The ANDHRA AGRICULTURAL JOURNAL Since 1954

The Andhra Agric. J 72 (3): 291-295, 2025
doi :10.61657/aaj.2025.211

Genetic variability studies for yield and its components in finger millet (*Eleusine coracana* (L.) Gaertn) accessions

N Bhagyasri, N Anuradha, D Ratna Babu and K Kiran Prakash
Department of Genetics and Plant Breeding, Acharya N G Ranga Agricultural University,
Agricultural College, Bapatla-522101, Andhra Pradesh, India

ABSTRACT

The present study was carried out using 50 finger millet accessions evaluated for 14 traits at Agricultural Research Station, Vizianagaram, during *kharif* 2024-25 in randomized complete block design with 2 replications. Analysis of variance revealed significant differences among genotypes for all traits, indicating presence of sufficient genetic variability. High genotypic and phenotypic coefficients of variation were observed for number of productive tillers per plant, finger width (cm), fodder yield per plant (g) and grain yield per plant (g) while days to 50% flowering, ear length (cm), finger length (cm) and 1000 grain weight (g) showed moderate GCV and PCV values. High heritability coupled with high genetic advance as percent of mean was recorded for days to 50% flowering, ear length, finger width, number of productive tillers per plant, thousand grain weight, fodder yield per plant and grain yield per plant indicating that these traits are largely governed by additive gene action and can be effectively improved through simple selection.

Keywords: *Finger millet, Genetic Advance, Heritability and Variability*

Finger millet (*Eleusine coracana* (L.) Gaertn), a member of the Poaceae family within the monocotyledon group, is commonly referred to as ‘Ragi’ or ‘Mandua’. The common name finger millet is derived from the finger-like branching of the panicle. The cultivated species, *Eleusine coracana*, is a predominantly self-pollinating allotetraploid (AABB) with a chromosome number of 2n = 4x = 36. Finger millet is primarily cultivated in arid and semiarid regions of Africa and Asia, including countries like India, Uganda, Ethiopia, Nepal and Kenya. It is very adaptable to a wide range of environmental and climatic conditions and thrives at higher elevations than most other tropical cereals and ability to withstand salinity better than most cereals.

It is the third most important millet crop after sorghum and pearl millet and the most important small millet in the tropics covering 12% of the global millet area. In India, finger millet ranks first in importance among all small millets with a share of 81% in production (Sajja *et al.* 2025). It is cultivated over an area of more than 12.14 lakh hectares with 16.69 lakh tones and 1375 kg/ha of production and productivity, respectively in India. While in Andhra Pradesh, it is cultivated in 27 thousand hectares with a production and productivity of 34.05 thousand tonnes and 1261 kg/ha, respectively (Ministry of Agriculture, 2023-24).

Finger millet is highly nutritious as it is rich source of calcium (344 mg/100 g) and also contains 65-75% carbohydrates, 5-8% protein, 15-20% dietary fibre and 2.5-3.5% minerals. Due to its gluten-free and low fat, it is easy to digest and non-allergic and that is why finger millet is also called “super cereal” (Singh *et al.,* 2023).

Expanding the genetic base of germplasm requires a thorough understanding of the existing genetic variation among available genotypes. Without genetic variation, selection and breeding cannot bring about improvement. When coupled with parameters like heritability and genetic advance, it helps to also determine effectiveness of selection particularly in improving complex traits like yield. It can be effectively estimated using phenotypic and genotypic coefficients of variation. Yield is a complex quantitative trait which cannot be improved by selecting individuals on performance basis. Thus, it can be improved by practicing selection for other traits which are highly heritable and are interrelated with the yield as well. Genetic advance indicates the amount of progress that could be expected with selection for a particular trait. Estimates of heritability along with estimates of genetic advance are more useful in selection rather than heritability or genetic advance alone (Johnson *et al.,* 1955)

MATERIAL AND METHODS

The experimental material consists of 50 finger millet accessions including two checks (VR 929 and VL 376) which were collected from different states like Karnataka, Andhra Pradesh, Orrisa, Bihar, Gujarat and Uttarakhand. The experiment was laid out in randomized complete block design (RCBD) with two replications at agricultural research station, Vizianagaram during *Kharif* 2024-25, with a spacing of 22.5 cm between rows and 10 cm between plants respectively. All the recommended agronomic packages of practices were followed during the entire crop period. In each replication, five random plants were chosen and observations were recorded on 14 yield and yield contributing characters *viz.,* days to 50% flowering, plant height (cm), flag leaf length (cm), flag leaf width (cm), peduncle length (cm), ear length (cm), finger length (cm), finger width (cm), finger number on main ear, number of productive tillers per plant, days to maturity, thousand grain weight (g), fodder yield per plant (g) and grain yield per plant (g).

