International Journal of Agriculture and Food Science 2025; 7(12): 389-391

ISSN Print: 2664-844X
ISSN Online: 2664-8458
NAAS Rating (2025): 4.97
IJAFS 2025; 7(12): 389-391
www.agriculturaljournals.com
Received: 19-09-2025
Accepted: 26-10-2025

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Genetic variability studies in finger millet (*Eleusine Corcana* L.)

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DOI: https://www.doi.org/10.33545/2664844X.2025.v7.i12e.1069

Abstract

Genetic diversity was assessed in finger millet (*Eleusine coracana* L.) germplasms with 33 genotypes of finger millet collected from various sources which were evaluated in RBD at ZARS, Igatpuri during *kharif* 2024. A treatment sum of squares was significant for all the characters studied indicated considerable amount of variability. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters studied indicating the role of environment in expression of characters. The characters *viz.*, fodder yield per plot (kg), number of productive tillers and grain yield per plot (kg) exhibited high GCV and PCV effects indicating the presence of large variation among the genotypes for these characters.

The traits plant height, iron content, fodder yield per plot, flag leaf length grain yield per plot, crude fibre, test weight and peduncle length showed high estimates of heritability (b.s.) accompanied by high genetic advance as per cent of mean signifying that these characters could be prominently governed by additive gene action and direct selection of these traits could be rewarded.

Keywords: Genetic advance as per cent of mean, Genotypes, GCV, heritability, Finger millet, PCV

Introduction

Finger millet *(Eleusine coracana* L.) belongs to the family *poaceae (gramineae)* subfamily *panicoideae* and genus *Eleusine*, considered a self-pollinated crop. It is an allotetraploid (2n = 4X = 36), mainly found in the arid and semiarid tropics and subtropics (Fakrudin *et al.* 2004), the domesticated crop of African origin and it is spread throughout the world. The crop is grown in a wide range of challenging environmental situations. It is a blessing for vast arid and semi-arid regions because it can be cultivated on low-fertility soils. Often regarded as a staple food, used as animal feed (straw) in industrialized countries and as food (grains) in underdeveloped. It is a major crop of semi-arid and arid regions and developing nations of Asia and Africa.

The southern states of India are where finger millet is primarily grown in Asia, and these regions have ideal growing conditions. Finger millet is the fourth most produced millet in the world after sorghum, pearl millet and foxtail millet. During the year 2022-23 India produced 1.70 million tonnes of finger millet, which is grown over 1.07 million hectare area (Anonymous, 2023) [1]. The states Karnataka, Andhra Pradesh, Tamil Nadu, Maharashtra, Kerala, Telangana, Uttarakhand, Jharkhand, Madhya Pradesh and Haryana are important producers of finger millet. The area and production under finger millet have reduced over the years in the state. In Maharashtra, Nashik and Kolhapur are major finger millet growing districts and from 1997-98 to 2023-24 they contributed about an average of 46 % area and 48 % production of finger millet in the state. The area and production of finger millet have been reducing over the years in the districts (Anonymous, 2024) [2].

Considering its nutritional composition, the declining production will affect the supply of finger millet to the increasing population across India. Hence, efforts are required to maintain and increase the area and production of finger millet. The use of varied, traditional landraces of finger millet maintained by farmers is one of the reasons for the low area and production hence, the identification of higher-yielding genetic resources to use in breeding programmes by evaluation of local germplasm is prerequisite.

Material and Methods

The experiment entitled, "Genetic diversity and nutraceutical composition analysis in finger millet (*Eleusine coracana* L)" was conducted at Zonal Agriculture Research Station, Igatpuri during *Kharif* 2024. The experimental material used for the study consisted of 31 newly collected finger millet genotypes from adjoining area of Igatpuri Tahasil of Nasik district along with two check varieties Phule Nachani and Phule Kasari. All were obtained from the Zonal Agriculture Research Station, Igatpuri. The net plot size was 3.0 m x 2.4 m. The spacing was 22.5 cm x 10.0 cm. The following data were collected for each replication for 14 characters *viz;* Days to 50% flowering, days to maturity, plant height (cm), number of tillers per plant, finger length (cm), number of fingers per plant, peduncle length (cm), flag leaf length (cm), Thousand seed weight (g), grain yield (kg/plot), fodder yield (kg/plot), Calcium content (mg/100g), Crude fiber content (%) and Iron content (mg/100g).

Analysis of variance for the Randomized Block Design were done as per the method suggested by Panse and Sukhatme (1967) [10]. The genotypic and phenotypic covariances were then calculated as per the formulae given by Johnson *et al.* (1955) [6]. Heritability estimates in broad sense (h^2) were computed by the formula suggested by Lush (1940) [9]. From heritability estimates the genetic advance was estimated by the formula given by Johnson *et al.* (1955) [6]. In order to estimate the relative utility of genetic advance among characters, genetic advance as percent for mean is usually calculated. The range of genetic advance as percent of mean was classified as per suggestion by Johnson *et al.* (1955) [6].

Results and Discussion

Analysis of variance exposed significant differences among the genotypes for all the quantitative characters as presented in Table 1. The mean of square due to genotype showed highly significant difference for all the traits *viz*., days to 50 per cent flowering, days to maturity, plant height, finger length, number of fingers per plant, peduncle length, flag leaf length, number of productive tillers per plant, Thousand seed weight, fodder yield per plot, crude fiber content, iron content, calcium content and grain yield per plot indicating that adequate variability was found in the genotype studied for these characters because of diverse genotypes. These results were confirmed by Charitha and Lal (2023) and Kumar *et al.* (2023) [4, 8].

