

Genetic Variability Studies in Finger Millet [*Eleusine coracana* (L.) Gaertn]

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ABSTRACT

An experiment was conducted to study the genetic variability, heritability and genetic advance by using 240 finger millet genotypes (including two checks) for eight traits during *Kharif* 2023 and summer 2023 at Zonal Agricultural Research Station, UAS, GKVK, Bengaluru. Analysis of variance for *Kharif*-23 and Summer-23 have exhibited the significant differences for all the characters studied indicating the presence of a substantial amount of genetic variability. The phenotypic coefficient of variation (PCV) was a little greater than genotypic coefficient of variation (GCV) for all the traits studied which shows the minor influence of the environmental effect on the traits. During *kharif* 2023, high PCV and GCV were observed for number of productive tillers/plant, number of fingers/earhead, earhead weight (g) and grain yield (g). Similar results were also obtained during summer 2023, except for number of fingers/earhead which exhibited low PCV and GCV indicating that the selection based on these characters would be effective for future finger millet crop improvement program. High heritability coupled with moderate genetic advance as per cent of mean was observed for plant height, days to 50 per cent flowering and test weight. High heritability coupled with high genetic advance as per cent of mean was observed for number of productive tillers/plant, number fingers/earhead, finger length (cm), ear head weight (g) and grain yield (g). These findings suggested the little influence of environment in trait expression; hence selection could be effective and can be used for finger millet crop improvement.

Keywords : Genetic variability studies in finger millet (*Eleusine coracana* (L) Gaertn, Finger millet, PCV, GCV, Grain yield, *Kharif*

MILLETS are highly nutritious grains, boasting significant amounts of protein, fiber and essential vitamins and minerals such as calcium, iron and magnesium. Their rich nutritional profile makes millets an excellent food choice, particularly for women and children, as they can help prevent malnutrition and ensure nutritional well-being. Small millets are especially valuable due to their ability to thrive in diverse agro-ecological

conditions and adapt to varied geographical environments (Patel *et al.*, 2018).

Due to their high fiber and protein content, millets are highly recommended as dietary supplements for individuals managing diabetes and cardiovascular diseases (Patil *et al.*, 2019). Finger millet (*Eleusine coracana* L.) is a prominent millet variety, ranking among the top three most cultivated millets, along

with pearl millet and great millet. Finger millet is well-suited for dry farming and is primarily grown as a rainfed crop (Vilas *et al.*, 2015).

This crop is significant, because it can be consumed both in its natural form (to make malted beverages and infant foods) and after processing, offering a valuable source of calcium and dietary fiber (Gopalan *et al.*, 1989 and Rao & Muralikrishna, 2001). In India, during 2021-2022, small millets were cultivated on 1.45 million hectares, with finger millet accounting for 1.004 million hectares, yielding 1.76 million tonnes at a productivity rate of 1747 kg/ha (Anonymous, 2023).

Low productivity of this crop is attributed to the use of low-yielding cultivars and a scarcity of stress-tolerant varieties (Madhavilatha *et al.*, 2019). While breeding programs often prioritize yield improvement (Yan *et al.*, 2002), Several morphological traits influence yield, possessing higher heritability than grain yield itself. Therefore, selection for these traits could be a more effective approach to enhance yield. Selection based on yield-contributing characteristics can be more successful than selection solely on yield performance (Fisher, 1918).

To develop high-yielding varieties, breeders need to understand the heritability of target traits and predict genetic gain under selection (Johnson *et al.*, 1955b). To devise effective breeding strategies for enhancing finger millet, a study was conducted using 238 Recombinant Inbred Lines (RILs) with two checks to examine grain yield and yield related traits, focusing on genetic parameters such as Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), heritability and genetic advance.