The analysis of variance for each character was calculated as per the standard statistical procedure given by Panse and Sukhatme (1978). Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed as per Burton and Devane (1953). Heritability in broad sense was computed as per Allard (1960). Heritability and genetic advance were categorized into low, medium and high as per Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Analysis of Variance

Analysis of variance revealed significant differences among all the characters indicating presence of sufficient variability in the studied material (Table 1). Thus, there is ample scope for selection of different quantitative characters for the genetic improvement of the crop through breeding. Based on mean values, the range for days to 50% flowering varied from 56 days (GE 2811) to 94 days (GE 162) with a mean of 74.20 days; days to maturity ranged from 84 days (GE 2811) to 128.5 days (GE 162) with a mean of 106 days; plant height ranged from 76.25 cm (GE 4468) to 123.12 cm (GE 1437) with a mean of 98.65 cm, number of productive tillers per plant varied from 2.10 (GE 4) to 7.30 (VL 376) with a mean of 4.34; finger number on main ear ranged from 6.45 (FM 220) to 11.44 (GE 4468) with a mean of 7.98, while ear length range varied from 5.81 cm (GE 390) to 11.22 cm (GE 6492) with a mean of 7.71 cm; peduncle length had 12.90 cm (VR 929) to 20.74 cm (GE 4468) with a mean of 16.73 cm; flag leaf length and width ranged from 23.48 cm (GE 390) to 37.30 cm (VL 376) with a mean of 29.70 and from 1.41 cm (GE 390) to 2.21 cm (GE 162) with a mean of 1.77 cm, respectively. Finger length ranged from 4.84 cm (GE 6614) to 9.71 cm (GE 6523) with a mean of 7.15 cm, finger width ranged from 0.53 cm (FM 505) to 1.51 cm (VL 376) with a mean of 0.81 cm, 1000 grain weight ranged from 1.37 g (FM 374) to 3.37 g (GE 2566) with a range of 2.56 g whereas fodder yield per plant varied from 10.18 g (GE 390) to 61.27 g (FM 2195) with a mean of 30.04 g and grain yield per plant ranged from 3.55 g (GE 390) to 21.78 g (VL 376) with an average of 10.52 g (Table 2).

Variability parameters

Crop improvement depends on the amount of genetic variability present in the germplasm. In the present study, phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits studied (Table 2). Phenotypic coefficient of variation ranged from 9.23% to 44.76% and genotypic coefficient of variation ranged from 4.35% to 43.26%. High PCV and GCV was recorded for number of productive tillers per plant (23.57, 21.20), finger width (29.02, 26.86), fodder yield per plant (33.78, 32.04) and grain yield per plant (44.76, 43.26). Hence, for these characters most of the variability is genetic and environmental effects are small. Similar results were reported by Sharma *et al.* (2022) and Hansalia *et al.* (2024) for number of productive tillers per plant, fodder yield per plant, grain yield per plant and Priya *et al.* (2023) for finger width. Moderate PCV and GCV was observed for days to 50% flowering (11.90, 11.80), ear length (17.39, 15.75), finger length (13.02, 10.80) and 1000 grain weight (15.21, 14.59). These conclusions were in accordance with Madhusri *et al.* (2022) and Jahnavi and Lal (2023). Low PCV and GCV was recorded for days to maturity (9.75, 9.64), plant height (9.92,

Table 1. Analysis of variance for 14 characters in 50 accessions of finger millet (*Eleusine coracana* (l.) Gaertn) Mean sum of squares

Source of variation	d.f	DFF	DM	PH	NPT	NFE	EL	PL	FLL	FLW	FL	FW	TW	FYP	GYP
Treatments	49	156.04**	213.31**	191.44**	2.10**	1.59**	3.59**	4.76*	22.68**	0.06**	1.73**	0.11**	0.30**	205.90**	44.33**
Replications	1	1.96	1.69	22.38	2.56	0.32	0.49	2.08	0.20	0.09	1.70	0.07	0.06	74.75	10.49
Error	49	2.61	4.75	44.27	0.40	0.58	0.64	3.71	10.96	0.02	0.54	0.02	0.02	20.66	2.93

*Significance at 5% level, ** Significance at 1% level.

d.f : Degrees of freedom, **DFF:** Days to 50% flowering, **PH:** Plant height (cm), **FLL:** Flag leaf length (cm), **FLB:** Flag leaf width (cm), **PL:** Peduncle length (cm), **EL:** Ear length (cm), **FL:** Finger length (cm), **FB:** Finger width (cm), **NFE:** Finger number on main ear, **NPT:** Number of productive tillers per plant, **DM:** Days to maturity, **TW:** 1000 grain weight (g), **FYP:** Fodder yield per plant (g), **GYP:** Grain yield per plant (g).