The parameters range, GCV and PCV, heritability in broad sense and genetic advance as per cent of mean have been presented in Table 2. Fodder yield per plot (59.03%) showed high estimates of GCV accomplished by grain yield per plot (37.79%), number of productive tillers per plant (24.81%), no. of fingers/plant (21.11), iron (21.08%). While test weight (12.79%), peduncle length (14.53%), flag leaf length (12.13%), finger length (15.50%), plant height (14.82%) and crude fibre (17.42%), calcium (12.73%) exhibited medium GCV. However, days to maturity (3.24%) and days to 50 per cent flowering (2.88%) exhibited low GCV.

Fodder yield per plot (59.47%) showed high estimates of PCV accomplished by grain yield per plot (39.36%) and productive tillers/plant (25.99%), iron (23.68%), no. of fingers/plant (21.78%). The medium PCV were recorded in crude fibre (18.69 %), finger length (16.78%), peduncle length (16.39%), plant height (15.71%), test weight (13.80%) flag leaf length (13.81%), calcium (13.13%), days to 50 per cent flowering (4.01%) and days to maturity (3.67%) exhibited low PCV.

Similar findings were reported by Patel *et al.* (2017) [11] reported high heritability with moderate GCV and genetic advance for days to flowering and maturity. Bharathi *et al.* (2023) [3] also noted high heritability for days to flowering, indicating potential for early maturing lines. Ramakrishnan *et al.* (2016) [12] reported low heritability for plant height in finger millet due to significant environmental effects.

This study depicted high heritability for all character except days to 50% flowering indicating that these traits are governed predominantly by additive gene action and have less environmental influence in their expression and direct phenotypic selection can be followed for these characters in breeding programme for development of high yielding genotypes.

Similar findings were reported by Ramesh *et al.* (2002) [13], who observed high heritability for grain yield, number of fingers per plant, and plant height in finger millet. Kumar *et al.* (2016) [7] observed high heritability for traits such as days to maturity, flag leaf length, and peduncle length, indicating the possibility of effective phenotypic selection.

Table 1: Analysis of variance (ANOVA) for fourteen characters in finger millet

Sr. No.	Character	Mean Sum of Square		
		Replication	Genotypes	Error
1	Days to 50 per cent flowering	5.47	23.32**	7.44
2	Days to maturity	0.97	37.92**	4.75
3	Plant height (cm)	2.97	316.18**	18.38
4	Finger length (cm)	0.04	2.85**	0.23
5	No. of Fingers/ Plant	0.288	3.264**	0.101
6	Peduncle length (cm)	0.05	7.98**	0.91
7	Flag leaf length (cm)	0.64	24.70**	3.19
8	Number of productive tillers per plant	0.0102	0.4666**	0.0217
9	Test weight (g)	0.29	0.26**	0.02
10	Fodder yield per plot (kg)	0.000002	0.21**	0.00
11	Crude Fibre %	0.089	0.918**	0.065
12	Iron (mg/100g)	0.22	3.54**	0.07
13	Calcium (mg/100g)	13.64	3170.99**	97.82
14	Grain yield per plot (kg)	0.00002	0.013**	0.00053

** indicate significant at 1 per cent level, respectively

Table 2: Parameters of genetic variability for yield and yield contributing characters in finger millet genotypes

Sr. No.	Name of the characters	GCV %	PCV %	ECV %	Heritability [h^2 (b.s.)] %	G.A.	G.A. as % of means
1.	Days to 50 % flowering	2.88	4.01	2.79	51.63	4.17	4.27
2.	Days to maturity	3.24	3.67	1.73	77.73	7.40	5.88
3.	Plant height (cm)	14.82	15.71	5.21	89.01	23.72	28.81
4.	Finger length (cm)	15.50	16.78	6.43	85.33	2.18	29.50
5.	No. of Fingers/ plant	21.11	21.78	5.33	94.02	2.51	42.18
6.	Peduncle length (cm)	14.53	16.39	7.58	78.61	3.33	26.54
7.	Flag leaf length	12.13	13.81	6.60	77.15	5.93	21.95
8.	Productive tillers/ plant	24.81	25.99	7.76	91.09	0.93	48.77
9.	Test weight (g)	12.79	13.80	5.18	85.92	24.42	12.79
10.	Fodder yield/plot (kg)	59.03	59.47	7.26	98.51	0.66	120.69
11.	Crude Fibre %	17.42	18.69	6.77	86.86	1.25	33.44
12.	Iron (mg/100g)	21.08	23.68	10.78	79.26	2.19	38.66
13.	Calcium (mg/100g)	12.73	13.13	3.21	94.01	78.30	25.44
14.	Grain yield /plot (kg)	37.79	39.36	11.00	92.19	0.16	74.74

Conclusion

The genotypic and phenotypic coefficient of variation (GCV and PCV) were categorized as high, medium, or low. The characters fodder yield per plot, number of productive tillers and grain yield per plot exhibited highest GCV and PCV effects. However, medium estimates of genotypic (GCV) and phenotypic coefficients of variation (PCV) had shown by plant height, finger length, test weight, peduncle length, flag leaf length, crude fibre and calcium. While days to 50 per cent flowering and days to maturity, showed low GCV and PCV effects.

In the present study the characters all characters except days to 50 % flowering and days to maturity showed high heritability coupled with low genetic advance, therefore selection of such character is not rewarding because of presence of non- additive gene action and heterosis breeding may be useful.

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