MATERIAL AND METHODS

The present study was carried out at Zonal Agricultural Research Station (ZARS), GKVK, Bengaluru for during *kharif*2023 and Summer 2023. The experiment was conducted using 238 RILs derived from parents GE 1746 and GPU 28 and both the parents were used as checks and these were evaluated in Alpha

lattice design with two replications. Each block consisted of 15 rows of 3m length with a spacing of 30×10cm. The observations were recorded on five random plants in each replication in both the seasons and their mean values were used for the statistical analysis. The data was recorded on eight quantitative traits *viz.*, days to 50 per cent flowering, plant height (cm), number of productive tillers, number of fingers, finger length (cm), ear head weight (g), test weight (g) and grain yield (g). Observations on eight characters were recorded on five competitive plants which were selected randomly from each genotype in replication. A Days to 50 per cent flowering was the only character which was recorded on whole plot basis.

To determine significant differences among the genotypes for the studied traits, the analysis of variance (ANOVA) technique, as outlined by Panse and Sukhatme (1978), was employed. The pooled analysis of variance and the parameters *viz.*, critical difference and coefficient of variation were calculated for all 8 traits for both the seasons and is represented in Table 1a and 1b. Genotypic, phenotypic and environmental variances were calculated using the formulas described by Johnson *et al.* (1955a). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were determined using Burton's (1952) formulas and classified into low, moderate and high categories, following the guidelines of Burton and De Vane (1953).

The proportion of phenotypic variability attributable to genetic factors (heritability) was calculated as a percentage, using Allard's (1960) formula. Heritability percentages for all traits were categorized based on the recommendations of Robinson *et al.* (1949). The expected genetic advance (GA) for each trait was estimated using the method proposed by Allard (1960) and the genetic advance as a percentage of the mean was calculated according to Johnson *et al.* (1955b).

RESULTS AND DISCUSSION

In this study, genetic variability in metric traits was assessed using statistical parameters *viz.*, mean, range,

variance components and coefficients of variation. Understanding genetic variability is crucial as it provides foundational insights into the genetic characteristics of a population, guiding the development of effective breeding strategies for crop improvement. These analyses help to determine the nature and extent of variability resulting from various factors, the crop's sensitivity to environmental influences, trait heritability and potential genetic advance.

For all the eight studied traits the analysis of variance has shown significant difference ($P < 0.001$)

among all the genotypes which are summarized in Table 1a & 1b, Fig. 1a & 1b. The substantial genetic variability observed among the genotypes indicates significant potential for enhancing yield and other desirable traits. Similar results were found by Meenakshi *et al.* (2024), Anand *et al.* (2024), Nagaraja *et al.* (2023), Yadav *et al.* (2023), Divya *et al.* (2022) and Sindhuja *et al.* (2019) in finger millet genotypes.

The mean, minimum and maximum values for all the eight traits among the 240 genotypes are presented in the Table 2a and 2b for *kharif* 2023 and Summer-2023 respectively. The estimates of GCV,

TABLE 1a
Pooled analysis of variance for eight traits under study in finger millet *Kharif* - 2023

Sources of variation	DF	Mean sum of Squares							
		PH	DFF	NPT	NF	FL	EHW	GY	TW
Replication	1	79.8 **	28.3 **	0.1291 **	0.1981 **	0.2113 **	50.9 **	20.5 **	0.059 **
Genotype	239	98.2 **	20.02 **	2.5996 **	2.318 **	1.6004 **	1435.7 **	1143.9 **	0.166 **
Replication × Block	15	548.2 **	171.3 **	0.7218 **	1.9494 **	1.9221 **	524.9 **	355.5 **	5.409 **
Pooled Error	224	1.8	0.62	0.0058	0.0093	0.0083	3.8	2.9	0.008
S.Em±		1.341 641	0.787 401	0.0761 58	0.0964 37	0.0911 04	1.9493 59	1.7029 39	0.08 9443
CD@5%		2.644 776	1.552 203	0.1501 3	0.1901 05	0.1795 94	3.8427 71	3.3570 03	0.17 6318
CV (%)		1.27	1.2	1.98	1.52	1.45	1.877	2	2.95

DF: Degrees of freedom, PH-Plant height (cm), DFF-Days to fifty per cent flowering, NPT- number of productive tillers/plant, NF-Number of fingers/ear head, FL- Finger length (cm), EHW- Ear head weight (g), GY- Grain yield (g), TW-Test weight (g)

