



Exploring the agro-morphological performance of mini core collection of finger millet [*Eleusine coracana* (L.) Gaertn] germplasm under sodic condition

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Abstract Sodidity refers to the excessive accumulation of sodium ions in soil, which adversely affects soil structure and thereby crop productivity. Finger millet is a highly adaptable crop that contributes significantly to global food security and nutrition. Although, it demonstrates tolerance to various abiotic stresses, cultivars suitable for sodic soils remain limited. To address this gap, a mini core collection of 76 finger millet accessions from ICRISAT, Hyderabad, along with four released cultivars, were evaluated under natural sodicity during the summer 24 and kharif 2024. Genetic variability and diversity analysis for 13 qualitative and 19 yield-related traits among the mini core collection revealed high diversity for ear shape and grain colour, while traits like discontinuity

of spikelets on fingers showed low diversity among the qualitative traits. Spearman rank correlation was used to examine trait interrelationships among the qualitative traits. Mixed model analysis using REML indicated significant variation in most yield traits, except for flag leaf breadth and peduncle length. High phenotypic and genotypic coefficients of variation (PCV and GCV) were recorded for flag leaf length, with moderate variation for most traits, and lower values for days to flowering and days to maturity. Heritability was found to be moderate to high, with genetic advance as a percent of mean (GAM) spanning low to high. Principal Component Analysis (PCA) identified six principal components with eigen values > 1, accounting for 76% of the total variability. Hierarchical clustering grouped accessions into eight clusters, suggesting the potential for selecting diverse parents for breeding. Promising accessions for high yield and other key traits under sodic stress have been identified for future breeding programs which aim at improving sodicity tolerance in finger millet.

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Introduction

Finger millet [*Eleusine coracana* (L.) Gaertn] is an important crop cultivated for food and fodder

purposes in Asia and Africa (Upadhyaya et al. 2007; Caesar et al. 2018). Finger millet is grown in approximately 2.1 million ha with a production of 3.4 million tonnes and a productivity of 1623 kg/ha (Rao et al. 2021). India has the largest finger millet area of 1.1 million hectares with a production of 1.6 million tonnes and an average yield of 1.5 tonnes per hectare (MAO 2023). Finger millet is a significant nutri cereal with high dietary fiber, 7–10% protein and essential amino acids such as cysteine, methionine and tryptophan (Mirza et al. 2014). The grains are also rich in the members of the vitamin B complex (Saleh et al. 2013). The micronutrient concentration in finger millet is relatively higher than that in rice and wheat (Rao and Deosthale 1983). It has high amount of iron (3.9 mg/100 g), zinc (2.3 mg/100 g) (Gopalan et al. 2004) and has remarkable amount of calcium (344 mg/100 g), which is 5 to 30 times higher than any other crop (Maharajan et al. 2021). Finger millet is termed as the ‘wonder crop’ for its nutritional significance and as ‘famine crop’ for its long storability and agronomic significance (Takan et al. 2004).

The crop exhibits tolerance to various biotic and abiotic stresses. It is tolerant to drought, saline and alkali conditions and could tolerate up to a pH of 5.0–8.2 (Duke 1978). This makes the crop extensively grown in arid and semi-arid regions across Asia and Africa (Fakrudin et al. 2004), where it serves as a staple food, primarily in regions vulnerable to food insecurity (Upadhyaya et al. 2007). These semi-arid and arid regions, have a prevalent abiotic stress of high salt accumulation leading to the salinity or alkalinity condition of the soil. Salinity refers to the buildup of soluble salts in the root zone of the soil where plants grow (Divya et al. 2022). Sodicty is a condition characterized by a high concentration of sodium ions occupying the soil’s exchangeable sites. Soil has a pH of > 8.5, EC < 4 dsm⁻¹, ESP > 15, SAR > 13 and the physical condition of the soil becomes poor owing to the dispersion of clay materials, thereby disturbing infiltration and aeration due to the formation of surface crust at the root zone and limited nutrient uptake (Stavi et al. 2021). Sodium-induced osmotic stress and ionic toxicity further impair water absorption and cellular metabolism, reducing photosynthetic efficiency and overall plant vigor (Munns and Tester 2008; Shrivastava and Kumar 2015). These physiological disturbances are known to adversely affect both vegetative and reproductive traits, resulting in

decreased plant height, fewer tillers, shorter panicles, and reduced grain filling (Ashraf 2004). Collectively, these factors contribute to significant yield reductions in crops grown under sodic conditions. Globally sodicity affected soils occupies 618 million hectares (FAO 2015; Daba 2025). In India, soils affected by sodicity cover an area of 3.77 million ha (Rai et al. 2018). Sodic soils occupy 47% of land in 11 states in India and salt affected soils account for approximately 5% of net cultivated area (Kumar and Sharma 2020). Thus, cultivation in sodic soils is unavoidable to meet the food demand of the upheaving population (Singh et al. 2012). The development and cultivation of sodic tolerant cultivars possessing natural adaptation mechanisms would be environmentally safer and more suitable for sustainable crop production in these regions (Sharma et al. 2016) than large-scale amendments (Rahi et al. 2013). Therefore, it is essential to develop finger millet cultivars suited to these regions, combining high yield potential with inherent sodicity tolerance, enabling farmers to achieve better productivity despite the challenging conditions.

Understanding the genetic resources of crops is the first stage in crop improvement programs, which helps to expand the crop’s genetic basis. Germplasm collections may contain accessions from diverse ecological zones, some of which may have naturally evolved mechanisms to cope with sodicity. Characterization of the germplasm is crucial for identifying accessions that are tolerant to sodicity. The presence of considerable diversity may suggest that soil sodicity may act as a selective force for shaping the expression of adaptive traits and influencing the underlying genetic structure of the population. In this regard, the mini core collection of finger millet (Upadhyaya et al. 2010) obtained from the International Crops Research Institute for Semi-Arid Tropics (ICRISAT) was screened to identify the accessions that provides high yield by tolerating sodic conditions. Several investigations have summarized the variability and diversity among finger millet accessions (Singh et al. 2023; Nagaraja et al. 2023), however information on their performance in sodic soil is limited. With these objectives, the present research includes various genetic analysis to study the genetic variability and diversity among the mini-core germplasm accessions of finger millet under sodicity and subsequent grouping was performed based on multivariate analysis.

Materials and methods

Experimental material, site and design

The experimental materials used in this study comprised 80 finger millet accessions with 76 mini-core accessions (Upadhyaya et al. 2010) collected from the ICRISAT, Patancheru and four released cultivars namely TRY 1, Co (Ra) 15, PYR 2 and ATL 1 (Supplementary Table 1). The mini-core accession used in this study represents different countries and is presented in Fig. 1. The experiment was carried out under naturally occurring sodic soil at Anbil Dharmalingam Agricultural College and Research Institute (ADAC &RI), Tamil Nadu Agricultural University (TNAU), Tiruchirappalli, Tamil Nadu, India for two seasons, viz., Summer 2024 and Kharif 2024. The chemical parameters of the soil under which the experiments were conducted are listed in Table 1. The experimental design used was an Augmented Complete Block Design. Each accession was sown in a single row plot of 4 m length, 30 cm between rows and 15 cm between plants. Recommended agronomic practices were meticulously followed to ensure optimal crop growth and development in the field.

Table 1 Soil parameters of the experiment field

Parameters	Season I Summer 2024 (sown in Feb)	Season II Kharif 2024 (sown in Sep)
pH	8.95	8.83
EC (dsm ⁻¹)	0.34	0.26
ESP	36.65	34.98

Data recorded

Morphological characteristics including 13 qualitative traits namely growth habit, pigmentation at leaf juncture, leaf sheath pubescence, culm branching, ear shape, finger branching, branching position, multiple whorls in inflorescence, discontinuity of spikelets on fingers, glume covering, grain color, lodging susceptibility and senescence score were recorded. Nineteen quantitative traits were measured including days to flowering (DF), days to maturity (DM), stem diameter (SD) (cm), plant height (PH) (cm), leaf blade length (LL) (cm), leaf blade width (LW) (cm), number of tillers (NT), number of productive tillers (NPT), flag leaf length (FLL) (cm), flag leaf width (FLB) (cm),

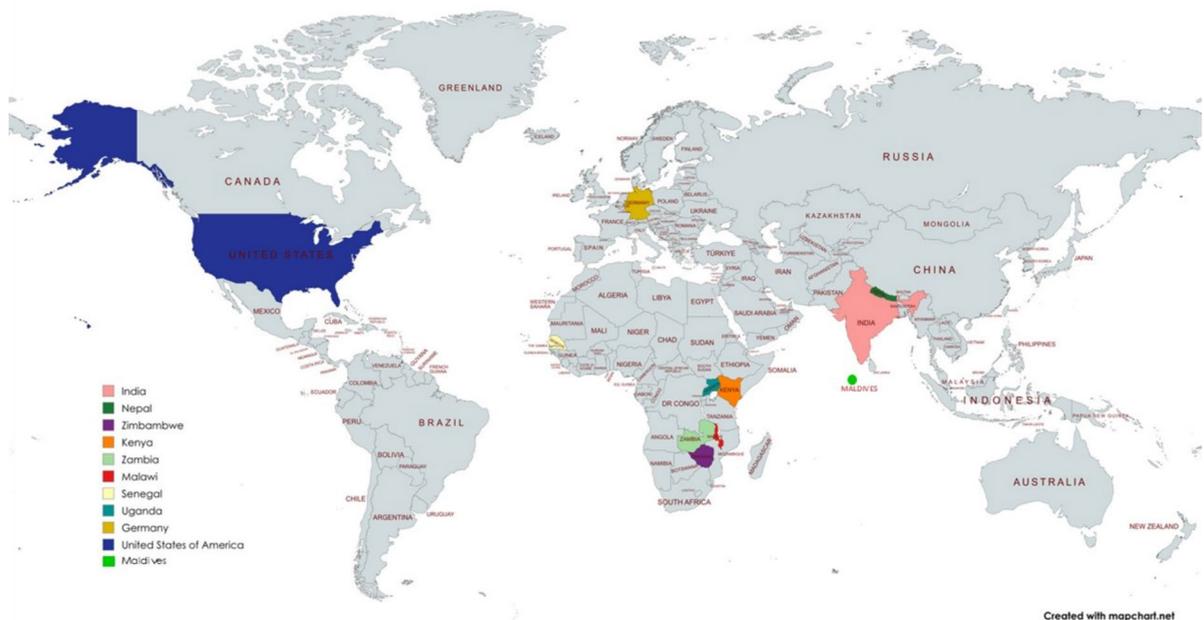


Fig. 1 Origin of different germplasm used in the study

peduncle length (PL) (cm), ear head length (EL) (cm), finger number/ear (FN), finger length (FL) (cm), finger width (FW) (cm), single ear head weight (SEW) (g), thousand grain weight (TGW) (g), fodder yield/ plant (FYP) (g) and grain yield/plant (g). All traits were recorded based on IBPGR descriptors (1985) at relevant growth stages. Quantitative data were recorded from five randomly selected plants from each accession and checks for further statistical analysis.

