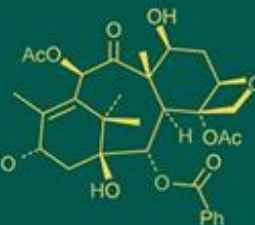
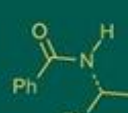
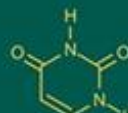
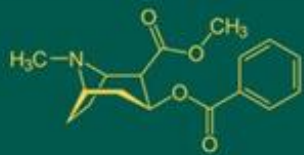


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Studies on variability for yield and yield attributing traits in finger millet [*Eleusine coracana* (L.) Gaertn.]

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Abstract

Assessment of genetic variation is fundamental to efficient selection and the genetic improvement of finger millet. In the present investigation, 35 genotypes were assessed across four locations during *Kharif* 2024 to determine the magnitude of variability, heritability, and genetic advance for yield and yield-related traits. Analysis of variance indicated significant differences among the genotypes for all the characters evaluated. In general, genotypic coefficient of variation values were lower than the corresponding phenotypic coefficient of variation values, demonstrating the influence of environmental conditions on trait expression. Moderate to high estimates of GCV, PCV, heritability, and genetic advance were recorded for main ear-head length, finger length, finger width, 1000-grain weight, grain yield per plant, and fodder yield per plant. These findings indicate the predominance of additive gene effects and suggest that direct selection for these traits would be effective in achieving genetic improvement.

Keywords: Genetic variability, finger millet, GCV, PCV, heritability, genetic advance

Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn.) is an important cereal crop of the family Poaceae and is extensively cultivated in the semi-arid regions of Asia and Africa. It is believed to have originated in the Ethiopian highlands and was later introduced into the Indian subcontinent, where it became an important part of traditional agricultural systems (Dida *et al.*, 2008) [1]. Finger millet is a self-pollinated allotetraploid species with a chromosome number of $2n=4x=36$. It is widely recognized for its ability to adapt to diverse agroclimatic conditions, particularly drought-prone areas and soils with low fertility (Upadhyaya *et al.*, 2007) [2]. Its tolerance to unfavourable climatic conditions makes it a valuable crop for sustainable agriculture, especially under rainfed farming systems.

Among the small millets, finger millet is considered nutritionally superior because of its high content of carbohydrates, dietary fibre, essential amino acids, and minerals, particularly calcium and iron (Devi *et al.*, 2014) [3]. The grains contain approximately 7–10 per cent protein and constitute an important source of nutrition for rural communities. In addition, its low glycaemic index and high antioxidant content have increased its significance as a healthpromoting cereal crop (Chandra *et al.*, 2016) [4].

India is the world's leading producer of finger millet. During 2024–25, the crop was cultivated over an area of 12.48 lakh hectares, producing 19.77 lakh tonnes with an average productivity of 1,584 kg ha⁻¹. In Gujarat, finger millet occupied approximately 0.10 lakh hectares, with a production of 0.08 lakh tonnes and an average productivity of 835 kg ha⁻¹ (Anonymous, 2025) [5]. The crop is mainly cultivated in the tribal and hilly areas of South Gujarat, particularly in the Dangs and Valsad districts. However, the productivity of finger millet in Gujarat remains considerably below the national average, highlighting the need for genetic enhancement and the development of high-yielding varieties.

The effectiveness of any crop-breeding programme largely depends on the availability of adequate genetic variability within the breeding material. Genetic variation provides the basic foundation for selection and creates opportunities to develop superior genotypes with desirable agronomic characteristics. A detailed understanding of the nature and magnitude of variability within a population is therefore necessary for designing an efficient breeding programme. The presence of substantial variation increases the possibility of identifying and selecting superior recombinants. Moreover, estimates of heritability and genetic advance provide valuable information regarding the inheritance of traits and their expected response to selection (Burton and DeVane, 1953) [6].

Grain yield is a complex quantitative trait controlled by several component characters and strongly affected by environmental conditions. Consequently, the estimation of genetic variability parameters is essential for developing effective selection strategies. Therefore, the present study was conducted to assess genetic variability, heritability, and genetic advance for yield and yield-contributing traits in finger millet genotypes evaluated across four different locations.

Materials and Methods

The experimental material consisted of 35 finger millet genotypes evaluated at four locations: the Centre for Millets Research, SDAU, Deesa (E1); the Agronomy Instructional Farm, SDAU, Sardarkrushinagar (E2); the Maize Research Station, SDAU, Bhiloda (E3); and the Agricultural Research Station, SDAU, Ladol (E4), during *Kharif* 2024. The experiment was conducted in a randomized block design with three replications. Each genotype was planted in a single row measuring 3.0 m in length, with a spacing of 30 cm × 10 cm. Standard agronomic and plant-protection practices recommended for the crop were followed throughout the growing season.