TABLE 1b
Pooled analysis of variance for eight characters under study in finger millet Summer - 2023

Sources of variation	DF	Mean sum of Squares							
		PH	DFF	NPT	NF	FL	EHW	GY	TW
Replication	1	110.1 **	37.41 **	0.142 **	0.2955 **	0.2018 **	203.1 **	26.3 **	0.057 **
Genotype	239	265.6 **	31.53 **	0.8623 **	0.6197 **	2.3756 **	3097.4 **	2112.2 **	0.165 **
Replication × Block	15	654.3 **	264.84 **	0.7781 **	1.9969 **	1.7974 **	594.7 **	349.9 **	5.374 **
Pooled Error	224	2.5	0.74	0.0034	0.0065	0.0094	19	5.2	0.009
S.Em±		1.581139	0.860233	0.05831	0.080623	0.096954	4.358899	2.280351	0.094868
CD@5%		3.11701	1.695837	0.11495	0.158937	0.191131	8.593003	4.495415	0.187021
CV (%)		1.35	1.16	1.46	1.25	1.5	4.12	2.65	5.88

TABLE 2a
Mean and range for all eight characters
during *kharif* - 2023

Characters	Range		Mean
	Min	Max	
Plant height (cm)	73.4	128.4	106.3
Days to 50% flowering	48	71.8	59.4
Number of productive tillers/plant	1.3	15.6	3.8
Number of fingers/earhead	4.2	20.6	6.3
Finger length (cm)	3.1	8.9	6.3
Ear head weight (g)	23.0	176.9	103.6
Grain yield (g)	19.2	170.6	85.1
Test weight (g)	2.4	4.0	3.1

TABLE 2b
Mean and range for all eight characters
during Summer-2023

Characters	Range		Mean
	Min	Max	
Plant height (cm)	64.6	148.1	116.2
Days to 50% flowering	59.5	84.2	73.6
Number of productive tillers	2.3	6.2	4.0
Number of fingers	3.8	8.3	6.4
Finger length (cm)	4.1	9.6	6.1
Ear head weight (g)	39.4	316.2	105.6
Grain yield (g)	28.8	239.2	85.6
Test weight (g)	2.3	4.0	3.1

PCV, h^2 (bs) and GAM for all the characters is presented in Table 3a & 3b, Fig. 1a & 1b, for *kharif*-23 and Summer-23 respectively.

The mean value of genotypes in *kharif*-23 for plant height was ranged from 73.4 to 128.3 cm with a mean of 106.3 cm; days to 50 per cent flowering ranged from 48 to 71.8 days with a mean of 59.4 days;