Statistical analysis

Handling of qualitative trait data

Diversity among the 80 accessions was studied using Shannon-Weaver Diversity index based on 13 qualitative traits. It is a commonly applied diversity measure that incorporates both the abundance and evenness of traits within a group (Shannon 1948). It was calculated based on the formula,

$$H' = \sum_{i=1}^s p_i \ln p_i$$

where H' = Shannon diversity index, S = total number of classes (species richness), p_i = percentage of individuals of one specific class (ie., $p_i = n_i/N$ where n_i = number of individuals in the particular class, and N = total number of individuals of all species), \ln = natural log, Σ = summation of the computations, s = number of traits

The analysis was performed using MS Excel 2021. Relationships among the different qualitative traits were studied by Spearman rank correlation using GRAPES software v.1.1.0 (Gopinath et al. 2021; Jarwar et al. 2019).

Handling of quantitative trait data

The data recorded in two environments were subjected to REML-BLUP (Restricted Maximum Likelihood/Best Linear Unbiased Prediction) analysis for individual and pooled data using 'lme4' package of R software v.4.5.1, considering the accessions as random effects and blocks in individual analysis and years in pooled analysis as fixed effect. The BLUP values obtained using data from the two seasons were used for further downstream analysis (Chaudhary et al. 2025). Significance of the variances was

tested using Likelihood Ratio Test (LRT) and Wald statistics. Phenotypic variance (σ_p^2) was obtained from the sum of the genotypic and error variances ($\sigma_p^2 = \sigma_g^2 + \sigma_e^2$) (Allard 1960). From the variances obtained, the phenotypic coefficient of variance, genotypic coefficient of variation, broad-sense heritability and genetic advance as percent of mean (GAM) were calculated (Lush et al. 1940; Johnson et al 1955a). They were classified as low, medium and high as suggested by Sivasubramanian and Madhavamenon 1973; Johnson et al. 1955a. The data were subjected to correlation analysis (Johnson et al. 1955b) and path analysis to study the relationship between yield attributes and grain yield/plant. The direct and indirect effects were graded as suggested by Lenka and Mishra (1973). The data were further subjected to multivariate analysis such as principal component analysis and hierarchical clustering. PCA aids in identifying the key traits contributing to the total variation and reduces the volume of data. Correlation analysis and the principal component analysis were performed using the GRAPES software v.1.1.0 (Gopinath et al. 2021). Genetic diversity was assessed with agglomerative hierarchical clustering based on Ward's approach and Euclidean distances, implemented through the 'stats' package in R software v.4.5.1.

Results and discussion

Assessment of discrete morphological variations in finger millet

Frequency distribution of accessions for thirteen qualitative traits

Eighty accessions were morphologically characterized using 13 discrete traits (Table 2 and Figs. 2 and 3). Of the 80 accessions, 25% showed a decumbent type of growth habit and 75% were erect. The growth habits, prostrate and decumbent types tend to suppress weed growth and combat moisture stress by covering the soil and reducing evapotranspiration. However, erect types are highly favoured because of their ability to gain high beneficial light interception and distribution, better radiation use efficiency, better canopy photosynthesis and more plant accommodation per unit area and thereby increasing the

Table 2 Frequency distribution of accessions for 13 qualitative traits

S. No	Traits	Phenotypic classes	Relative frequency	Frequency of accessions (%)	Shannon-Weaver Diversity Index (H')
<i>Growth traits</i>					
1	Growth habit	Decumbent	20	25.00	0.562
		Erect	60	75.00	
2	Pigmentation at leaf juncture	Present	17	21.25	0.517
		Absent	63	78.75	
3	Leaf sheath Pubescence	Absent	33	41.25	0.678
		Present	47	58.75	
4	Culm branching	Present	29	36.25	0.655
		Absent	51	63.75	
<i>Ear traits</i>					
5	Ear shape	Droopy	1	1.25	1.271
		Open	15	18.75	
		Semi-compact	37	46.25	
		Compact	21	26.25	
		Fist	6	7.50	
6	Finger branching	Absent	74	92.50	0.266
		Present	6	7.50	
7	Branching position	All fingers	3	3.75	0.693
		Thumb	3	3.75	
8	Multiple whorls in inflorescence	Present	6	7.50	0.266
		Absent	74	92.5	
9	Discontinuity of spikelets	Present	1	1.25	0.067
		Absent	79	98.75	
<i>Grain traits</i>					
10	Glume covering	Enclosed	17	21.25	0.736
		Intermediate	58	72.50	
		Exposed	5	6.25	
11	Grain colour	White	3	3.75	1.364
		Light brown	37	46.25	
		Copper brown	23	28.75	
		Brown	2	2.50	
		Dark brown	10	12.50	
12	Lodging susceptibility	Purple brown	5	6.25	0.980
		Low	32	40.00	
		Intermediate	38	47.50	
		High	10	12.50	
		Dead	4	5.00	
13	Senescence score	Actively growing	76	95.00	0.199
Mean					0.635

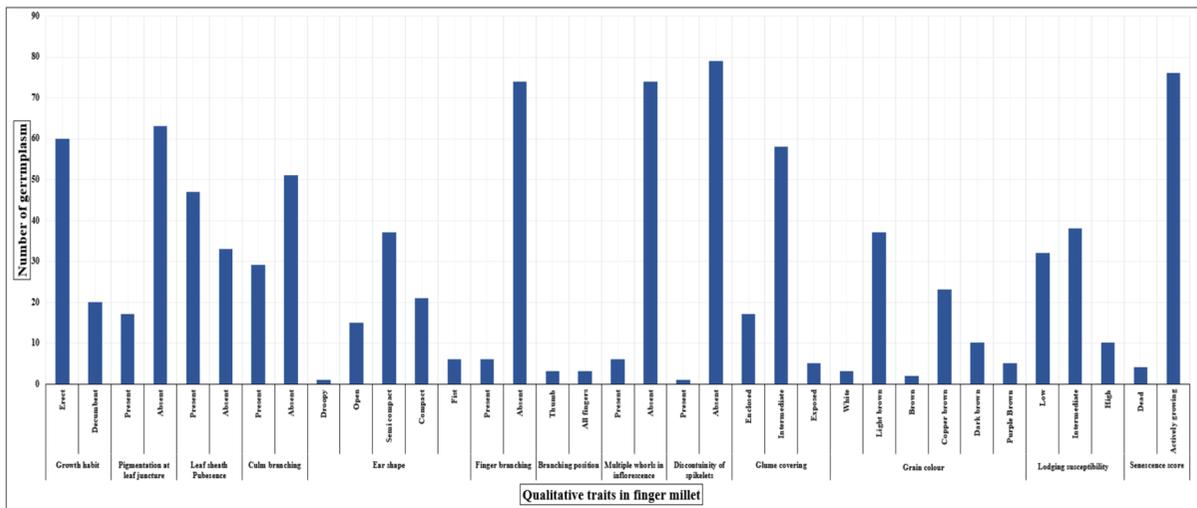


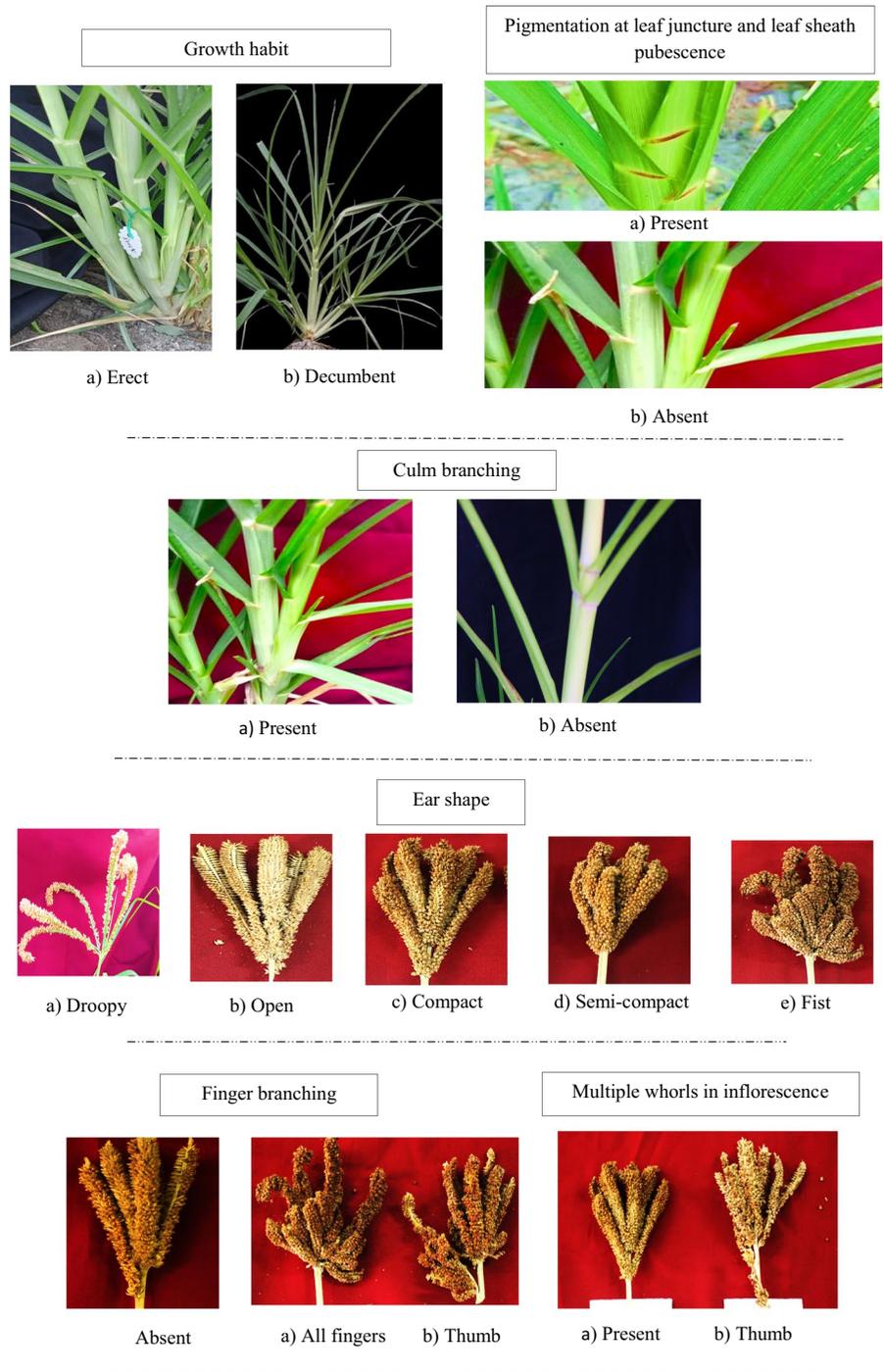
Fig. 2 Distribution of accessions for variation in discrete morphological features in finger millet