Data were collected from five randomly selected competitive plants in each plot for all the characters, except days to 50 per cent flowering and days to maturity, which were recorded on a plot basis. Protein content was estimated using the Kjeldahl method (AOAC, 2005). Iron and zinc concentrations were determined through atomic absorption spectrophotometry following wet-acid digestion, while calcium content was measured using the versenate titration method described by Jackson (1967)^[7].

Statistical analysis

Analysis of variance was performed to determine the extent of variation among the genotypes. The analysis was conducted separately for each environment and subsequently pooled across environments using the randomized block design model described by Panse and Sukhatme (1978)^[8]. Different genetic variability parameters were estimated using the standard formulae proposed by the respective researchers.

Coefficients of variation

The magnitude of variation present within a crop population can be effectively determined by estimating the genotypic and phenotypic coefficients of variation. The genotypic coefficient of variation represents the extent of genetic differences among the genotypes and indicates the heritable component of the observed variation. Conversely, the phenotypic coefficient of variation reflects the total variation expressed by a trait, including both genetic and environmental effects.

These parameters are commonly employed in plant-breeding research to quantify the available variability and identify traits with greater potential for improvement through selection. In the present investigation, the genotypic coefficient of variation and phenotypic coefficient of variation were estimated according to the method proposed by Burton (1952)^[9].

Phenotypic coefficient of variation (PCV %)

$$PCV (\%) = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

Genotypic coefficient of variation (GCV %)

$$GCV (\%) = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Where, σ_p^2 = Phenotypic variance, σ_g^2 = Genotypic variance and $\bar{X}$ = Population mean.

Heritability (broad sense) $h^2(b)$

In most plant-breeding experiments, broad-sense heritability [$h^2(b)$] is estimated more frequently than narrow-sense heritability. Narrow-sense heritability represents the ratio of additive genetic variance to the total phenotypic variance. However, the overall genotypic variance consists of both additive and non-additive genetic components. Therefore, estimating narrow-sense heritability requires the separation of additive genetic variance from the total genetic variance, which is often difficult, time-consuming, and mathematically complex.

In contrast, broad-sense heritability is defined as the ratio of total genetic variance to phenotypic variance and does not require the separation of additive and non-additive genetic effects. It is an important parameter that indicates the proportion of total phenotypic variation within a population that is attributable to overall genetic differences. In the present study, broad-sense heritability [$h^2(b)$] was estimated using the formula proposed by Allard (1960)^[10]:

$$h^2(b) (\%) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where, $H^2(b)$ = Heritability (broad sense), σ_p^2 = Phenotypic variance and σ_g^2 = Genotypic variance.

Expected genetic advance (GA) (Genetic gain):

Genetic advance represents the expected improvement in the mean genotypic value of selected plants over that of the original population. It was estimated according to the method proposed by Allard (1960)^[10], assuming a selection intensity of 5 per cent and using a constant 'k' value of 2.06.

$$G.A. = h^2(b) \times K \times \sigma_p$$

Where, G.A. = Genetic advance, $h^2(b)$ = Heritability (broad-sense), K = Selection intensity at 5 percent (2.06) and σ_p = Phenotypic standard deviation

Genetic advance expressed as percent of mean:

Genetic advance as a percentage of the mean was calculated using the formula proposed by Johnson *et al.* (1955)^[11].

$$GA (\% \text{ of mean}) = \frac{GA}{\bar{X}} \times 100$$

Where, GA = Expected Genetic advance, $\bar{X}$ = Mean of character under study

Table 2 showed the categorization of genetic estimations. Sivasubramanian and Madhavamenon (1973)^[12] categorized GCV and PCV, Robinson *et al.* (1949)^[13] categorized heritability and Johnson *et al.* (1955)^[11] categorized GAM.

Results and Discussion

The mean squares due to replications were non-significant for all the traits in each environment, demonstrating uniformity within the experimental sites. In contrast, the mean squares due to genotypes were highly significant for all the characters across all environments. This indicated the presence of considerable genetic variability among the evaluated genotypes, which could be effectively utilized for selecting and improving grain yield and its associated traits (Table 3).

In the pooled analysis, the mean squares due to replications were non-significant for all the characters except days to 50 per cent flowering, further indicating the general homogeneity of the experimental conditions. Significant genotypic mean squares for all the traits confirmed the existence of substantial genetic variation among the genotypes. Environmental and genotype $\times$ environment interaction effects were significant for most morphological traits, except 1000-grain weight. However, these effects were non-significant for biochemical traits, including protein, calcium, iron, and zinc contents. The significant environmental and genotype $\times$ environment interaction effects indicated that environmental conditions influenced the expression of different genotypes and that the genotypes responded differently across the test locations. Therefore, further evaluation of these traits across multiple environments is necessary to identify stable and consistently performing genotypes (Table 4).

