., 2016). The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) holds 6804 finger millet accessions, making it a valuable resource for genetic diversity studies (Goron and Raizada, 2015). By incorporating finger millet into cropping systems, farmers can diversify their income sources and reduce their dependence on a limited number of crops, thereby enhancing their livelihoods and reducing vulnerability to climate change (Mbinda *et al.,* 2019; Makate *et al*., 2016). Genetic diversity analysis is a fundamental component of modern crop improvement strategies. Goron and Raizada (2015) discussed the genetic diversity and genomic resources available for small millet crops, including finger millet, highlighting the importance of utilizing genomic resources to accelerate crop improvement and achieve a new Green Revolution. Agronomic traits, including grain morphology, serve as focal points in breeding programs that enhance crop yield and quality, given their significant impact on crop productivity and resilience to environmental challenges (Biselli *et al*., 2015). Although the assessment of quantitative traits such as yield, plant height, days to maturity, grain test weight, and disease resistance has gained paramount importance in agriculture, it is imperative to underscore the significant role that qualitative traits play in the analysis of genetic diversity. Qualitative traits with discrete, easily distinguishable characteristics offer a unique lens to explore the diversity of finger millet germplasm.

This research article focused on understanding the genetic basis of these qualitative traits and their potential implications for crop improvement in finger millet. The findings of this study contribute to our understanding of the genetic diversity and potential applications of finger millet germplasm.

A collection comprising 154 genotypes of Finger millet (*Eleusine coracana*), encompassing 150 diverse accessions and four checks (KMR301, GPU67, ML365, VR847), was procured from ICAR-NBPGR (National Bureau of Plant Genetic Resources), New Delhi, and ICAR-IIMR (Indian Institute of Millets Research) Rajendranagar, Hyderabad, India. The experiment was laid out in the CCS Haryana Agricultural University research farm, located at coordinates 29.14°N 75.70°E in Hisar, Haryana, during the rainy (*kharif*) seasons of 2019 and 2020. Across the experimental years, the observed annual precipitation exhibited a range between 264.0 and 285.6 mm, with temperatures ranging from 17.8°C and 30.6°C. The germplasm lines were sown in an augmented block design, in single row plots of 2 meters with a plant to plant spacing of 20 cm between adjacent rows and 15 cm between plants. All recommended cultivation practices were followed for better crop growth and establishment.

Observations on 16 qualitative traits, namely, growth habit, vigor, culm branching, lodging, pigmentation, leaf sheath pubescence, ear head color, ear head shape, finger branching, finger position of branching, finger multiple whorls, spikelets discontinuity, seed shattering, grain shape, grain color, and pericarp persistence were recorded as per Finger millet descriptor (IBPGR, 1985). Post-harvest assessments included grain shape, categorized as round, reniform, or ovoid, and grain color, including white creamy, light brown, copper brown, or dark brown. The persistance of the pericarp was examined based on the intactness of pericarp after maturation and drying. Frequency distribution analysis, diversity index computation, principal component analysis (PCA) and Spearman’s rank correlation assessment were conducted using MS Excel, RStudio, and SPSS software. Shannon-Weaver diversity index (1949) was calculated for qualitative traits in MS Excel using the formula

$$H' = -\sum_{i=1}^{n} Pi \log e\, Pi$$

Assessment of Genotypes Based on Qualitative Traits: Sixteen qualitative traits were meticulously evaluated to comprehensively assess all 154 genotypes, as outlined in **Table 1**. The growth-related traits were categorized into four groups: growth habit, vigor, culm branching, and lodging. The decumbent growth habit was the most prevalent, observed in 122 genotypes

Table 1. Proportion of phenotypic classes for 16 qualitative traits studied in finger millet accessions