yield (Wu and Ma 2019). Pigmentation at leaf junctures in 21.25% of the accessions was found with purple pigmentation and 78.75% were without pigmentation. This trait can be utilized as a morphological marker for identifying and selecting cultivars. Pubescence on the leaf sheath was absent in 41.25% of the accessions studied and 58.75% of the accessions had pubescence on the leaf sheath. Leaf sheath pubescence is a vital feature that protects the plant from several abiotic stresses such as moisture deficit and heat stress by maintaining the canopy temperature and biotic stresses such as insects and pathogens (Basavaraj et al. 2021). Culm branching was present in 36.25% of the accessions and was absent in 63.25% of the studied accessions. This trait prevents the plant from lodging (Choudhary et al. 2025). Different categories were found for the ear shape in finger millet such as droopy, open, semi-compact, compact and fist types. Out of 80 accessions, the predominant type of ear shape was semi-compact (46.25%) followed by compact types (26.25%), open (18.75%), fisty (7.5%) and droopy (1.25%).

Among the different types, compact and semi-compact are preferred by farmers owing to their less shattering nature, neck and finger blast resistance and reduced bird damage due to their dense arrangement of fingers compared to open and droopy types (Owere et al. 2014). Finger branching was present in 7.5% of the accessions studied and was absent in 92.5% of the accessions studied. In that 7.5% of the

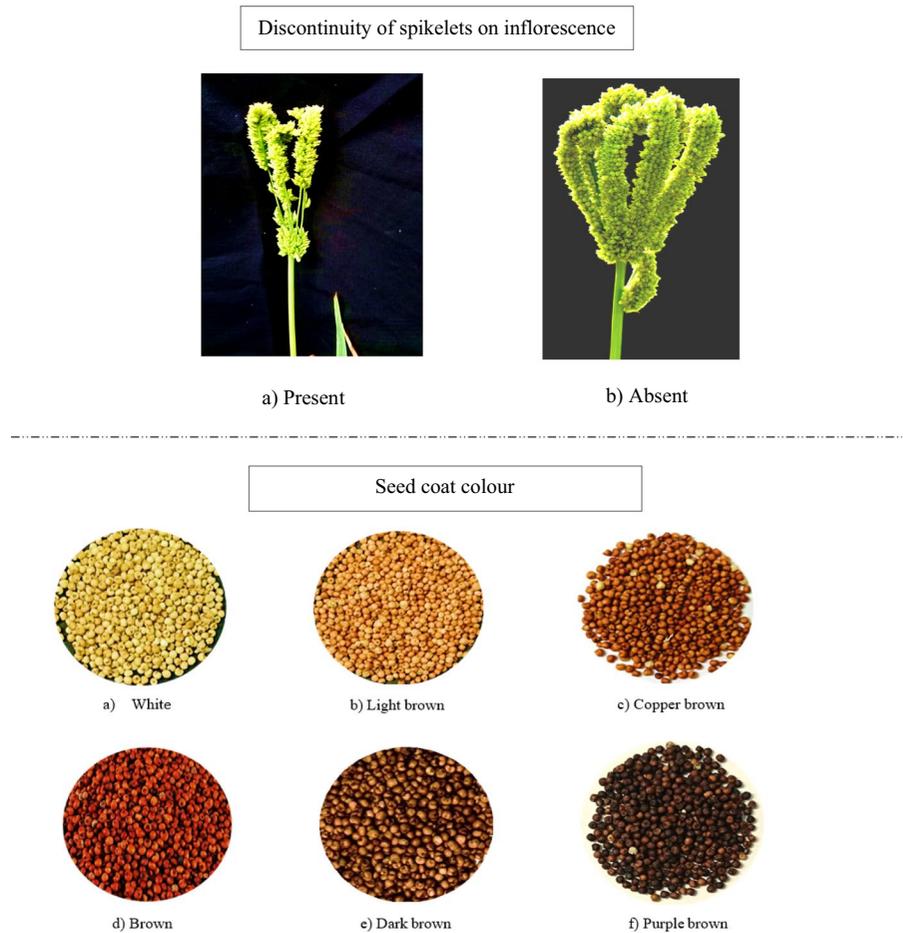
accessions, half of the accessions had branching in thumb (3.75%) and half had branching in other fingers addition to thumb (3.75%). Multiple whorls on the inflorescence is an essential yield attribute, which has more number of fingers and can lead to high yield (Choudhary et al. 2025). In the present study, multiple whorls in inflorescences were observed in 7.5% of the accessions and 92.5% of them lacked multiple whorls in the inflorescence. Spikelets were continuous on the inflorescence in 98.75% of the accessions and 1.25% had a discontinuous arrangement of spikelets on the inflorescence. Covering of seeds by the glumes was complete in 21.25% of the accessions (enclosed), intermediate in 72.5% of the accessions and 6.25% of the accessions had exposed seeds. Grains enclosed by glumes pose difficulty in post-harvest processing, and exposed seeds have a high chance of bird damage and thus intermediate ones are preferred to avoid such disadvantages. Grain colour ranged from white to purple brown of which, 3.75% had white grains, 46.25% had light brown seeds, 28.75% were copper brown, ragi brown was found in 2.5% of the accessions, 12.5% had dark brown seed and 6.25% had purple brown seeds. Grain colour influences the quality, consumer preference and value of the grains in the market. White and ragi brown seeds are economically preferred over other coloured grains (Tsehay and Kebebew 2002). Lodging susceptibility was low in 40% of accessions, 47.5% of accessions had intermediate susceptibility to lodging and

Fig. 3 Morphological variations observed for different discrete traits in finger millet accessions for Growth habit (A), Pigmentation at leaf juncture and leaf sheath pubescence (B), Culm branching (C), Ear shape (D), Multiple whorls in inflorescence (E), Finger branching (F), Discontinuity of spikelets on inflorescence (G), Seed colour (H)



12.5% were highly susceptible to lodging. Lodging is a vital trait to be considered in breeding programs, as it can lead to seed shattering and viviparous germination thereby affecting the economic yield and quality of grains (Dasanayaka and Kaluthanthri 2017). The

senescence score showed that 95% of the accessions were green when primary inflorescence on each culm reached maturity and 5% were not green at maturity. Similar variations in qualitative traits were observed

Fig. 3 (continued)

and reported by Itreddy et al. 2023; Patil et al. 2019; Reddy et al. 2009 for finger millet.

Shannon-Weaver diversity Index (H') for thirteen qualitative traits studied in the germplasm studied

The Shannon diversity Index (H') was computed using the frequency distribution of accessions for the 13 qualitative attributes studied (Hennink and Zeven 1991) (Table 2). The qualitative characteristics correspond to the genetic locus and the phenotypic classes denote the alleles. The allelic evenness *i.e.*, relative abundance of accessions for all the traits was given by H' index and the frequency of classes denote the allelic richness (Maruthi et al. 2025). A high H' value indicates that the traits are diverse for phenotypic classes and have an even distribution of accessions for those classes. Lower values indicate that the diversity is low and an uneven frequency class exists (Hennink

and Zeven 1991). The mean diversity index value was 0.635, indicating the prevalence of genetic diversity in the traits studied.

The H' values for the studied traits ranged from 0.067 to 1.364. The diversity indices were classified as low when the H' value was ≤ 0.4 , medium when it was 0.401–0.6 and high when H' values was ≥ 0.601 (Eticha et al. 2005). The highest Shannon diversity index was found for the trait grain colour (1.364), followed by ear shape (1.271), lodging susceptibility (0.98), grain covering (0.736), position of finger branching (0.693), leaf sheath pubescence (0.678) and culm branching (0.655). The highest H' value for the traits grain colour, ear shape, lodging susceptibility and glume covering indicates that these characters have high diversity and even distribution of accessions for the phenotypic classes of these traits. Medium diversity was found for traits, growth habit (0.562) and pigmentation at leaf juncture (0.517).

Table 3 Mean performance and variability parameters for yield attributes in finger millet accessions

Traits	Mean	Range		Season I σ_g^2	Season II σ_g^2	Pooled		PCV (%)	GCV (%)	h ² b (%)	GAM (%)
		Min	Max			σ_g^2	σ_{ge}^2				
DF	85.00	42.17	96.55	64.11*	49.92*	54.48*	3.14*	9.07	8.68	91.56	17.12
DM	115.75	73.26	128.82	61.72*	45.76*	52.98*	1.68 ^{ns}	6.73	6.29	87.40	12.11
SD (cm)	1.34	1.03	1.67	0.035*	0.048*	0.022*	0.01*	13.56	11.07	66.67	18.62
PH (cm)	83.78	41.06	117.77	169.56*	174.08*	169.08*	2.36*	15.78	15.52	96.69	31.44
NT	4.50	3.20	6.19	0.55*	0.40*	0.34*	0.13*	15.36	12.96	71.13	22.51
NP	3.75	2.80	5.40	0.35*	0.37*	0.26*	0.09*	15.96	13.60	72.63	23.87
LL (cm)	35.32	22.93	48.89	45.63*	41.39*	38.35*	4.60*	19.60	17.53	80.01	32.31
LW (cm)	1.01	0.60	1.30	0.03*	0.029*	0.02*	0.01*	17.23	14.00	66.01	23.43
FLL (cm)	24.27	14.53	36.28	29.74*	40.59*	30.60*	4.57*	24.54	22.79	86.25	43.61
FLB (cm)	1.12	0.97	1.26	0.032*	0.069*	0.039 ^{ns}	0.05*	26.74	17.63	43.48	8.48
PL (cm)	9.82	9.02	10.44	3.05*	4.43*	0.05 ^{ns}	3.69*	19.82	2.28	1.32	5.66
EL (cm)	7.98	5.43	14.82	1.63*	2.13*	1.81*	0.06	17.32	16.86	94.71	33.80
FL (cm)	7.33	5.30	13.89	1.49*	1.94*	1.61*	0.10*	17.96	17.31	92.85	34.36
FW (cm)	0.80	0.51	1.17	0.017*	0.02*	0.017*	0.002*	17.41	16.30	87.63	31.43
FN	6.75	5.60	8.06	0.88*	0.52*	0.63*	0.000 ^{ns}	15.64	11.76	56.55	18.22
SEW (g)	7.35	5.58	9.29	1.66*	1.13*	0.68*	0.72*	16.24	11.22	47.72	15.97
TGW (g)	3.06	2.05	3.9	0.29*	0.31*	0.29*	0.006*	17.81	17.60	97.68	35.83
FYP (g)	29.95	18.83	42.03	22.31*	31.46*	18.78*	8.066*	24.01	19.82	68.15	33.71
GYP (g)	23.05	14.12	32.16	13.19*	17.37*	11.66*	3.58*	13.83	11.97	74.88	21.33