For traits such as main ear-head length, finger length, finger width, 1000-grain weight, protein content, calcium content, iron content, and zinc content, genotypic variance closely followed phenotypic variance. This narrow difference indicated that environmental factors contributed relatively little to the observed variation and that selection based on phenotypic performance would likely be effective. In contrast, environmental variance exceeded genotypic variance for days to 50 per cent flowering, days to maturity, plant height, productive tillers per plant, number of fingers per ear head, grain yield per plant, fodder yield per plant, and harvest index. Consequently, direct phenotypic selection may be less effective for improving these traits. A combination of selective breeding, multi-location evaluation, and intensive phenotypic selection may therefore be more suitable for their improvement (Table 5). Low estimates of GCV and PCV were observed for days to 50 per cent flowering, with values of 3.77 and 5.89 per cent, respectively, and days to maturity, with corresponding values of 3.50 and 5.88 per cent. Similar low estimates of GCV and PCV for flowering and maturity traits were reported by John (2006) [14], Ulaganathan and Nirmalakumari (2011) [15], and Suryanarayana *et al.* (2014) [16]. Low GCV accompanied by moderate to high PCV was recorded for plant height (8.65 and 14.21%), productive tillers per plant (9.16 and 34.15%), and number of fingers per ear head (9.32 and 23.75%). These findings were consistent with the results reported by John (2006) [14], Ulaganathan and Nirmalakumari (2011) [15], Anuradha *et al.* (2017) [17], and Patel *et al.* (2020) [18] (Table 6 and Figure III).

Moderate GCV and moderate to high PCV were recorded for main ear-head length (15.54 and 17.64%), finger length (18.09 and 24.49%), finger width (11.58 and 15.97%), 1000-grain weight (14.27 and 15.03%), grain yield per plant (15.62 and 36.01%), fodder yield per plant (16.61 and 28.21%), harvest index (10.63 and 18.72%), protein content (19.95 and 20.06%), and calcium content (19.13 and 19.27%). These observations agreed with the findings of Mahanthesha *et al.* (2017) [19], Anuradha *et al.* (2017) [17], Devaliya *et al.* (2018) [20], Keerthana

et al. (2019) [21], Madhavilatha *et al.* (2021) [22], Bharathi *et al.* (2022) [23], Madhusri *et al.* (2022) [24], and Udamala *et al.* (2022) [25]. High estimates of both GCV and PCV were observed for iron content (33.92 and 34.02%) and zinc content (38.57 and 38.69%). Comparable findings were also reported by Savitha *et al.* (2013) [26] and Udamala *et al.* (2022) [25] (Table 6 and Figure III).

The highest estimate of broad-sense heritability was recorded for iron content (99.41%), followed by zinc content (99.38%), protein content (98.85%), calcium content (98.49%), 1000-grain weight (90.10%), and main ear-head length (77.65%). Moderate heritability was recorded for finger length (54.58%), finger width (52.61%), days to 50 per cent flowering (40.85%), plant height (37.00%), days to maturity (35.37%), fodder yield per plant (34.65%), and harvest index (32.26%). Low heritability was observed for grain yield per plant (18.82%), number of fingers per ear head (15.39%), and productive tillers per plant (7.20%) (Table 6 and Figure III).

High genetic advance as a percentage of the mean was recorded for zinc content (79.22%), followed by iron content (69.67%), protein content (40.85%), calcium content (39.10%), main ear-head length (28.21%), 1000-grain weight (27.90%), finger length (27.54%), and fodder yield per plant (20.14%). Moderate genetic advance as a percentage of the mean was observed for finger width (17.31%), grain yield per plant (13.96%), harvest index (12.44%), and plant height (10.83%). In contrast, low estimates were recorded for number of fingers per ear head (7.53%), productive tillers per plant (5.07%), days to 50 per cent flowering (4.96%), and days to maturity (4.29%) (Table 6 and Figure III).

High heritability accompanied by high genetic advance as a percentage of the mean was observed for main ear-head length, 1000-grain weight, protein content, calcium content, iron content, and zinc content. This combination indicated that these traits were predominantly governed by additive gene action and could therefore be effectively improved through direct selection. Similar observations for different traits were reported by John (2006) [14], Haradari *et al.* (2011) [27], Priyadharshini *et al.* (2011) [28], Ulaganathan and Nirmalakumari (2011) [15], Lule *et al.* (2012) [29], Reddy *et al.* (2013) [30], Wolie and Dessalegn (2013) [31], Suryanarayana *et al.* (2014) [16], Saundaryakumari and Singh (2015) [32], Mahanthesha *et al.* (2017) [19], Devaliya *et al.* (2018) [20], Keerthana *et al.* (2019) [21], Anuradha *et al.* (2020) [33], Gopal *et al.* (2021) [34], Madhavilatha *et al.* (2021) [22], Bharathi *et al.* (2022) [23], Madhusri *et al.* (2022) [24], Udamala *et al.* (2022) [25], Ketema *et al.* (2025) [35], Pavithra *et al.* (2025) [36], and Ujjainkar *et al.* (2025) [37].

Grain yield per plant exhibited low heritability combined with moderate genetic advance as a percentage of the mean. This suggested that the trait was strongly influenced by environmental factors, although some additive genetic effects were also involved. Therefore, direct phenotypic selection may not be sufficiently effective, and improvement may be achieved more successfully through progeny selection and recurrent selection in advanced generations. These findings were consistent with those reported by Savitha *et al.* (2013) [26].