S. No.	Descriptors	Score/Short form	Sub-Descriptors	No. of Genotypes	Frequency (%)	Shannon-Weaver Diversity Index (H')
			Growth Traits			
1	Growth Habit	DC (1)	Decumbent	122	79.22	0.540
		ER (2)	Erect	31	20.13	
		PR (3)	Prostrate	1	0.65	
2	Vigour	1	Low	66	42.86	1.040
		2	Medium	60	38.96	
		3	High	28	18.18	
3	Culm Branching	1-2	Low	98	63.64	0.779
		3-4	Medium	50	32.47	
		5	High	6	3.90	
4	Lodging	0	Absent	113	73.38	0.860
		1	Low	19	12.34	
		2	Medium	13	8.44	
		3	High	9	5.84	
			Leaf Traits			
5	Pigmentation	0	Absent	125	81.17	0.484
		1	Present	29	18.83	
6	Leaf Sheath Pubescence	1	Low	74	48.05	0.969
		2	Medium	62	40.26	
		3	High	18	11.69	
			Ear Head Traits			
7	Ear Head Color	LG (1)	Light Green	37	24.03	1.055
		DG (2)	Dark Green	90	58.44	
		LP (3)	Light Purple	6	3.90	
		DP (4)	Dark Purple	21	13.64	
8	Ear Head Shape	D (1)	Droopy	11	7.14	1.320
		O (2)	Open	58	37.66	
		SC (3)	Semi-Compact	60	38.96	
		C (4)	Compact	17	11.04	
		F (5)	Fist type	8	5.19	
9	Finger: Branching	0	Absent	133	86.36	0.398
		1	Present	21	13.63	
10	Finger: Position of Branching	T (1)	Thumb	141	91.56	0.289
		F (2)	Fingers	13	8.44	
11	Finger: Multiple Whorl	0	Absent	145	94.16	0.223
		1	Present	9	5.84	
12	Spikelets Discontinuity	0	Absent	100	64.94	0.892
		1	Low	32	20.78	
		2	Medium	13	8.44	
		3	High	3	1.95	
13	Seed Shattering	0	Absent	88	57.14	1.097
		1	Low	38	24.68	
		2	Medium	17	11.04	
		3	High	11	7.14	
			Grain Traits			
14	Grain Shape	RD (1)	Round	91	59.09	0.908
		RF (2)	Reniform	47	30.52	
		O (3)	Ovoid	16	10.39	
15	Grain Color	WC (1)	White Creamy	2	1.30	0.982
		LB (2)	Light Brown	14	9.09	
		CB (3)	Copper Brown	80	51.95	
		DB (4)	Dark Brown	58	37.66	
16	Pericarp Persistence	0	Absent	0	0.00	0.00
		1	Present	154	100.0	