*Significant at 5% Level of significance for LRT; ns- non-significant

Note: GV, Genotypic Variance; PV, Phenotypic variance; PCV – Phenotypic Co-efficient of Variation; GCV – Genotypic Co-efficient of Variation; h²b—Broad-sense heritability; GAM- Genetic Advance as Percent of Mean. DF – Days to flowering; DM- Days to maturity; SD – Stem diameter; PH- Plant height; NT- Number of tillers; NP- Number of productive tillers; LL- Leaf length; LW- Leaf width; FLL – Flag leaf length; EL – Ear head length; FL – Finger length; FW- Finger width; FN- Finger number/ear; SEW- Single earhead weight; TGW- 1000 grain weight; FYP – Fodder yield/ plant; GYP – Grain yield/plant

Low H' values were noticed for finger branching (0.266), presence of multiple whorls in inflorescence (0.266), senescence score (0.199) and discontinuity of spikelets on fingers (0.067). Low index values indicate an uneven distribution of accessions for the phenotypic classes under the trait and the trait has low genetic diversity. Similar results for H' values (0.122–0.908) were found for the traits ear shape, grain covering, lodging susceptibility, grain colour by Ghimire et al. 2023 in finger millet; for grain colour, ear shape, culm branching, growth habit, pigmentation at leaf juncture, leaf sheath pubescence with H' range of 0.00–1.097 by Singh et al. 2024 in finger millet. H' values were noticed low (0.05–0.458) for the trait's growth habit, ear shape, grain colour, glume covering by Lule et al. 2012 since the accessions failed to show more variations for the traits studied.

Spearman rank correlation for qualitative traits

Spearman rank correlation was worked out between the 13 qualitative traits (Fig. 4). Plant growth habit showed a significant positive correlation with pigmentation at leaf junctures and was negatively correlated with lodging susceptibility. Prostrate ones were easily susceptible to lodging than that of erect ones. Semi-compact and compact types were found with finger branching and it was found in the thumb and the fist had branching in all fingers. Coloured seeds were enclosed by glumes and the white ones seemed to be exposed. Culm branching is negatively correlated with discontinuity of spikelets, glume covering, senescence score, lodging susceptibility. More number of culm branches can cause the plant stay strong and were erect. Ear shape is negatively correlated with multiple whorls on inflorescence, discontinuity of spikelets and grain colour. The trait multiple whorls on inflorescence was not seen in droopy and

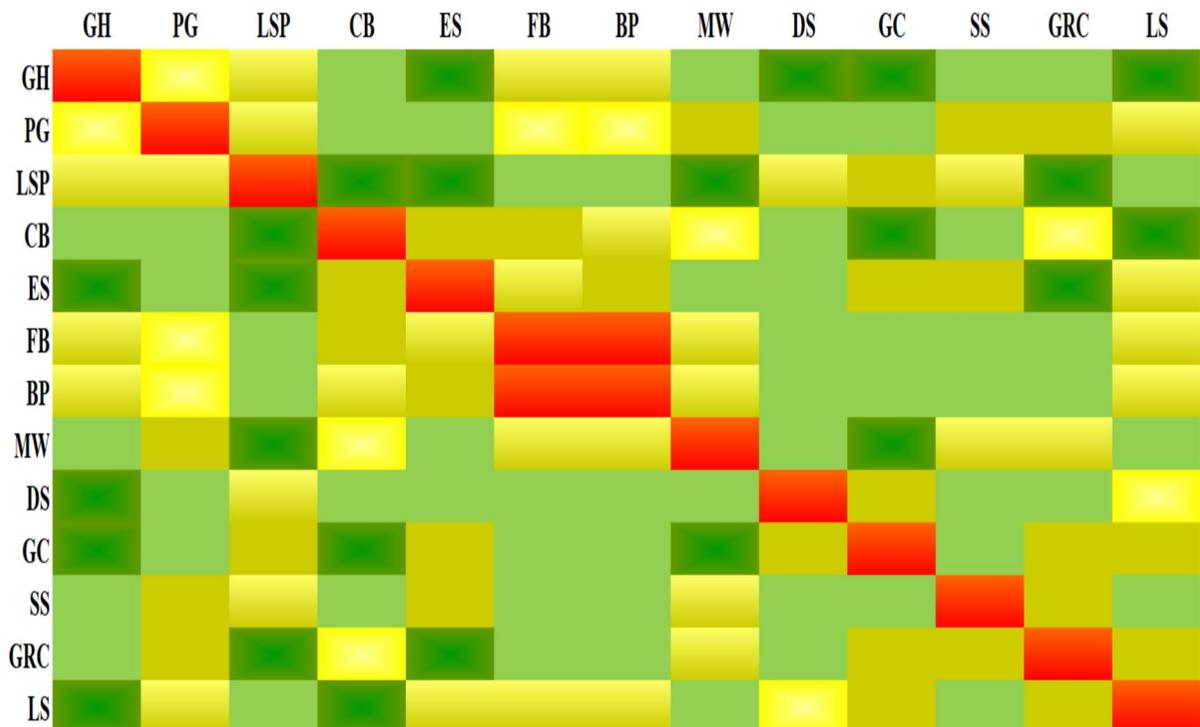


Fig. 4 Heat map representing the relationship among the 13 qualitative traits studied. Note: GH- Growth habit; PG- Pigmentation at leaf juncture; LSP- Leaf sheath Pubescence; CB- Culm branching; ES- Ear shape; FB- Finger branching;

BP – Branching position; MW- Multiple whorls in inflorescence; DS- Discontinuity of spikelets; GC- Glume covering; SS- Senescence score; GRC- Grain colour; LS- Lodging susceptibility

open types of inflorescences and discontinuity of spikelets affect the compactness of the ear. Finger branching is negatively correlated with discontinuity of spikelets, glume covering, senescence score, grain colour. Branching position is negatively correlated with discontinuity of spikelets on inflorescence, glume covering, senescence and grain colour. These results indicate that ears with finger branching had continuous arrangement of spikelets. Multiple whorls on inflorescences were negatively correlated with the discontinuity of spikelets, glume covering, and lodging susceptibility. The development of fingers from single whorls showed a continuous arrangement of spikelets and an enclosed and intermediate covering of glumes. Similar associations were reported by Singh et al. (2024) in finger millet.

Assessment of continuous variations in finger millet germplasm

REML variance component analysis

Observations recorded in both seasons were used to obtain BLUPs for individual seasons and pooled data for both seasons. All traits showed significant genotypic variance in both seasons. This indicates the prevalence of genetic variability among the accessions. Considering the pooled data, all yield attributes except flag leaf width and peduncle length showed significant genotypic variances. The G×E variance was significant for all traits except days to maturity and finger number/ear, which showed stable performance in both seasons. All the other 17 yield attributes showed a significant interaction between genotype and season for phenotypic expression. Only the traits that were significant were used for further downstream biometric analyses.

Variability parameters

Variability prevailing among the accessions lines for the 17 yield contributing traits were studied using phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV), broad-sense heritability (h^2) and Genetic Advance as percent of mean (GAM) as presented in Table 3. Genetic variability is the basis for selection and a pre-requisite for plant breeding. The greater the genetic variability in the population enhances the potential for effective selection during the cultivar development process (Hussain et al. 2022). High PCV and GCV were found for flag leaf length (24.54% and 22.79%). A high PCV and moderate GCV was found for fodder yield/plant (24.01% and 19.82% respectively). High PCV and GCV values indicate the presence of a larger variation in the trait and scope of efficient selection (Islam et al. 2022). Moderate PCV and GCV was found for all the other traits studied except days to flowering and maturity where these traits showed low PCV and GCV. Similar results have been reported by Mahalle et al. 2024; Tejasree et al. 2022; Madhavalatha et al. 2021 in finger millet. In the current study, high and moderate magnitudes of PCV and GCV were observed for almost all traits. Moreover, the small difference between PCV and GCV indicated that environmental effects were minimal, and the expression of these traits was predominantly governed by genetic factors. Heritability in broad-sense determines the extent to which the traits are passed on from one generation to the succeeding generation (Akhter et al. 2021). Broad-sense heritability was noticed high for almost all the traits except finger number/ear and single ear head weight. High to moderate heritability for all the traits indicate the negligible effect of environment in the trait expression. Reliable heritability estimates are necessary for the improvement of the yield attributes and phenotypic selection based on these traits can improve the hereditary framework (Mohamed et al. 2012; Yadav et al. 2024). Genetic advance is yet another important parameter which indicates the possibility of efficient selection (Pooja et al. 2022). GAM was high for traits such as plant height, number of tillers and productive tillers, leaf length, leaf width, flag leaf length, ear head length, finger length, finger width, 1000 grain weight, fodder yield/plant and single-plant yield. Moderate GAM was found for days to flowering, days

to maturity and stem diameter, finger number/ear and single ear head weight. Estimates of heritability, when considered along GAM are useful for predicting the effectiveness of selection gain. Traits with higher h^2 do not necessarily have a high GAM. In the current investigation, all traits exhibited moderate to high heritability along with a high GAM. This indicates that these traits showed additive gene effect, where the genes work together equally without dominance and selection would be effective. The greater the number of genes for the trait, the stronger the phenotypic expression (Dutta et al. 2013). The trait finger width has moderate heritability and low GAM which indicates that non-additive gene action exists and selection in this trait may not be rewarding.