Moderate heritability associated with moderate genetic advance as a percentage of the mean was observed for plant height, finger width, and harvest index. In contrast, days to 50 per cent flowering and days to maturity exhibited moderate heritability together with low genetic advance. These combinations suggested the involvement of both additive and non-additive genetic effects in the expression of the traits. Breeding approaches that efficiently utilize additive genetic variation,

such as the development of transgressive segregants, may therefore be combined with appropriate hybridization and selection procedures to achieve substantial improvement.

Finger length and fodder yield per plant exhibited moderate heritability coupled with high genetic advance as a percentage of the mean. This indicated that these traits were largely controlled by additive gene effects, although environmental factors also contributed to their expression. Selection based on phenotypic performance could therefore be useful, and improvement may be achieved through simple breeding methods such as mass selection or pedigree selection. In contrast, productive tillers per plant and number of fingers per ear head showed low heritability and low genetic advance as a percentage of the mean. These findings indicated a strong environmental influence and suggested that improvement through direct selection would be difficult.

Days to 50 per cent flowering, days to maturity, plant height, productive tillers per plant, and number of fingers per ear head displayed low to moderate estimates of GCV and PCV, indicating limited variability for these characters in the existing population. Their low to moderate estimates of heritability and genetic advance further suggested that the potential for improvement through direct selection within the present material was restricted.

When broad-sense heritability is mainly attributable to non-additive gene effects, the expected genetic gain from selection is generally low. Conversely, when high heritability results primarily from additive gene effects, substantial genetic advance may be expected. Genetic gain provides an estimate of the improvement likely to be achieved for a trait under an appropriate selection procedure. High heritability combined with high genetic advance indicates the predominance of additive gene action and a greater possibility of improving the trait through selection. High heritability accompanied by low genetic advance suggests that direct selection may not produce substantial improvement. Similarly, low heritability combined with low genetic advance indicates the importance of non-additive gene action and environmental effects. Moderate heritability associated with low genetic advance in some traits also suggests that non-additive genetic effects may contribute to trait expression, thereby limiting progress through simple selection procedures.

Overall, days to 50 per cent flowering and days to maturity exhibited low GCV and PCV together with low to moderate heritability and genetic advance. These traits are therefore expected to respond poorly to selection within the current population. This limitation may be addressed by increasing the genetic diversity of the breeding material through the introduction of germplasm from diverse sources. Greater genetic diversity would provide a broader range of potentially

useful alleles and increase the likelihood of identifying genotypes with substantial variation for the targeted characters. Selection should subsequently be directed towards plants exhibiting desirable phenotypic variability for these traits.

Plant height, productive tillers per plant, and number of fingers per ear head exhibited low GCV but moderate to high PCV, together with low to moderate estimates of heritability and genetic advance. Improvement of these traits would require increasing the relative contribution of genetic effects while minimizing environmental variation. This may be achieved by identifying and selecting favourable genes or alleles associated with the targeted traits and by ensuring greater consistency in phenotypic evaluation. Evaluation of breeding lines across multiple environments would further help assess performance and stability under diverse growing conditions. Such testing would enable breeders to distinguish genuine genetic effects from environmentally induced variation and identify lines that consistently express desirable characteristics.

Moderate to high GCV and PCV, accompanied by moderate to high heritability and genetic advance, were observed for main ear-head length, finger length, finger width, 1000-grain weight, grain yield per plant, and fodder yield per plant. As these characters are agronomically important, their improvement may be strengthened by broadening the genetic base of the breeding population. New genetic material may be introduced through the collection and utilization of germplasm from diverse geographical regions, collaboration with other breeding programmes, and exploration of centres of origin and diversity. Such approaches would enhance genetic variability and create greater opportunities for selecting superior genotypes.

Table 1: List of finger millet genotypes used for study

Sr. No.	Name of genotypes	Sr. No.	Name of genotypes
1	FM 4005	19	FM 3003
2	FM 3015	20	FM 3011
3	FM 4002	21	FM 4007
4	FM 3013	22	FM 3014
5	FM 3023	23	FM 3028
6	FM 3010	24	FM 4010
7	FM 3024	25	WN 494
8	FM 3018	26	FM 3021
9	FM 3019	27	FM 3004
10	FM 3020	28	FM 3025
11	FM 3022	29	FM 4008
12	FM 3001	30	ICFV 221036
13	FM 3027	31	FM 4006
14	FM 3017	32	FM 4004
15	FM 3008	33	FM 4001
16	FM 4011	34	FM 4009
17	FM 3007	35	FM 4003
18	FM 3026	-	-

Table 2: Categorization of genetic estimates

Estimates	GCV & PCV (%)	Heritability (h^2_b) (%)	GAM (%)
Low	0 to 10	0 to 30	0 to 10
Moderate	10 to 20	30 to 60	10 to 20
High	More than 20	More than 60	More than 20

Table 3: Analysis of variance (mean sum square) for the experimental design under individual environment for different characters in finger millet