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(79.22%). The erect growth habit was exhibited by 31 genotypes (20.13%), while only one genotype displayed the prostrate growth habit. Our study revealed the prevalence of the decumbent growth habit, contrasting with the predominant erect habit observed in African finger millet germplasm (Lule *et al*., 2012). The observed variation in growth habits across continents may be due to genetic, edaphic, or environmental factors that impact adaptability. The genotypes revealed varying degrees of vigor indices. Notably, 42.86% of the genotypes exhibited a low vigor index, while 38.96% demonstrated a medium vigor index, while 18.18%, displayed a high vigor index, providing insights into the diversity of vigor levels among the genotypes. About 18.18% of the genotypes were observed to produce more than five branches, while , 64% exhibited 1-2 branches and 32.47% displayed 3-4 branches in the culm which is indicative of existence of high diversity among the genotypes. With respect to lodging maximum number of genotypes (73.38%) were observed to be non-lodging. The existence of varying degree of lodging among the genotypes contribute valuable insights into the lodging patterns and diversity by revealing plant structural stability variations. Among the accessions, 125 genotypes (81.17%) exhibited absence of pigmentation on plant surfaces, while 29 genotypes (18.83%) displayed pigmentation characteristics. This is consistent with the findings of Upadhyaya *et al*., 2007 and Louis *et al*., 2023. Seventy four genotypes (48.05%) exhibited a low degree, and 62 genotypes (40.26%) displayed moderate pubescence, while 18 genotypes (11.69%) exhibited a high pubescence. Majority of the genotypes showed dark green colour (58.44%), followed by light green (24.03%), dark purple (13.64%), and light purple (3.90%). Most of the genotypes (60) manifested the semi-compact form, followed by open type (58), while eight genotypes exhibited compact ear head shape. In the studied population, branching on fingers was identified in 21 genotypes while 141 genotypes displayed branching. Fingers with multiple whorls were observed in nine genotypes which underscores the rarity of finger multiple whorls as a distinct trait. Regarding spikelet discontinuity and seed shattering, four different categories were observed. A total of 100 genotypes displayed no discontinuity in spikelets, while 88 genotypes did not exhibit seed shattering. The remaining genotypes demonstrated varying degrees of spikelet discontinuity and seed shattering, ranging from low to high levels. This categorization provides valuable insights into the prevalence and distribution of spikelet discontinuity and seed-shattering traits among the studied genotypes. Round-shaped grains predominated (59.09%) among finger millet genotypes, followed by reniform (30.52%) and ovoid (10.39%) shapes. Regarding grain color, copper brown was the most common (51.95%), followed by dark brown at 37.66%, light brown at 9.09%, and white creamy at 1.30%. Similar diverse seed colours were reported by Karki *et al*., 2020. No variation was observed among the genotypes for persistence of pericarp. Genotypes with persistent pericarp in grains could provide resistance to bird damage, reduce grain spoilage from mold, especially in high-humidity or rainy areas, and exhibit tolerance to shattering.

Shannon-Weaver Diversity (H') Index: The Shannon-Weaver diversity (H') index accesses the germplasm’s phenotypic diversity, allelic richness, and even distribution within the germplasm. Among the examined traits, “ear head shape” displayed the highest H' value (1.320), followed by seed shattering (1.097) and ear head color (1.055). Conversely, the traits “finger: multiple whorl” (0.223) and “finger: position of branching” (0.289) exhibited the lowest H' values, *i.e*., 0.223 & 0.289, respectively (**Table 1**). These findings provide insights into the relative diversity levels among the assessed traits within the germplasm. Application of Shannon-Weaver diversity index (H') for diversity studies was demonstrated by Vetriventhan and Upadhyaya, 2018 in prosomillet and by Ghimire *et al*. 2020 in finger millet.

Spearman’s Rank Correlation: The present research established a significant positive correlation of growth habit with vigor (0.294^{**}), lodging (0.204^{**}), and distinct visual traits *viz*., ear head color (0.204^{*}), pigmentation (0.209^{**}) as illustrated in **Fig. 1**. It demonstrates that prostrate genotypes manifest heightened vigor in plant growth habits compared to their decumbent and erect habits. The elevated vigor also renders prostrate genotypes more susceptible to lodging because of high vigor. Lodging entails the inclination of plant stems to bend/fracture under external influences such as wind, precipitation, or the sheer biomass weight of the plant itself. Thus, prostrate genotypes are inherently predisposed to lodging events. The current research shows a significant negative correlation (-0.170^{**}) between leaf sheath pubescence and seed shattering. This implies that genotypes with higher leaf sheath pubescence tend to exhibit increased seed shattering. Both of these traits hold significance in plant breeding, as leaf sheath pubescence aids in abiotic stress tolerance, such as drought and extreme temperature. To mitigate this undesirable linkage, cross-breeding efforts are necessary to develop superior genotypes with improved traits. Seed shattering exhibited a positive correlation with lodging (0.204^{*}), indicating that it is more likely to occur in genotypes prone to lodging. This relationship underscores the adverse impact of lodging on yield, as it can lead to increased seed loss during harvesting, thereby reducing overall crop productivity. Managing and mitigating these interconnected traits is crucial for optimizing yield and agricultural productivity. Lodging was observed to be significantly influenced by culm branching (0.339^{**}), wherein an increase in the number of culms correlates with an increase in plant biomass, rendering the plant more susceptible to lodging. This highlights the importance of simultaneously enhancing culm strength when breeding for culm branching, as culm branching is a valuable trait contributing to yield improvement. Balancing these traits is essential for developing robust and high-