Association analysis

Correlation analysis

Correlation indicates the strength and direction of the association between yield and other traits. The interrelationships between yield and its contributing attributes is illustrated in the correlogram (Fig. 5). Yield is a complex trait, influenced by many other quantitative traits. Studying the relationship between the yield and its contributing attributes would aid in the simultaneous enhancement of the yield and its attributes. This helps plant breeders to decide the selection intensity and direction, while working for yield enhancement (Monika 2021). The correlation among traits is influenced by the linkage of loci or major QTLs responsible for trait variation, which are positioned on specific chromosomes (Singh et al. 2023). A high significant positive correlation (at 1% level of significance) of grain yield/plant was noticed with yield attributes such as plant height (0.38), number of tillers (0.61), number of productive tillers/plants (0.64), ear head length (0.42), finger length (0.46), finger width (0.32), fodder yield/plant (0.98). These results indicate that the plants with more tillers, lengthy panicle, more fingers and more biomass will result in high yield per plant. Significant positive correlation of grain yield (5% level of significance) was found with traits such as leaf width (0.25) and flag leaf length (0.26). Enhancing these traits would lead to a concurrent increase in plant yield. Reddy and Gowda (2023) reported similar results. Significant

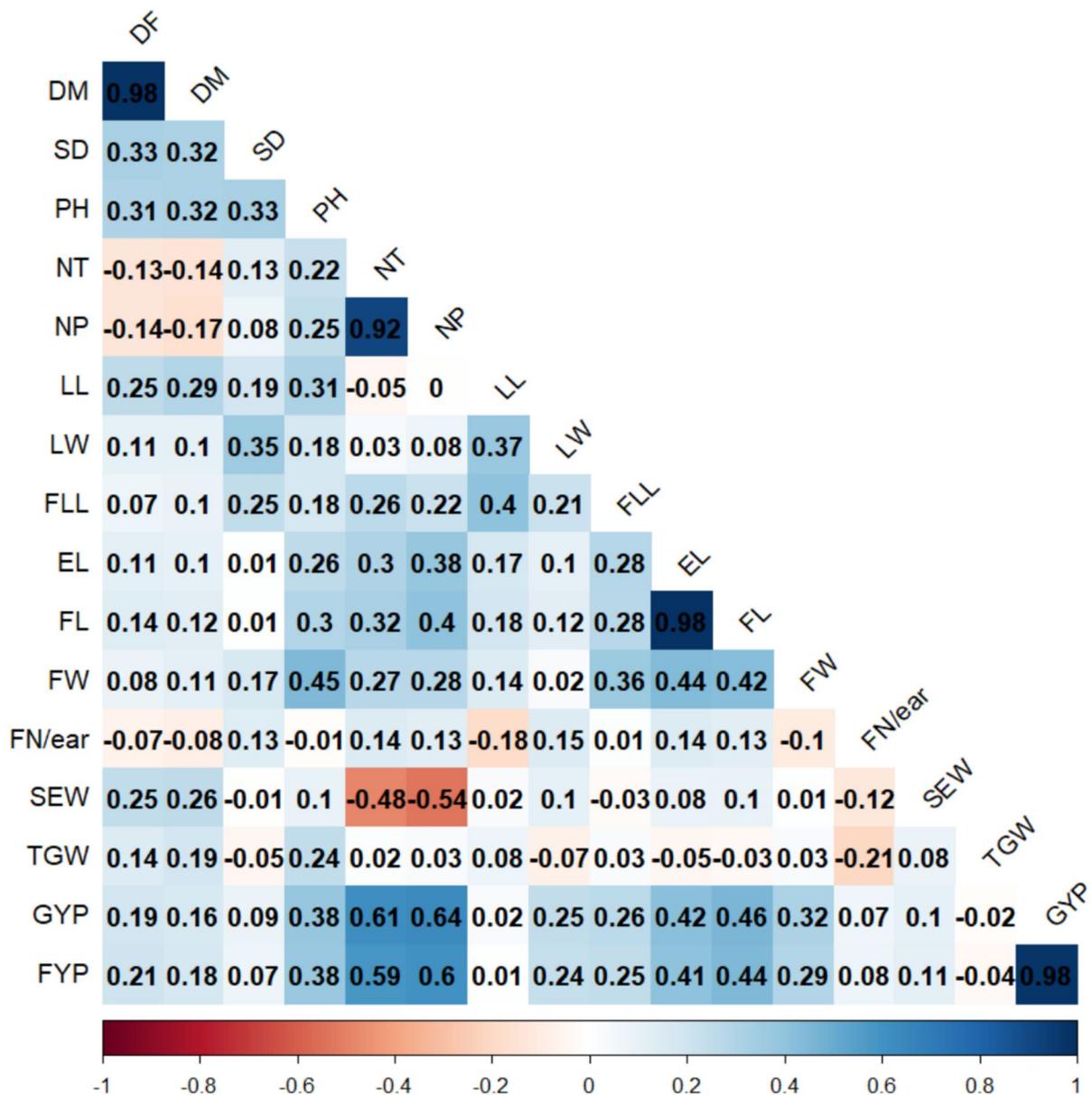


Fig. 5 Correlogram representing the relationship between the yield attributes in the finger millet accessions (Note: DF – Days to flowering; DM- Days to maturity; SD – Stem diameter; PH- Plant height; NT- Number of tillers; NP- Number of productive tillers; LL- Leaf length; LW- Leaf width; FLL

– Flag Leaf length; EL – Ear head length; FL – Finger length; FW- Finger width; FN- Finger number/ear; SEW- Single ear head weight; TGW- 1000 grain weight; FYP – Fodder yield/ plant; GYP – Grain yield/plant)

high positive correlation was found between days to flowering with days to maturity, stem diameter and plant height; between days to maturity and stem diameter, plant height, leaf length; between stem diameter and plant height, leaf width; between plant height and leaf length, finger length, finger width,

fodder yield/ plant; between number of tillers/ plant and number of productive tillers/ plant, ear head length, finger length, fodder yield/ plant; leaf length and leaf width, flag leaf length; between flag leaf length and finger width; between ear head length and finger length, finger width; between finger

length with finger width; finger width with fodder yield/ plant. This suggests that these traits can be simultaneously enhanced and may contribute to the indirect improvement of plant yield (Naik et al. 2021; Chavan et al. 2020; Singh et al. 2023). A significant negative correlation was observed between single ear head weight and the number of tillers/ plant (-0.482) and number of productive tillers/ plant (-0.540).

Path analysis

Correlation analysis indicated only the direction and strength of the relationship between the yield-related traits. However, path analysis is essential to understand how each trait affects yield individually and through its influence on other traits. Path coefficient splits the correlation between the traits as direct and indirect effects of the independent yield contributing traits on the dependent variable, the yield. Path analysis helps to identify key component traits that are useful for indirectly evaluating complex characteristics (Faysal et al. 2022) with low heritability and high sensitivity to environmental factors. This helps in selecting traits more effectively for yield enhancement while minimizing undesirable effects that could compromise selection efficiency. The direct and indirect effects of the yield contributing traits on yield are shown in Table 4. In the present study, plant height and fodder yield per plant had a strong positive direct influence on grain yield/plant. These traits can be used in direct selection to improve yield (Nikunj et al. 2023). Similar results have been reported by Patel et al. 2023. The number of productive tillers exerted a moderate positive direct effect, whereas finger length had a low positive direct influence. Traits such as stem diameter, leaf width, finger width, and single earhead weight had negligible direct impacts on grain yield. Conversely, days to flowering had a strong negative direct effect on yield, and earhead length had a low negative direct effect.

Regarding indirect effects, days to flowering showed a strong positive indirect influence on grain yield through days to maturity. Similarly, plant height, number of tillers, productive tillers/plant, earhead length, and finger length positively and indirectly influenced grain yield indirectly through fodder yield/plant. The number of tillers also had a moderate positive indirect effect via productive tillers per plant.

Leaf width, flag leaf length, and finger width had a moderate positive indirect effect on yield through fodder yield/plant. Both days to flowering and maturity contributed to low positive indirect effects on grain yield via the fodder yield. Stem diameter and plant height also exhibited low positive indirect effects on yield through days to maturity, whereas earhead length had a low indirect effect via finger length. Fodder yield per plant had a low positive indirect effect on grain yield through the number of productive tillers. On the other hand, days to flowering exerted a low negative indirect impact on grain yield through stem diameter. Similarly, low negative indirect effects were noted for finger length via earhead length and single earhead weight based on number of productive tillers per plant. Other traits expressed negligible indirect effects on one another. Similar results are seen in the report of Aruna et al. 2023; Sapkal et al. 2019; Chavan et al. 2019.

The residual effect was found to be minimum of 0.19 which indicating that the significant variability existed in the accessions was covered by most of the traits studied.

Multivariate analysis

Principal component analysis

Principal Component Analysis (PCA) transforms a group of correlated variables into a smaller set of uncorrelated and meaningful components known as principal components, without losing its original variability (Sharma et al. 2022). The principal component analysis helps plant breeders to aim for trait-specific crop improvement. The significant principal components are those which exhibit eigen values more than one. These principal components exhibit the key traits which contribute to the variation prevailing in the accessions population. In PCA, the number of principal components obtained is equal to the number of variables present in the study. Supporting the context, seventeen principal components was obtained out of which six exhibited more than one eigen value. The variation contributed by the principal components to divergence is depicted in the Scree Plot (Fig. 6). Together these significant PCs contribute 76.64% of the variability in the population. PC1 showed 27.31% of the variation followed by PC2 (16.80%). Together these two PCs contribute to 44.1% of the total

Table 4 Direct and indirect effects of the different yield attributes with grain yield/plant in finger millet accessions

DF	DM	SD	PH	NT	NP	LL	LW	FLL	EL	FL	FW	FN	SEW	TGW	FYP	GYP
DF	-0.320	0.004	-0.005	0.008	-0.032	-0.004	0.002	0.001	-0.018	0.020	0.001	0.001	0.024	-0.002	0.180	0.19
DM	-0.315	0.331	-0.005	0.008	-0.039	-0.004	0.002	0.001	-0.016	0.019	0.002	0.001	0.024	-0.003	0.153	0.16
SD	-0.105	0.105	0.013	-0.005	-0.007	0.018	0.006	0.002	-0.001	0.001	0.003	-0.001	-0.001	0.001	0.062	0.09
PH	-0.098	0.106	0.004	-0.015	-0.013	0.058	0.003	0.002	-0.041	0.045	0.007	0.000	0.009	-0.003	0.325	0.38**
NT	0.042	-0.047	0.002	-0.003	-0.059	0.214	0.001	0.002	-0.049	0.049	0.004	-0.001	-0.046	0.000	0.505	0.61**
NP	0.044	-0.056	0.001	-0.004	-0.054	0.233	0.000	0.001	-0.062	0.060	0.005	-0.001	-0.052	0.000	0.517	0.63**
LL	-0.080	0.096	0.002	-0.005	0.003	0.000	-0.015	0.007	-0.028	0.028	0.002	0.002	0.002	-0.001	0.006	0.02
LW	-0.034	0.034	0.005	-0.003	-0.002	0.018	-0.006	0.017	-0.016	0.019	0.000	-0.001	0.010	0.001	0.205	0.25*
FLL	-0.024	0.032	0.003	-0.003	-0.015	0.051	-0.006	0.004	0.009	-0.045	0.042	0.006	-0.003	0.000	0.211	0.26*
EL	-0.035	0.034	0.000	-0.004	-0.018	0.090	-0.003	0.002	0.003	-0.161	0.148	0.007	-0.001	0.008	0.350	0.42**
FL	-0.043	0.041	0.000	-0.004	-0.019	0.093	-0.003	0.002	0.003	-0.158	0.150	0.007	-0.001	0.009	0.378	0.46**
FW	-0.027	0.037	0.002	-0.007	-0.016	0.065	-0.002	0.000	0.003	-0.070	0.063	0.016	0.001	0.000	0.250	0.32**
FN	0.022	-0.027	0.002	0.000	-0.008	0.029	0.003	0.003	0.000	-0.023	0.019	-0.002	-0.009	0.003	0.066	0.07
SEW	-0.080	0.085	0.000	-0.001	0.028	-0.126	0.000	0.002	0.000	-0.013	0.015	0.000	0.096	-0.001	0.099	0.1
TGW	-0.046	0.062	-0.001	-0.004	-0.001	0.007	-0.001	-0.001	0.000	0.007	-0.005	0.000	0.008	-0.014	-0.032	-0.02
FYP	-0.067	0.059	0.001	-0.006	-0.035	0.140	0.000	0.004	0.002	-0.066	0.066	0.005	0.011	0.001	0.860	0.98**