Table 2 Estimates of genetic parameters for 14 characters in 50 finger millet accessions (*Eleusine coracana* (L.) Gaertn).

S. No.	Character	Mean	Range		Coefficient of Variation		Heritability (broad sense) (%)	Expected Genetic advance as % of mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1	DFF	74.2	56.00	94.00	11.90	11.80	98.33	24.11
2	DM	105.95	84.00	128.50	9.75	9.64	97.77	19.63
3	PH	98.65	76.25	123.12	9.92	8.70	76.87	15.70
4	NPT	4.34	2.10	7.30	23.57	21.20	80.92	39.29
5	NFE	7.98	6.45	11.44	11.18	8.91	63.56	14.64
6	EL	7.71	5.81	11.22	17.39	15.75	82.10	29.40
7	PL	16.73	12.90	20.74	9.23	4.35	22.17	4.21
8	FLL	29.70	23.48	37.30	11.34	8.15	51.67	12.07
9	FLB	1.77	1.41	2.21	9.71	8.33	73.52	14.71
10	FL	7.15	4.84	9.71	13.02	10.80	68.88	18.47
11	FB	0.81	0.53	1.51	29.02	26.86	85.70	51.23
12	TW	2.56	1.37	3.37	15.21	14.59	91.98	28.82
13	FYP	30.04	10.18	61.27	33.78	32.04	89.97	62.61
14	GYP	10.52	3.55	21.78	44.76	43.26	93.39	86.11

PCV: Phenotypic coefficient of variation, **GCV:** Genotypic coefficient of variation**, DFF:** Days to 50% flowering, **PH:** Plant height (cm), **FLL:** Flag leaf length (cm), **FLB:** Flag leaf width (cm), **PL:** Peduncle length (cm), **EL:** Ear length (cm), **FL:** Finger length (cm), **FB:** Finger width (cm), **NFE:** Finger number on main ear, **NPT:** Number of productive tillers per plant, **DM:** Days to maturity, **TW:** 1000 grain weight (g), **FYP:** Fodder yield per plant (g), **GYP:** Grain yield per plant (g).

8.70), peduncle length (9.23, 4.35), flag leaf width (9.71, 8.33). Moderate PCV and low GCV were reported by finger number on main ear (11.18, 8.91) and flag leaf length (11.34, 8.15). These results are in accordance with previous reports of Gayatri *et al.* (2022) for plant height, Sharma *et al.* (2023) for peduncle length and days to maturity, Anuradha *et al.* (2017) for finger number on main ear, Singh *et al.* (2023) for flag leaf width and Anuradha *et al.* (2020) for flag leaf length.

Assessment of heritability provides an idea into the extent to which a trait is governed by genetic factors and plays a crucial role in determining its response to selection. When combined with the genetic advance as per cent of mean, heritability estimates become more useful in predicting gain under selection than heritability estimate alone. High heritability along with high genetic advance as per cent of mean (GAM) was observed for days to 50% flowering, ear length, finger width, number of productive tillers per plant, 1000 grain weight, fodder yield per plant and grain yield per plant indicating that these traits was less influenced by environment and governed by additive gene action which may be exploited through simple selection procedures. Similar conclusions were reported by Kumar *et al.* (2022) for finger width, 1000 grain weight, Jahnavi and Lal (2023) for days to 50% flowering and ear length, Priya *et al.* (2023) for fodder yield per plant, Sharma *et al.* (2023) for number of productive tillers per plant and grain yield per plant. High heritability coupled with moderate genetic advance as per cent of mean was recorded for days to maturity, plant height, finger number on main ear, flag leaf length, flag leaf width and finger length, indicating the predominance of both additive and non-additive gene action. Similar results were reported by Kumar *et al.* (2022) for finger number on main ear and finger length, Madhusri *et al.* (2022) for flag leaf length and flag leaf width and Singh *et al.* (2023) for days to maturity.