Source of variation	D. F.	Days to 50 % flowering				Days to maturity				Plant height (cm)			
		E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4
Replications	2	2.66	3.27	3.80	2.90	0.09	0.18	2.01	4.20	17.31	46.20	4.09	33.06
Genotypes	34	38.33**	41.72**	28.46**	42.60**	59.65**	98.16**	50.77**	78.50**	355.42**	351.64**	551.87**	597.62**
Error	68	2.47	2.19	2.29	2.31	11.36	5.77	5.22	5.17	20.76	20.56	29.66	29.55

Source of variation	D. F.	Productive tillers per plant				Main ear head length				Finger length			
		E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4
Replications	2	0.01	0.002	0.0004	0.01	0.08	0.43	0.14	0.54	0.10	0.08	0.23	0.09
Genotypes	34	0.73**	0.46**	1.00**	0.42**	5.08**	4.68**	5.51**	4.80**	3.99**	2.78**	3.13**	2.73**
Error	68	0.03	0.02	0.03	0.01	0.21	0.32	0.25	0.27	0.09	0.06	0.11	0.05

Source of variation	D. F.	Finger width				Number of fingers per ear head				1000 grain weight			
		E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4
Replications	2	0.001	0.02	0.002	0.01	0.01	0.12	0.16	0.19	0.01	0.0003	0.01	0.001
Genotypes	34	0.04**	0.05**	0.12**	0.06**	3.17**	1.63**	3.51**	7.81**	0.40**	0.35**	0.36**	0.42**
Error	68	0.003	0.005	0.01	0.004	0.37	0.27	0.30	0.30	0.01	0.01	0.01	0.02

Source of variation	D. F.	Grain yield per plant (g)				Fodder yield per plant (g)				Harvest Index (%)			
		E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4
Replications	2	0.40	1.13	0.98	0.15	0.42	1.61	0.31	0.67	3.78	11.39	2.95	2.77
Genotypes	34	14.00**	7.42**	15.53**	22.93**	54.10**	40.10**	38.12**	80.87**	47.83**	56.02**	61.72**	62.65**
Error	68	1.08	0.85	1.03	0.79	3.71	3.48	3.22	2.88	10.16	9.96	9.65	8.05

Source of variation	D. F.	Protein (%)				Calcium content (mg/100g)			
		E1	E2	E3	E4	E1	E2	E3	E4
Replications	2	0.02	0.15	0.10	0.01	10.17	3.80	64.61	207.23
Genotypes	34	5.96**	6.06**	5.78**	5.75**	8554.90**	8608.89**	8467.19**	9122.54**
Error	68	0.05	0.07	0.04	0.06	49.83	82.48	79.82	54.51

Source of variation	D. F.	Iron content (mg/100g)				Zinc content (mg/100g)			
		E1	E2	E3	E4	E1	E2	E3	E4
Replications	2	0.005	0.02	0.02	0.0003	0.002	0.01	0.0002	0.0003
Genotypes	34	3.54**	3.64**	3.70**	3.80**	1.33**	1.39**	1.37**	1.41**
Error	68	0.01	0.02	0.01	0.01	0.001	0.004	0.004	0.01

* and ** significant at 5% and 1% levels of significance, respectively. E1: Deesa, E2: Sardarkrushinagar, E3: Bhiloda and E4: Ladol

Table 4: Analysis of variance (mean sum square) for the experimental design over environments for different characters in finger millet

Source of variation	Degree of freedom	Mean sum of square							
		Days to 50% flowering	Days to maturity	Plant height	Productive tillers per plant	Main ear head length	Finger length	Finger width	Number of fingers per ear head
Replications	2	8.41*	0.40	48.97	0.001	0.40	0.06	0.006	0.29
Environments	3	1177.14**	2127.6**	375.17**	7.824**	1.22**	18.35**	2.380**	13.11**
Genotypes	34	114.21**	205.58**	1352.45**	1.019**	18.75**	10.58**	0.217**	8.3**
G × E	102	12.3**	27.17**	168.03**	0.527**	0.44**	0.69**	0.015**	2.61**
Pooled Error	278	2.29	6.77	24.96	0.021	0.26	0.08	0.004	0.30
S.Em ±		0.87	1.50	2.88	0.083	0.29	0.16	0.038	0.32
CD at 5%		2.43	4.18	8.03	0.233	0.82	0.45	0.107	0.89
CV (%)		1.96	2.36	4.35	6.58	6.43	5.64	5.93	7.47

Source of variation	Degree of freedom	Mean sum of square							
		1000 grain weight	Grain yield per plant	Fodder yield per plant	Harvest index	Protein content	Calcium content	Iron content	Zinc content
Replications	2	0.008	0.68	1.42	8.60	0.10	129.08	0.001	0.001
Environments	3	0.108**	180.69**	160.09**	384.46**	0.03	10.91	0.006	0.002
Genotypes	34	1.488**	33.39**	151.48**	157.76**	23.48**	34620.97**	14.657**	5.491**
G × E	102	0.014	8.83**	20.57**	23.49**	0.02	44.18	0.007	0.002
Pooled Error	278	0.012	0.93	3.26	9.34	0.06	66.34	0.012	0.003
S.Em ±		0.063	0.56	1.04	1.76	0.14	4.70	0.065	0.034
CD at 5%		0.176	1.55	2.90	4.91	0.38	13.09	0.182	0.097
CV (%)		4.48	10.54	9.08	9.71	3.39	2.90	3.49	3.45