Residual effect: 0.19 Bold values indicate the direct effect of the yield attributes on Grain yield/plant. Last column gives the correlation values between the yield attributes and grain yield / plant. *, Significance at 5% level and **, Significance at 1% level. DF – Days to flowering; DM– Days to maturity; SD – Stem diameter; PH– Plant height; NT– Number of tillers; NP– Number of productive tillers; LL– Leaf length; LW– Leaf width; FLL – Flag Leaf length; EL – Ear head length; FL – Finger length; FW– Finger width; FN– Finger number/ear; SEW– Single earhead weight; TGW– 1000 grain weight; FYP – Fodder yield/ plant; GYP – Grain yield/plant

Bold values in the diagonal indicate the direct effect of the yield attributes on grain yield/plant; Bold values in the last column indicate the correlation values between the respective traits and grain yielded/plant. *, Significance at 5% level and **, Significance at 1% level

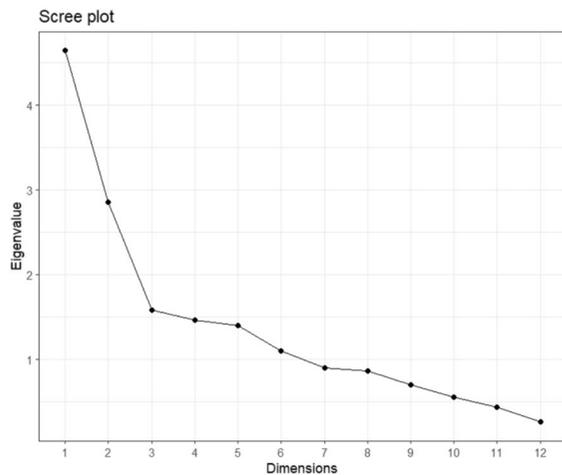


Fig. 6 Scree plot for different principal components in finger millet accessions

variation related to the agronomic characteristics. Similar results were obtained by Singh et al. 2023 for finger millet in which 5 PCAs were reported.

The key traits that contribute to significant variation are the characters which show high positive

loading in the principal components (Das et al. 2024). Almost, all traits except single ear head weight showed positive loading in the biplot (Table 5). The contribution of different traits to the principal components are presented in Table 5. In PC1, the traits that showed high positive loading were GYP (0.385), FYP (0.376), FL (0.337), EL (0.325), NP (0.333), NT (0.318) and the other traits except SEW showed positive loading. Genotype selection based on the yield attributes of the first PC can be effective for yield improvement. In PC1, the traits grain yield/plant, fodder yield, finger length, number of productive tillers, number of tillers/ plant and ear head length are the highest contributors of variation in the accessions population. In PC2, the traits, days to flowering, days to maturity, leaf length and single ear head weight were the highest contributors to divergence.

The loading biplot (Fig. 7) showed the relationship between different traits and their contribution towards divergence. The length of a trait vector is directly proportional to its contribution to overall genetic divergence among the accessions. The vector length was observed to be the highest for the number of productive tillers per plant, number of tillers/plant, days to

Table 5 Eigen value, Percentage of variance and Cumulative percentage of variance of different principal components and contribution of the yield attributes to significant principal components (PC)

Variables	PC1	PC2	PC3	PC4	PC5	PC6
Eigen value	4.643	2.856	1.575	1.461	1.398	1.097
Percentage of variance	27.31	16.80	9.267	8.591	8.223	6.452
Cumulative percentage of variance	27.31	44.109	53.377	61.968	70.191	76.643
Contribution of the yield attributes to significant PCs						
Days to flowering	0.129	0.467	-0.052	0.273	-0.122	0.293
Days to maturity	0.124	0.481	-0.054	0.256	-0.077	0.284
Stem diameter	0.131	0.21	-0.464	-0.125	-0.155	0.16
Plant height	0.267	0.197	-0.096	0.085	0.178	-0.019
Number of tillers/plant	0.318	-0.323	-0.219	0.181	0.069	0.06
Number of productive tillers/plant	0.333	-0.332	-0.183	0.15	0.087	0.066
Leaf length	0.127	0.266	-0.204	-0.371	0.275	-0.152
Leaf width	0.143	0.14	-0.291	-0.321	-0.289	-0.407
Flag leaf length	0.223	0.064	-0.158	-0.35	0.207	-0.115
Ear head length	0.325	-0.016	0.412	-0.273	0.004	0.247
Finger length	0.337	-0.005	0.406	-0.246	0.002	0.216
Finger width	0.262	0.041	0.115	-0.136	0.308	0.092
Finger Number/ear	0.054	-0.132	-0.097	-0.172	-0.521	0.359
Single earhead weight	-0.025	0.336	0.415	0.000	-0.212	-0.402
1000 grain weight	0.019	0.136	-0.007	0.308	0.456	-0.073
Grain yield/plant	0.385	-0.064	0.058	0.258	-0.198	-0.308
Fodder yield/plant	0.376	-0.055	0.068	0.271	-0.225	-0.302

Table 6 Accessions placed in each cluster, grouped based on the 17 yield attributes

Clusters	Cluster size	Accessions
Cluster I	15	TRY 1, IE 518, IE 3077, IE 4570, IE 4671, IE 4734, IE 4757, IE 5306, IE 5367, IE 6059, IE 6154, IE 6165, IE 6240, IE 6294, IE 2296
Cluster II	25	Co (Ra) 15, PYR 2, IE 2790, IE 2872, IE 2911, IE 3045, IE 3104, IE 3317, IE 3391, IE 3470, IE 1055, IE 3475, IE 4057, IE 2034, IE 4565, IE 2042, IE 4816, IE 5537, IE 2217, IE 6350, IE 6533, IE 7079, IE 7320, IE 2312, IE 2430
Cluster III	15	ATL1, IE 2437, IE 2457, IE 2821, IE 2871, IE 3392, IE 3614, IE 3945, IE 4073, IE 4121, IE 4497, IE 4795, IE 5091, IE 6221, IE 7018
Cluster IV	5	IE 501, IE 2606, IE 2619, IE 2710, IE 4797
Cluster V	4	IE 2572, IE 3952, IE 3973, IE 5201
Cluster VI	10	IE 2589, IE 4028, IE 4329, IE 4545, IE 4622, IE 4646, IE 5066, IE 5106, IE 6473, IE 6514
Cluster VII	1	IE 2957
Cluster VIII	5	IE 4491, IE 5817, IE 5870, IE 6326, IE 6421