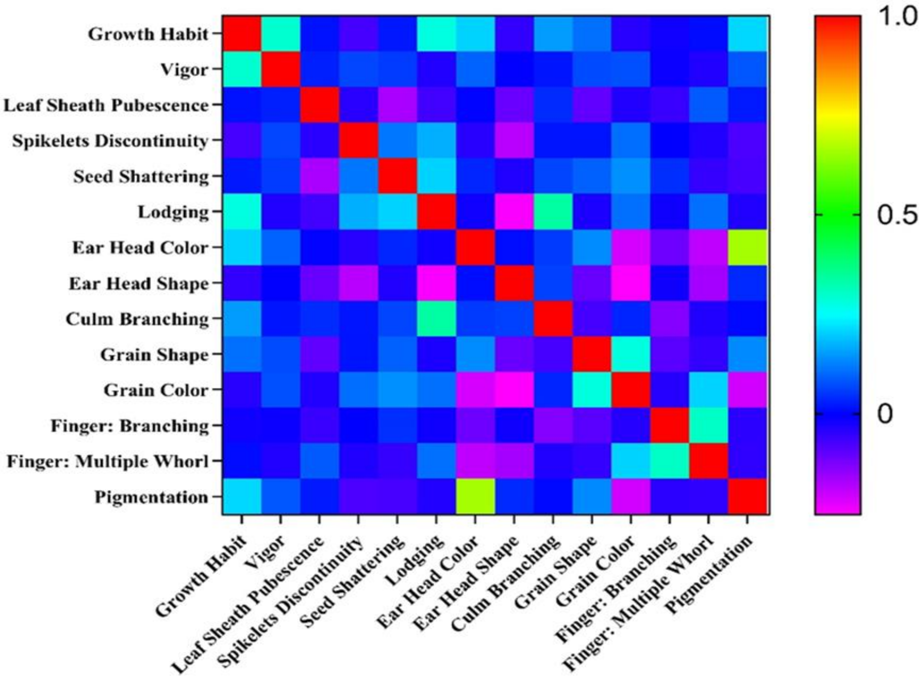

Fig. 1. Investigating Spearman's rank correlation among the qualitative traits of finger millet. The color scheme employs indigo to depict negative correlations between traits, while green and red signify strong positive correlations within the traits

yielding cultivars. A significant negative correlation was observed between ear head color and grain color (-0.211**), indicating that finger millet genotypes with purple-colored ears tend to have whitish grains. This observation aligns with the preference for white-grain genotypes, which are more preferred for consumption as food compared to brown-colored grains, potentially influencing culinary and dietary choices related to finger millet. Significant negative correlation was observed between ear head shape and traits like spikelets discontinuity (-0.185*), lodging (-0.248**), grain color (-0.253**), and finger: multiple whorls (-0.165*) (**Fig. 1**). Notably, droopy ear shapes were associated with lower spikelet discontinuity, indicating a more closely spaced arrangement of spikelets than semi-compact and compact ear shapes. Furthermore, droopy and open ear shapes exhibited greater resistance to lodging. Additionally, grain color correlates with ear shape, with semi-compact and compact genotypes having whitish/creamy grains and droopy and open ears displaying dark brown grains. Lastly, multiple whorls in the inflorescence were more pronounced in droopy and open ears than in semi-compact and compact ears. These findings offer valuable insights into the relationship between ear head shape and essential agronomic traits, with potential applications in crop breeding and management. In the study, grain color exhibited a positive correlation (0.204*) with multiple whorls in inflorescence and a negative correlation (-0.209*) with pigmentation. Pigmentation was positively correlated with ear head color and negatively associated with grain color, revealing intricate relationships among these traits in finger millet genotypes. A robust positive correlation was observed by Singh *et al.* (2023) in finger millet for grain yield per plant with productive tillers, plant height, flag leaf blade length and a significant negative correlation with days to 50% flowering. The correlation between yield and other agronomic traits assists in refining selection proficiency. Analysing the correlation between yield and various agronomic traits is an important tool for selection processes in agricultural breeding programs. Manyasa *et al.*, 2019 reported significant negative correlation of finger millet panicle blast with panicle shape (r= -0.189) and plant color (r= -0.134), which highlights the importance of qualitative traits in disease diagnosis