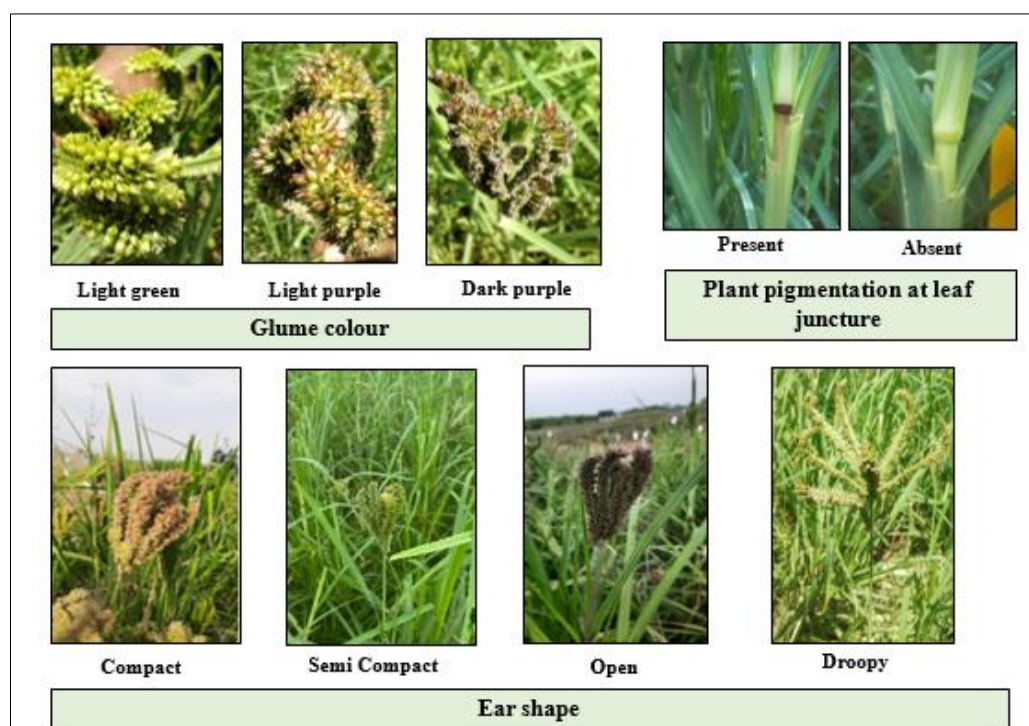
* and ** significant at 5% and 1% levels of significance, respectively

Table 5: Mean, minimum and maximum values along with respective genotypic, environmental and phenotypic variances over environments for different characters in finger millet

Sr. No.	Characters	Range		Mean	Variance		
		Minimum	Maximum		Genotypic	Environmental	Phenotypic
1	Days to 50 % flowering	68.00	89.33	77.37	8.49	12.30	20.79
2	Days to maturity	97.00	128.00	110.23	14.87	27.17	42.03
3	Plant height (cm)	76.80	141.20	114.91	98.70	168.03	266.73
4	Productive tillers per plant	1.20	4.00	2.21	0.04	0.53	0.57
5	Main ear head length (cm)	5.60	11.70	7.95	1.53	0.44	1.97
6	Finger length (cm)	3.20	8.80	5.02	0.82	0.69	1.51
7	Finger width (cm)	0.69	1.94	1.12	0.02	0.02	0.04
8	Number of fingers per ear head	4.80	10.32	7.39	0.47	2.61	3.08
9	1000 grain weight (g)	1.60	3.20	2.46	0.12	0.01	0.13
10	Grain yield per plant (g)	3.36	15.89	9.16	2.05	8.83	10.88
11	Fodder yield per plant (g)	7.40	29.85	19.89	10.91	20.57	31.48
12	Harvest index (%)	20.42	42.99	31.46	11.19	23.49	34.68
13	Protein content (%)	3.58	10.03	7.01	1.95	0.02	1.98
14	Calcium content (mg/100g)	187.07	388.47	280.66	2881.40	44.18	2925.58
15	Iron content (mg/100g)	1.95	6.01	3.26	1.22	0.01	1.23
16	Zinc content (mg/100g)	0.84	3.85	1.75	0.46	0.001	0.461

Table 6: Genotypic and Phenotypic Coefficient of Variation (GCV and PCV) for different characters along with respective heritability, genetic advance and genetic advance (% of mean)