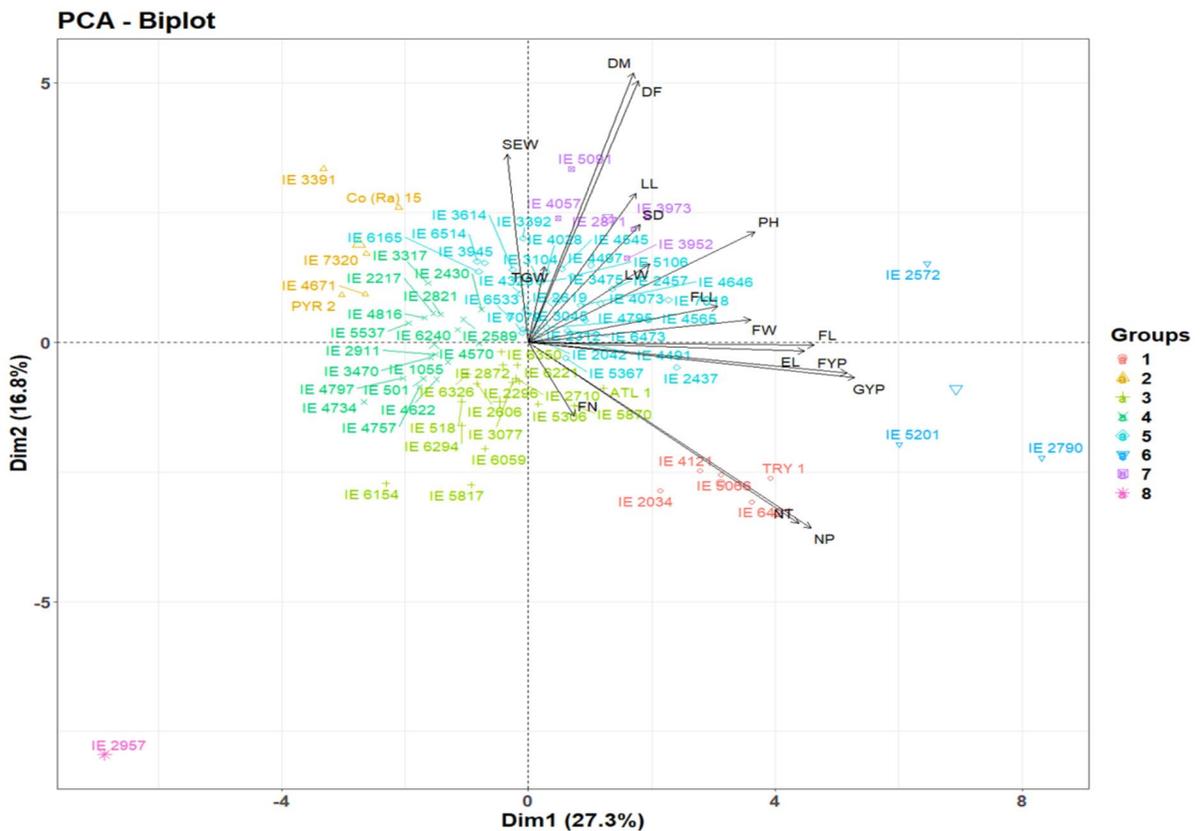
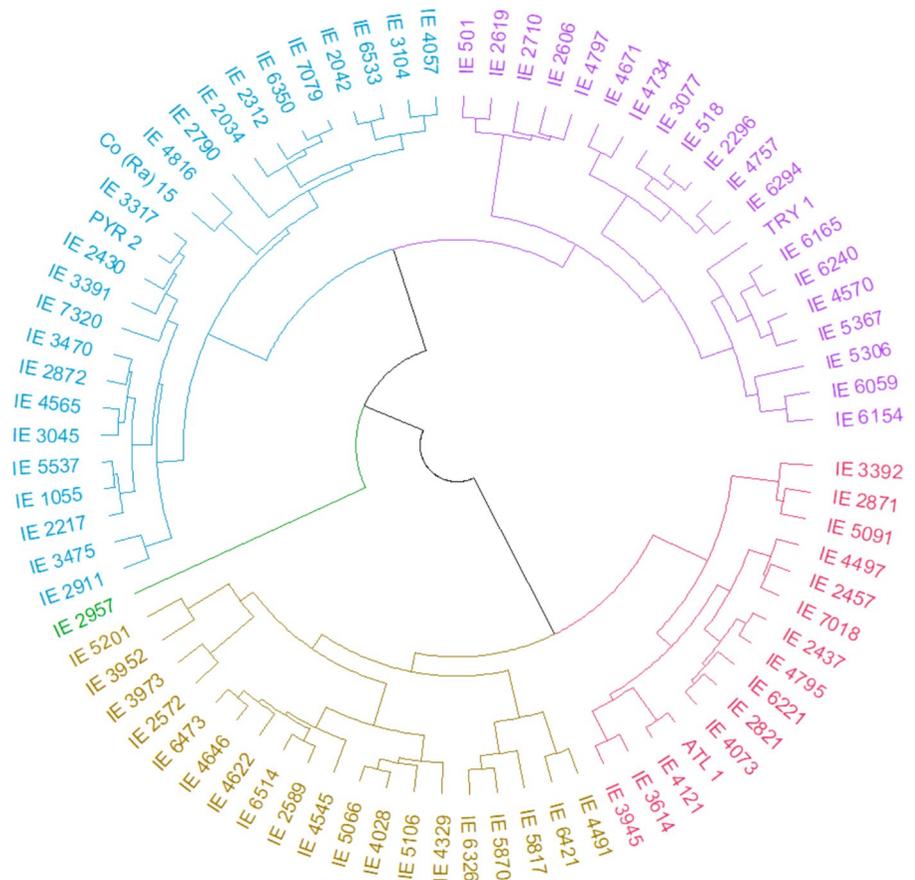


Fig. 7 Principal component (PC) 1 (PC1) vs PC2 biplot showing the distribution of the 80 accessions and contribution of the yield attributes in the two PCAs. Note: DF – Days to flowering; DM- Days to maturity; SD – Stem diameter; PH- Plant height; NT- Number of tillers; NP- Number of productive till-

ers; LL- Leaf length; LW- Leaf width; FLL – Flag Leaf length; EL – Ear head length; FL – Finger length; FW- Finger width; FN- Finger number/ear; SEW- Single earhead weight; TGW- 1000 grain weight; FYP – Fodder yield/ plant; GYP – Grain yield/plant

Fig. 8 Hierarchical cluster grouping of the 80 finger millet accessions based on the yield attributes



flowering and days to maturity, grain yield/ plant, earhead length, fodder yield/plant and finger length. These traits stay far away from the origin, indicating that these traits had higher loading and show maximum influence on the prevailing variation. The angle between the vectors indicates the relationship between the yield attributes. An acute angle ($<90^\circ$) between the vectors specifies the positive correlation between the traits and an obtuse angle ($>90^\circ$) denotes the negative correlation between the traits and the right angle (90°) shows zero correlation (Sulthana et al. 2021). The traits days to flowering, days to maturity, stem diameter, plant height, number of tillers, number of productive tillers/plants, leaf length, leaf width, flag leaf length, ear head length, finger length, finger width, number of fingers/ear, fodder yield/plant are positively correlated with grain yield and are clustered together in the same or near quadrants. The quadrants in the opposite quadrants such as the relation between the number of tillers and the

number of productive tillers/ plant, finger number/ear and single ear head weight.

The biplot between the PC1 and PC2 showed significant variability among the accessions (Fig. 7). The accessions IE 2957, IE 2970, IE 5201, IE 2572, IE 4121, IE 5066, IE 2034, TRY 1, IE 6437 are placed away from the origin and exhibit their divergence from other accessions present. These accessions can be used to develop cultivars suitable for sodic conditions. Accessions positioned along the trait vectors within the same quadrant exhibit superior performance for those specific yield attributes.

Cluster analysis

The present study was conducted to identify accessions that perform better for yield and other agronomically desirable traits in sodic soil. Grouping these accessions is an important step in characterizing the accessions and to serves as a vital source for finger

Table 7 Cluster mean for the yield attributing quantitative traits (Note: DF – Days to flowering; DM- Days to maturity; SD – Stem diameter; PH- Plant height; NT- Number of tillers; NP- Number of productive tillers; LL- Leaf length; LW- Leaf width; FLL – Flag Leaf length; EL – Ear head length; FL – Finger length; FW- Finger width; FN- Finger number/ear; SEW- Single ear head weight; TGW- 1000 grain weight; FYP – Fodder yield/plant; GYP – Grain yield/plant)

Traits	Cluster I		Cluster II		Cluster III		Cluster IV		Cluster V		Cluster VI		Cluster VII		Cluster VIII	
	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range
DF	80.06	72.91–86.14	88.19	82.36–96.46	86.53	78.11–95.13	88.41	85.67–90.87	90.05	83.78–96.55	87.04	82.83–90.40	42.17	0.00	76.31	71.96–79.05
DM	111.26	104.07–117.14	118.62	111.07–128.82	117.59	110.22–126.02	118.17	114.34–122.28	120.65	112.48–128.82	117.52	113.41–121.81	73.26	0.00	107.99	103.60–110.14
SD (cm)	1.33	1.15–1.52	1.35	1.10–1.67	1.38	1.11–1.54	1.26	1.12–1.34	1.33	1.26–1.41	1.41	1.25–1.49	1.03	0.00	1.29	1.22–1.41
PH (cm)	74.84	65.56–79.61	80.20	70.86–87.05	90.22	81.82–98.68	61.23	55.96–64.33	108.45	98.68–117.77	97.31	89.70–107.92	41.06	0.00	93.40	87.24–102.50
NT	4.46	4.06–5.82	4.39	3.20–6.19	4.59	3.63–5.76	4.40	4.06–4.48	4.80	4.06–5.76	4.48	4.06–6.19	4.48	0.00	4.82	4.48–6.19
NP	3.72	3.23–4.95	3.65	2.80–5.39	3.80	3.23–4.98	3.66	0	4.10	3.67–4.96	3.79	3.23–5.40	3.67	0.00	3.93	3.66–4.97
LL (cm)	32.54	24.63–42.65	34.37	26.24–46.48	42.72	38.34–48.89	32.13	28.32–36.48	38.86	32.58–44.90	33.76	27.78–38.28	22.93	0.00	32.16	27.52–36.58
LW (cm)	1.05	0.90–1.26	0.97	0.60–1.19	1.11	0.94–1.30	0.97	0.82–1.08	1.01	0.92–1.08	1.04	0.88–1.18	0.82	0.00	0.93	0.86–1.02
FLL (cm)	24.13	14.53–35.90	22.54	18.27–29.98	29.06	19.29–36.28	24.13	19.71–29.75	27.00	24.38–28.32	20.62	15.37–26.25	17.23	0.00	25.63	17.54–32.34
EL (cm)	7.70	6.45–8.40	7.97	6.11–14.82	8.02	5.43–10.35	7.87	7.28–8.59	10.14	8.35–11.90	7.75	6.99–8.50	6.55	0.00	7.79	6.55–8.45
FL (cm)	6.96	5.92–7.61	7.32	5.88–13.89	7.34	5.30–9.69	7.23	6.70–7.85	9.64	8.19–11.23	7.21	6.50–7.95	5.97	0.00	7.15	6.41–7.66
FW (cm)	0.76	0.51–0.99	0.79	0.58–0.93	0.83	0.65–1.07	0.68	0.55–0.81	0.92	0.70–1.17	0.83	0.65–1.00	0.65	0.00	0.90	0.77–0.96
FN	6.71	6.03–8.04	6.65	5.94–7.72	6.64	5.60–7.29	7.09	6.70–8.06	6.93	6.27–7.72	6.93	6.08–7.72	6.95	0.00	6.83	6.08–7.70
SEW (cm)	7.39	5.79–8.66	7.37	5.86–9.29	7.12	5.64–8.61	7.34	6.64–7.93	8.05	6.63–8.87	7.30	5.58–8.37	6.74	0.00	7.58	7.08–8.99
TGW (g)	3.01	2.32–3.79	3.10	2.30–3.86	3.16	2.27–3.90	2.50	2.39–2.62	3.12	2.28–3.62	3.21	2.28–3.84	2.41	0.00	3.06	2.28–3.77
FYP (g)	29.75	23.40–38.18	28.99	20.76–40.23	29.97	24.71–34.08	30.25	26.02–34.68	36.63	33.14–42.03	29.71	25.61–36.49	18.83	0.00	32.44	25.77–40.19
GYP (g)	23.15	18.66–31.57	22.11	15.48–31.14	22.89	19.21–25.75	23.09	20.52–25.91	28.03	25.10–32.16	23.07	20.86–27.19	14.12	0.00	25.09	19.37–31.46