Principal Component Analysis (PCA): PCA is valuable as it reveals the importance of certain traits that are more critical and aid in formulating precise breeding programs. PCA resulted in 15 independent principal components (PCs) with a cumulative explained variance of 100% (**Table 2**). The corresponding eigenvalues of PCs showed their importance to a character. The outcomes of PCA divulge that the first seven PCs with eigenvalues greater than unity accounted for >65% of the total variability in 154 genotypes for qualitative traits. PC1 holds 14.85% of the total variation. The traits which positively contribute to PC1 were ear head color (0.86), growth habit (0.45), fingers: multiple whorls (0.33), vigor (0.30), grain shape (0.26), fingers branching (0.24), ear head shape (0.22), spikelets discontinuity (0.20), culm branching (0.11),

Table 2. Principal components (PCs) for qualitative traits studied among the germplasm of finger millet

S. No.	Traits	PC1	PC2	PC3	PC4	PC5
1.	Growth Habit	0.303	-0.325	0.058	0.087	-0.124
2.	Vigor	0.202	-0.278	-0.210	-0.186	-0.211
3.	Pigmentation	-0.531	0.094	-0.270	0.143	-0.094
4.	Finger: Branching	0.162	-0.021	-0.417	0.488	-0.111
5.	Finger: Position of Branching	-0.143	-0.213	0.258	-0.181	0.292
6.	Finger: Multiple Whorl	0.223	0.199	-0.448	0.115	0.200
7.	Leaf Sheath Pubescence	0.019	0.032	0.345	0.304	-0.457
8.	Spikelets Discontinuity	0.136	0.197	0.031	0.107	-0.367
9.	Seed Shattering	0.049	0.240	0.362	0.293	-0.107
10.	Lodging	0.024	0.407	-0.011	-0.269	-0.380
11.	Ear Head Color	0.573	-0.088	0.139	-0.088	0.095
12.	Ear Head Shape	0.144	0.440	-0.224	-0.057	0.209
13.	Culm Branching	0.070	-0.224	0.000	0.521	0.250
14.	Grain Shape	0.171	-0.182	-0.275	-0.296	-0.320
15.	Grain Color	-0.284	-0.415	-0.199	0.028	-0.261
16.	Eigen values	2.23	1.67	1.36	1.26	1.17
17.	Proportion of variance	14.85	11.11	9.06	8.41	7.82
18.	Cumulative proportion	14.85	25.97	35.02	43.43	51.25