Sr. No.	Characters	GCV (%)	PCV (%)	ECV (%)	Heritability (Broad sense %)	Genetic advance	Genetic advance (% of mean)
1	Days to 50 % flowering	3.77	5.89	4.53	40.85	3.84	4.96
2	Days to maturity	3.50	5.88	4.73	35.37	4.72	4.29
3	Plant height	8.65	14.21	11.28	37.00	12.45	10.83
4	Productive tillers per plant	9.16	34.15	32.90	7.20	0.11	5.07
5	Main ear head length	15.54	17.64	8.34	77.65	2.24	28.21
6	Finger length	18.09	24.49	16.50	54.58	1.38	27.54
7	Finger width	11.58	15.97	10.99	52.61	0.19	17.31
8	Number of fingers per ear head	9.32	23.75	21.85	15.39	0.56	7.53
9	1000 grain weight	14.27	15.03	4.73	90.10	0.69	27.90
10	Grain yield per plant	15.62	36.01	32.44	18.82	1.28	13.96
11	Fodder yield per plant	16.61	28.21	22.81	34.65	4.01	20.14
12	Harvest index	10.63	18.72	15.40	32.26	3.91	12.44
13	Protein content	19.95	20.06	2.15	98.85	2.86	40.85
14	Calcium content	19.13	19.27	2.37	98.49	2.89	39.10
15	Iron content	33.92	34.02	2.60	99.41	2.27	69.67
16	Zinc content	38.57	38.69	3.04	99.38	1.39	79.22