CONCLUSION

In the present study high PCV and GCV, coupled with high heritability and genetic advance as percent of mean was recorded for number of productive tillers per plant, finger width, fodder yield per plant besides grain yield per plant in finger millet accessions suggesting that these traits are under strong genetic control and direct selection for these traits would be effective for overall improvement in accessions included in the study.

LITERATURE CITED

Allard R W 1960. Principles of Plant Breeding. John Wiley and Sons Inc, New York. 485.

Anuradha N, Patro T S S K, Divya M, Rani Y S and Triveni U 2017. Genetic variability, heritability and association in advanced breeding lines of finger millet [Eluesine coracana (L.) Gaertn.]. *International Journal of Chemical Studies.* 5 (5): 1042-1044.

Anuradha N, Patro,T S SK, Triveni U and Rao P J 2020. Heritability and trait association in finger millet [*Eleusine Coracana* (L.)]. *Journal of Pharmacognosy and Phytochemistry.* 9 (4): 768-771.

Burton G W and Devane E M 1953. Estimating heritability in tall Fescue (*Festuca arundinaceae*) from replicated clonal material. *Agronomy Journal*. 51: 515-518.

Gayatri C U, Lal G M, Elangovan M and Anwar S 2022. Estimation of Genetic Variability Direct and Indirect Effects of Yield Contributing Traits on Grain Yield in Finger Millet [*Eleusine coracana* (L.)]. *International Journal of Environment and Climate Change*. 3355–3360.

Hansalia M A and Pali V 2024. Assessment of genetic variability for morphological and nutritional traits in finger millet [*Eleusine Coracana* L. Gaertn.]. *Plant Archives*. 24 (2): 2695-2699.

Jahnavi A and Lal G M 2023. Genetic variability for yield and yield attributing traits in finger millet [*Eleusine coracana* L. Gaertn] under irrigation in central India. *International Journal of Plant & Soil Science*. 35 (19): 392-403.

Johnson H W, Robinson H F and Comstock R E 1955. Estimates of genetic and environmental variability in soyabean. *Agronomy Journal.* 47: 314-318.

Kumar R, Jaiswal M, Mishra A, Yadav D, Prajapati P K and Mishra U K 2022. Genetic variability studies for yield and related attributes in finger millet (*Eleusine Coracana*) genotypes. *International Journal of Plant & Soil Science*. 34 (23): 1763-1770.

Madhusri D, Lavanya G R and Elangovan M 2022. Phenotypic diversity of finger millet [*Eleusine coracana* (L.) Gaertn.] genotypes for grain yield characters. *International Journal of Plant & Soil Science*. 34 (20): 139-148.

Ministry of Agriculture, 2023-2024. Government of India. http://www.indisatat.com

Panse V G and Sukhatme P V 1978. *Statistical Methods for Agricultural Workers*. ICAR, New Delhi.

Priya P K, Anuradha N, Ganapathy K N, Patro T S S K, Kumar P R and Ramesh D 2023. Assessment of variability, heritability and genetic advance for quantitative characters in finger millet [*Eleusine coracana* (L.) Gaertn] Germplasm. *The Andhra Agricultural Journal.* 70 (1): 034-038.

Sajja S, Pranati J, Shyamala S, Vinutha K S, Reddy R, Joshi P, Pannem S, Rakshit P., Jadhav Y, Kumar C V and Mayes S 2025. Rapid Ragi: A speed breeding protocol for finger millet. *Plant Methods*. 21 (1): 1-10.

Sharma M, Madhusudan K, Vasisth P and Gupta P 2023. Characterization of novel germplasm for yield and yield related traits in finger millet [*Eleusine coracana* L. Gaertn.]. *Annals of Agricultural Research*. 44 (1): 106-114.

Sharma NIDHI, Bandyopadhyay B B, Chand SUBHASH, Pandey P K, Baskheti D C, Malik A and Chaudhary R 2022. Determining selection criteria in finger millet [*Eleusine coracana* (L.) Gaertn.] genotypes using multivariate analysis. *The Indian Journal of Agricultural Sciences.* 92(6): 763-68.

Singh A, Sehrawat K D, Sehrawat ANISH, Singh M and Sehrawat R A 2023. Assessing the genetic diversity of finger millet [*Eleusine coracana* (L.) Gaertn.] germplasm for agronomic traits. *The Indian Journal of Agricultural Sciences.* 93 (5): 489-494.

Received on 12.08.2025 and Accepted on 14.09.2025