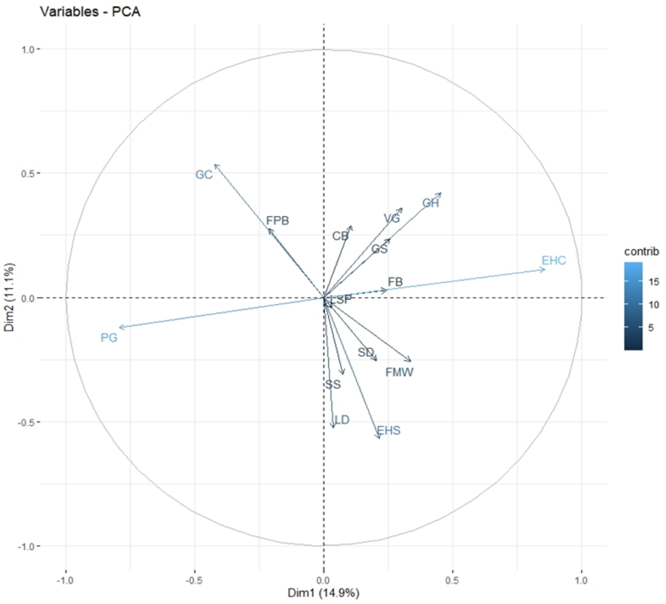

Fig. 2. PCA biplot of variables representing the contribution of qualitative traits for dimensions 1 and 2. Abbreviations used to describe the different qualitative traits of PCA plot.: Growth Habit (GH), Vigor (VG), Pigmentation (PG), Finger: Branching (FB), Finger: Position of Branching (FPB), Finger: Multiple Whorl (FMW), Leaf Sheath Pubescence (LSP), Spikelets Discontinuity (SD), Seed Shattering (SD), Lodging (LD), Ear Head Color (EHC), Ear Head Shape (EHS), Culm Branching (CB), Grain Shape (GS), Grain Color (GC)

seed shattering (0.07), lodging (0.04), and leaf sheath pubescence (0.03) while traits pigmentation (-0.79), grain color (-0.42), and finger: position of branching (-0.21) contribute negatively in PC1 (**Table 2, Fig. 2**).

PC2 holds 11.11% of the total variation, and the traits that govern the highest variation of PC2 were grain color (0.54), growth habit (0.42), and vigor (0.36). PC3 accounted for 9.06% variance and 35.02% cumulative proportion.

Likewise, PC4 and PC5 accounted for 8.41 and 7.82 proportions of variance, respectively. The contributing agronomic traits in PC1 and PC2 were shown in the PCA biplot in **Fig. 2** (Dim1/*x-axis* & Dim2/*y-axis* give the values of PC1 and PC2, respectively). The angle between variables indicates their degree of association, with a smaller angle denoting a stronger relationship and vice versa. Singh *et al*. (2023) studied the genetic diversity of finger millet germplasm for quantitative agronomic traits using PCA and found that the first five PCs with eigen values greater than unity accounted for 74% of the total variability. PCA is a powerful technique for dimensionality reduction and data exploration, it is crucial to provide a biological interpretation of the results explaining why certain traits are grouped in specific principal components. For instance, in finger millet breeding, the biological reasons behind traits like ear head shape and grain color being grouped in a particular PC should be explored. Ear head shape and other related traits contributed significantly positive to PC1, while grain color negatively contributed to PC1. The positive and negative contributions to the same principal component may indicate shared genetic regulation or pleiotropy, where a single gene influences multiple, seemingly unrelated, phenotypic traits. Exploring the genetic loci and molecular pathways governing ear head shape and grain color could provide insights into shared genetic underpinnings. Researchers can uncover valuable insights into the genetic and molecular mechanisms governing these traits by delving deeper into the biological interpretation of the relationship between ear head shape and grain color. This knowledge can be instrumental in developing effective breeding strategies and promoting the genetic improvement of finger millet for enhanced agricultural productivity and quality.

In conclusion, good deal of genetic variability was identified among the finger millet genotypes studied. Spearman's rank correlation analysis revealed valuable trait associations, such as the positive correlations between growth habit and vigor, lodging, ear head color, and pigmentation. Conversely, the negative correlation between leaf sheath pubescence and seed-shattering guides breeding programs. Principal Component Analysis (PCA) revealed that ear head color, growth habit, and grain color contributed to genetic diversity. Finger millet, as an underutilized yet highly nutritious crop, holds promise for enhancing nutritional security and supporting sustainable agriculture, particularly in regions vulnerable to climate change and water scarcity. This research contributes significantly to our knowledge and paves the way for a more resilient and diversified agricultural landscape, ultimately benefiting global food security and sustainability.

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