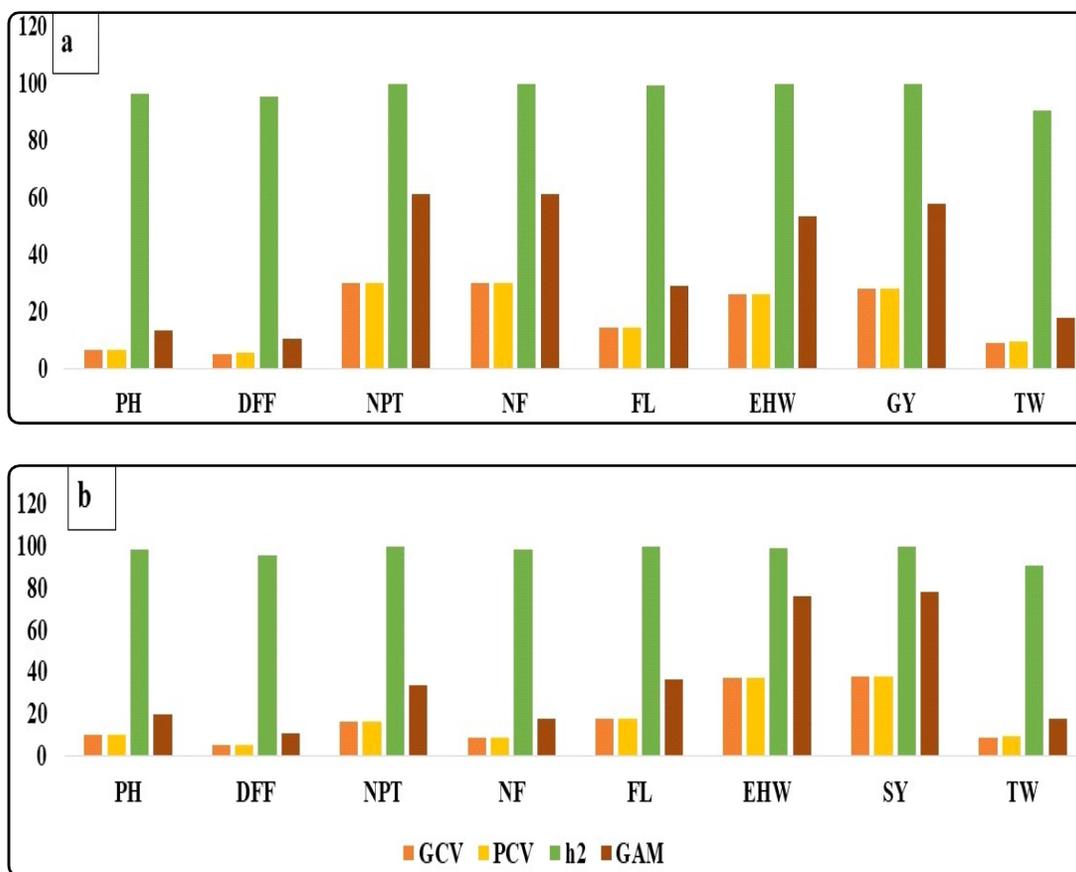


Fig. 1 : Histogram representation of genetic variability parameters of eight characters during a) *kharif*, 2023, b) summer, 2023 - Where, GCV Genotypic co-efficient of variation PCV-Phenotypic co-efficient of variation, h^2 -heritability in broad sense, GAM-Genetic advance as per cent over mean character

number of productive tillers/plant ranged from 1.3 to 15.6 with mean of 3.8; number of fingers/ear head ranged from 4.2 to 20.6 with a mean of 6.3; finger length ranged from 3.1 to 8.9 cm with mean of 6.3 cm; ear head weight ranged from 23.0 g to 176.9 g with mean of 103.5 g; grain yield for five plants varied from 19.2 to 170.6 g with mean 85.1 g and test weight varied from 2.3 to 4.0 g with mean of 3.1g.

PH-Plant height, DFF-Days to fifty per cent flowering, PT- number of productive tillers, NF-Number of fingers, FL- Finger length, EHW- Ear head weight, GY- Grain yield, TW-Test weight, Su- Summer.

The mean value of genotypes during summer 2023 season Summer-23 for plant height was ranged from 64.6 to 148.1 cm with a mean of 116.2; days to 50 per cent flowering ranged from 59.5 to 84.2 with a mean of 73.6 days; number of productive tillers/plant ranged from 2.3 to 6.24 with mean of 4.00; number of fingers ranged from 3.8 to 8.3 with a mean of 6.4; finger length ranged from 4.1 to 9.6 cm with mean of 6.1 cm; ear head weight ranged from 39.4 g to 316.2 g with mean of 105.6 g; grain yield varied from 28.8 to 239.2 g with mean 85.6 g and test weight varied from 2.3 to 4.0 g with mean of 3.1g. Similar results were observed by Chavan *et al.*, (2019) in finger millet for plant

TABLE 3a
Genetic variability parameters for eight characters in finger millet during *kharif* 2023