Table 8 Top 10 high performing accessions for yield attributes

Traits	Class	Accessions	Range
GYP	High	IE 2572, TRY 1, IE 6421, IE 2790, IE 5201, IE 4545, IE 4491, IE 3973, IE 3077, IE 2606	25.91–32.16 g
FYP	High	IE 2572, IE 2790, IE 6421, TRY 1, IE 5201, IE 4545, IE 3077, IE 2606, IE 3973, IE 2437	34.08–42.03 g
PH	High	IE 3945, IE 3973, IE 5066, IE 4028, IE 2572, IE 4491, IE 5106, IE 4329, IE 3952, IE 5201	73.25–110.14 cm
NT	High	IE 2790, IE 5066, IE 6421, TRY 1, IE 2437, IE 5201, IE 2457, IE 2572, IE 4816, IE 6059	4.91–6.19
NP	High	IE 5066, IE 2790, IE 4121, IE 6421, IE 5201, IE 2034, TRY 1, IE 2437, IE 5306, IE 2572	4.09–5.40
EL	High	IE 2790, IE 5201, IE 2572, IE 5091, IE 7018, ATL 1, IE 4057, IE 3045, IE 4565, IE 4121	8.69–14.82 cm
FL	High	IE 2790, IE 5201, IE 2572, IE 5091, IE 7018, ATL 1, IE 4057, IE 3045, IE 3952, IE 3973	8.19–13.89 cm
FW	High	IE 2572, IE 7018, IE 2296, IE 5201, IE 6326, IE 6473, IE 5870, IE 6421, IE 5306, IE 2430	0.93–17.17 cm
DF	Low*	IE 2957, IE 5817, IE 6154, IE 5870, TRY 1, IE 6326, IE 6059, IE 6294, IE 5367, IE 6421	42.17–79.05 days
DM	Low*	IE 2957, IE 5817, IE 6154, TRY 1, IE 5870, IE 6059, IE 6294, IE 4491, IE 6326, IE 4570	73.25–110.14 days

*Low values are preferable for agronomic benefits. Note: DF – Days to flowering; DM- Days to maturity; SD – Stem diameter; PH- Plant height; NT- Number of tillers; NP- Number of productive tillers; LL- Leaf length; LW- Leaf width; FLL – Flag Leaf length; EL – Ear head length; FL – Finger length; FW- Finger width; FN- Finger number/ear; SEW- Single ear head weight; TGW- 1000 grain weight; FYP – Fodder yield/ plant; GYP – Grain yield/plant)

millet improvement (Singh et al. 2023). In order to group the eighty accessions, cluster analysis was performed. The divergence among the accessions was calculated studied using the Euclidean distance and grouped following the ward's method. All accessions were classified into eight different clusters using the 17 quantitative traits studied (Table 6 and Fig. 8). Among the eight clusters, Cluster II is the largest cluster with 25 members, followed by Clusters I and III with 15 members each. Cluster VII was a solitary cluster with genotype IE 2957.

The distance between clusters V and VII was the highest followed by the distance between the clusters II and VII. The minimum inter-cluster distance was found between clusters III and VI indicating the similarity between the members of both the clusters.

The means and ranges of the eight clusters are presented in Table 7. Cluster VII had the genotype IE 2957 with low mean for days to flowering (42.17 days) and maturity (73.26 days), which can be used as parents in breeding programs for developing early maturing cultivars. Considering the cluster means for selection, selecting accessions with more than one desired trait may be valuable in crop improvement. The cluster mean for single plant yield and fodder yield/ plant was high for cluster V, which indicates that the members of this cluster can be exploited to develop cultivars that produce high grain and fodder yields under sodic conditions. Members in cluster V also had high mean for some of the useful yield attributes like plant height, number of

productive tillers/plant, earhead length and finger length. Cluster IV had accessions with high number of fingers in an ear. Cluster VI had members with sturdy stems, high thousand weight, indicating the possibility of developing non-lodging, bold-seeded finger millet cultivars. Similarly, 145 accessions from IIMR were grouped into 5 clusters by Sharma et al. 2022; 37 accessions were grouped into 6 clusters by Charitha and Lal 2023 in finger millet; Yadav et al 2024 in rice where 20 accessions were grouped into 7 clusters. Utilizing accessions from distant clusters in hybridization programs would maximize the chance of obtaining transgressive segregants since the unrelated individuals can contribute unique alleles at multiple loci (Beer et al. 1993). These transgressive segregants can be further bred as homozygous cultivars, suitable for sodic soil conditions (Nagarajan et al. 2024).

Promising accessions for yield attributes under sodicity

Yield under sodicity is a useful measure of sodicity tolerance which has practical implications in breeding program. Screening and characterization of mini core collection under natural sodic environments identified promising finger millet accessions for different yield contributing traits. High soil sodicity leads to poor soil structure, restricted root development, and nutrient deficiencies, which in turn reduce photosynthetic efficiency and overall plant

Table 9 Finger millet accessions with high values for multiple yield attributes

Genotype	DF*	DM*	SD	PH	NT	NP	LL	LW	FLL	EL	FL	FW	FN	SEW	TGW	FYP	GYP	Country	Region	Biological type
TRY 1	75.76	107.28	1.50	77.72	5.82	4.95	34.91	1.23	28.65	7.94	7.42	0.92	6.74	7.55	2.69	38.18	31.57	India	Asia	Released variety
IE 2437	87.09	117.14	1.54	88.54	5.76	4.52	39.19	1.08	28.93	7.23	6.50	0.79	7.04	7.05	3.72	34.08	25.75	Kenya	Africa	Landrace
IE 2572	96.55	128.82	1.37	101.54	4.91	4.09	37.36	0.92	27.88	11.76	10.94	1.17	7.72	8.87	2.28	42.03	32.16			Landrace
IE 2790	88.98	117.61	1.34	83.56	6.19	5.39	37.60	1.19	27.09	14.82	13.89	0.88	6.70	6.86	2.47	40.23	31.14	Malawi		Landrace
IE 3973	95.13	125.55	1.26	98.68	4.06	3.67	40.59	1.08	27.41	8.54	8.19	0.84	6.95	8.20	3.49	34.26	26.70	Uganda		Landrace
IE 4491	78.11	109.21	1.26	102.50	4.48	3.66	29.61	0.90	28.81	8.15	7.37	0.93	6.08	8.99	3.77	33.74	26.85	Zimbabwe		Landrace
IE 5201	83.78	112.48	1.41	117.77	5.76	4.96	32.58	0.98	24.38	11.90	11.23	0.98	6.76	6.63	3.09	37.06	28.16	India	Asia	Landrace
IE 5367	78.11	110.14	1.50	75.67	4.48	3.67	35.85	1.26	31.05	8.30	7.61	0.63	8.04	8.14	2.96	32.05	24.67	Kenya	Africa	Landrace
IE 5870	75.74	107.34	1.41	87.24	4.48	3.67	36.58	0.98	23.96	8.45	7.66	0.93	7.70	7.55	2.51	32.42	24.69	Nepal	Asia	Landrace
IE 6421	79.05	110.14	1.26	97.83	6.19	4.97	30.55	0.86	32.34	6.55	6.41	0.93	6.34	7.08	3.41	40.19	31.46	Uganda	Africa	Landrace

* Low values are preferable for agronomic benefits. Note: Bold values indicate the highest values for the respective yield attributes

DF, Days to flowering (days); DM, Days to maturity (days); SD, Stem diameter (cm); PH, Plant height (cm); NT, Number of tillers/plant (cm); NP, Number of productive tillers/plant (cm); LL, Leaf length (cm); LW, Leaf width (cm); FLL, Flag leaf length (cm); EL, Ear head length (cm); FL, Finger length (cm); FW, Finger width (cm); FN, Finger number/ear; SEW, Single earhead weight (g); TGW, 1000 grain weight (g); FYP, Fodder yield/plant (g); GYP, Grain yield/plant (g)

Bold values indicate the highest values for the respective yield attributes

growth. These physiological and structural stresses negatively impact both vegetative and reproductive traits, ultimately resulting in significant yield reductions under sodic conditions. This study identified finger millet accessions that exhibited superior performance for various yield-related traits under sodic soil conditions, suggesting the presence of inherent tolerance mechanisms. Top performing accessions with high values for yield and yield attributes which showed positive correlation with yield are presented in Table 8. The highest-performing accessions for key yield-contributing traits recorded grain yields ranging from 25.91 to 32.16 g/plant, fodder yields between 34.08 and 42.03 g/plant, 4 to 5 productive tillers per plant, earhead lengths of 8.69 to 14.82 cm, and finger lengths of 8.19 to 13.89 cm. The duration to flowering varied from 42 to 79 days, while days to maturity ranged from 73 to 110 days. These superior accessions represent valuable genetic resources for trait-specific breeding programs aimed at developing high-yielding finger millet cultivars suitable for sodic soil conditions. The top ten accessions exhibiting multiple superior yield traits originated from diverse geographical regions including India, Kenya, Malawi, Uganda, Zimbabwe, and Nepal. Among these, accessions IE 2572 and TRY 1 demonstrated superior performance in nine yield-related traits, followed by IE 2790 and IE 6421 with high values for eight traits. Accessions IE 2437 and IE 5367 were superior in seven traits, while IE 3973, IE 4491, and IE 5201 excelled in six traits. IE 5870 exhibited high performance with four yield attributes (Table 9). IE 2572 was high yielder and was found to be a promising source for a greater number of productive tillers, lengthy earhead, lengthy and wider fingers and more biomass. The sodic tolerant check TRY 1 showed high yield, had a greater number of productive tillers and matured early, with more biomass. Among the eighty accessions, IE 2957 was found with short duration, which can serve as a favourable source for developing early maturing finger millet accessions suitable for a sodic environment. Top performing accessions include a released variety and nine other landraces. Such differential performance under stress is often attributed to genotypic variation in osmotic adjustment, ion homeostasis, and efficient nutrient uptake (Munns and Tester 2008; Ashraf 2004). Identifying and utilizing these tolerant genotypes is essential for

breeding programs aimed at improving yield stability and resilience in sodic environments.

Conclusion and future prospects

Finger millet is a resilient and highly nutritious cereal crop, predominantly cultivated in arid and semi-arid regions. Despite extensive research on various abiotic stresses in finger millet, limited attention has been given to screening for sodicity tolerance. Variability analysis indicated moderate to high genetic diversity among yield-related traits, suggesting potential for effective selection and genetic improvement. Association research and principal component analysis (PCA) showed that traits such as productive tillers, finger length, plant height, and fodder yield/plant positively influence grain yield, making them valuable for indirect selection. Multivariate analyses such as PCA and cluster analysis offered insight into genotype performance, aiding the identification of donor lines for trait-specific breeding. The top ten high-performing accessions for individual and multiple yield-contributing traits were identified and hold promise for use in breeding programs aimed at improving yield under sodic conditions. These elite accessions should be further explored through advanced omics approaches to uncover the genetic basis and mechanisms of sodicity tolerance that contribute to high yields.

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Author's contribution MS conducted field experiment, collected data, statistical analysis and manuscript drafting, CV framing out the research work, Designing the experiment, Manuscript editing, MV guided in conducting field experiments and reviewing article, KS Manuscript editing, TR guided in conducting field experiments, SM Guided in conducting field experiments. All authors read and approved the final manuscript.

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Declarations

Conflicts of interest The authors declare no competing interests.

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