**Fig 1:** Descriptors of finger millet genotypes for glume colour, plant pigmentation at leaf juncture and ear shape

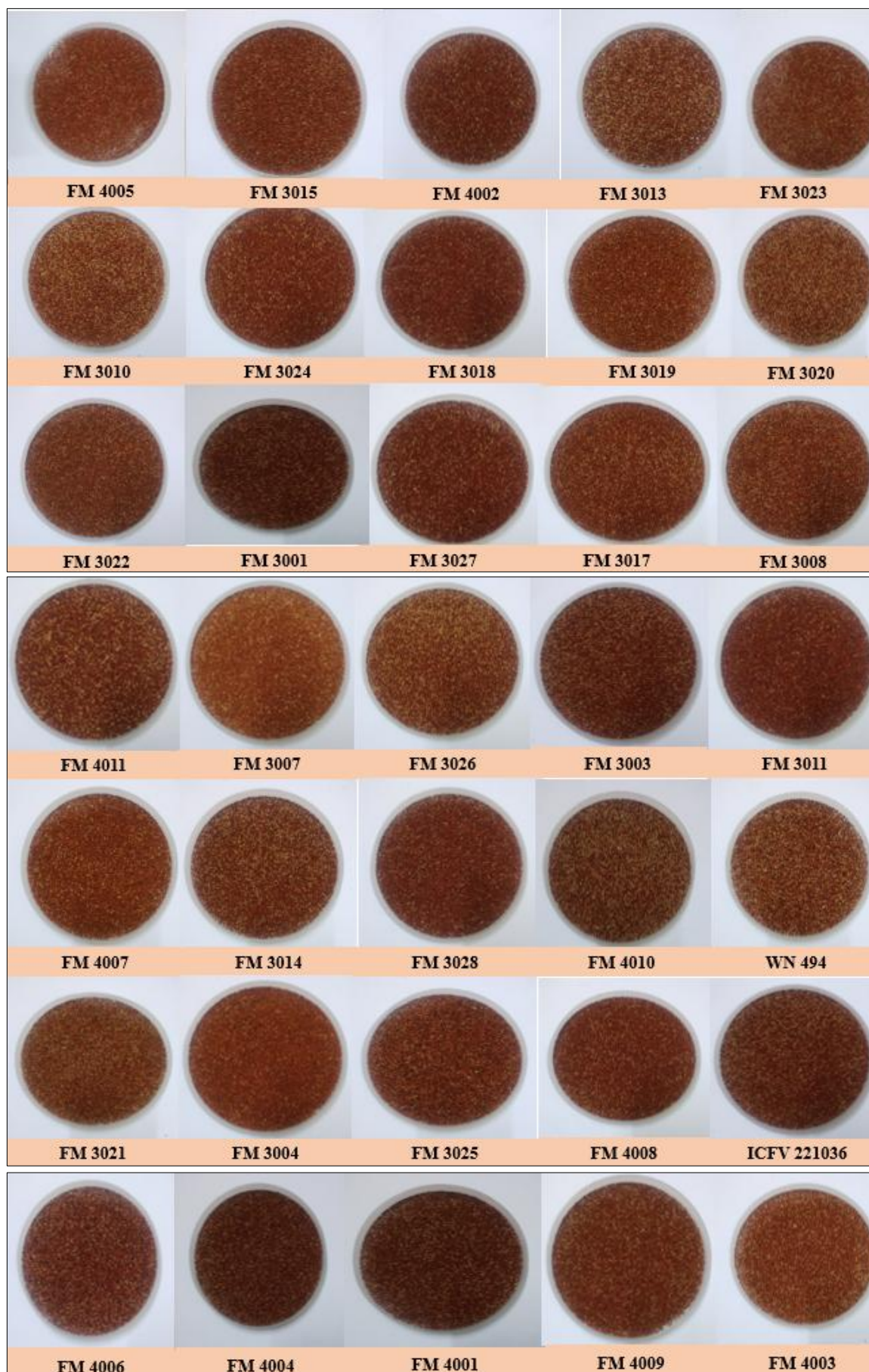


Fig 2: Variability present among finger millet genotypes for seed colour

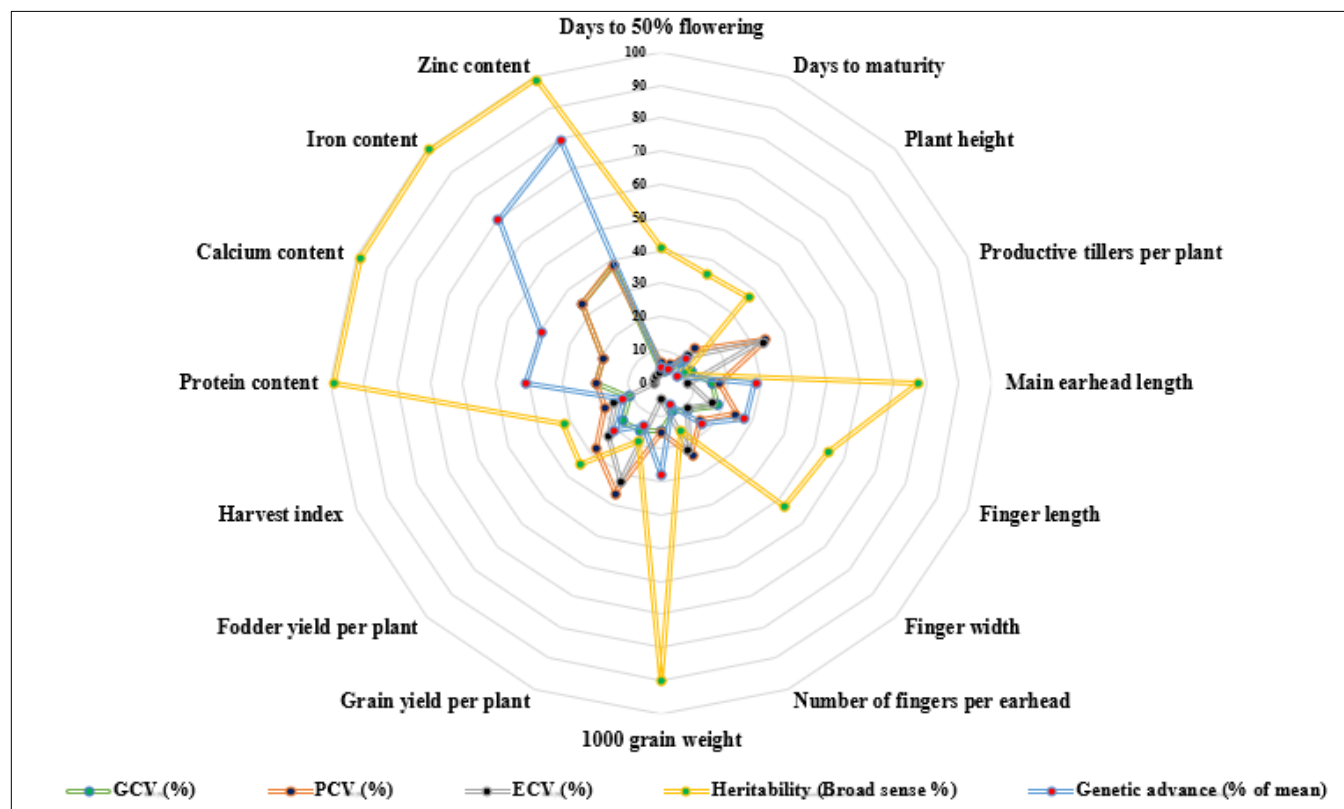


Fig 3: GCV, PCV and ECV for different characters along with respective heritability and genetic advance (% of mean)

Conclusion

The present investigation demonstrated significant genetic variability among the finger millet genotypes for all the traits studied, indicating adequate opportunities for genetic improvement through selection. Significant genotype $\times$ environment interactions for most morphological characters revealed that the genotypes responded differently across environments, emphasizing the need for multi-environment evaluation to identify stable and widely adapted genotypes.

High heritability accompanied by high genetic advance as a percentage of the mean was observed for main ear-head length, 1000-grain weight, protein content, calcium content, iron content, and zinc content. These results indicated the predominance of additive gene action and suggested that direct selection for these traits would be effective in future breeding programmes. In contrast, grain yield per plant, productive tillers per plant, and number of fingers per ear head were strongly affected by environmental factors. Improvement of these traits would therefore require progeny selection, recurrent selection, and evaluation across multiple locations.

Overall, traits exhibiting high heritability and substantial genetic advance can be effectively utilized for developing high-yielding and nutritionally superior finger millet cultivars. The promising genotypes identified in the study may also serve as valuable parents in future hybridization and crop-improvement programmes.

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