Characters	GCV (%)	PCV (%)	Heritability (Broad sense %)	Genetic advance	Genetic advance (% of mean)
Plant height (cm)	6.5	6.7	96.3	14.0	13.2
Days to 50% flowering	5.3	5.4	94.9	6.3	10.6
Number of productive tillers/plant	29.8	29.8	99.6	2.3	61.1
Number of fingers/earhead	29.8	29.8	99.6	2.3	61.1
Finger length (cm)	14.2	14.3	98.	1.8	29.1
Ear head weight	25.8	25.9	99.5	54.9	53.1
Grain yield (g)	28.1	28.1	99.5	49.1	57.7
Test weight (g)	9.0	9.5	90.3	0.6	17.7

TABLE 3b
Genetic variability parameters for eight characters in finger millet during summer 2023

Characters	GCV (%)	PCV (%)	Heritability (Broad sense %)	Genetic advance	Genetic advance (% of mean)
Plant height (cm)	9.9	9.9	98.2	23.4	20.1
Days to 50% flowering	5.3	5.4	95.4	7.9	10.7
Number of productive tillers/plant	16.4	16.5	99.2	1.3	33.7
Number of fingers/earhead	8.7	8.7	97.9	1.1	17.6
Finger length (cm)	17.9	17.9	99.2	2.2	36.7
Ear head weight	37.1	37.4	98.9	80.3	76.0
Grain yield (g)	37.9	38.0	99.5	66.7	77.9
Test weight (g)	8.9	9.5	90.1	0.6	17.6

height, number of fingers/earhead, finger length, test weight.

The phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the characters studied (Table 3a and 3b) and there was a little difference between the values of PCV and GCV indicating the lower influence of environment for the studied characters. Similar results were obtained by Dantie *et al.*, (2019) and Meenakshi *et al.*, (2024) in finger millet genotypes. Low PCV and GCV were observed for days to 50 per cent flowering, plant height (cm) and test weight (g). Moderate PCV and GCV was observed for finger length (cm) and high PCV and GCV were observed for number of productive tillers/plant, number of fingers, ear head weight (g) and grain yield/plant (g). Similar results were obtained in Summer season also except for number of fingers/earhead which had exhibited low PCV and GCV.

The high magnitude of PCV and GCV suggested the presence of sufficient amount of variation for the studied characters, which provides ample scope for selection and crop improvements, these outcomes were consistent with Bhavsar *et al.*, (2020) Shashibhushan *et al.* (2022) and Meenakshi *et al.*, (2024), whereas low to moderate GCV and PCV provides limited scope for selection and crop improvement.

Heritability, representing the heritable component of phenotypic variance, serves as a valuable indicator of how characters are transmitted from parents to offspring (Falconer, 1964). Johnson *et al.*, (1955a) suggested that using heritability and genetic advance in combination is more effective for predicting superior individuals than relying on either measure alone. To ensure effective selection, a character with high heritability should ideally also exhibit a substantial genetic advance.

In *kharif*-23, all the genotypes under the study exhibited high heritability coupled with moderate GAM for plant height, days to 50 per cent flowering, and test weight (g) similar results were obtained by Meenakshi *et al.*, (2024) for plant height and days to

50 per cent flowering. High heritability coupled with high GAM was observed for number of productive tillers/plant, number fingers/earhead, finger length (cm), ear head weight (g) and grain yield (g). These results are in accordance with Bhavsar *et al.*, (2020) for plant height, days to 50 per cent flowering, productive tillers/plant, number of fingers/earhead, finger length and Meenakshi *et al.*, (2024) for number of productive tillers/plant, number of fingers/earhead, finger length and ear head weight.

Similar results were found for summer-23 for all the genotypes except for characters *viz.*, plant height which has shown high heritability coupled with GAM and Number of fingers / earheads which exhibited high heritability with moderate GAM. Similar results were obtained by Mahalle *et al.*, (2024). Since most of the traits have exhibited high heritability and GAM, indicating that the variability in these genotypes can be used in breeding and crop improvement programmes.

High magnitude of PCV, GCV, heritability and GAM for the characters *viz.*, number of productive tillers/plant, earhead weight and grain yield have indicated the presence of ample amount of variation, which provides scope for selection and improvement of the crop.

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