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ASSESSMENT OF GENETIC VARIABILITY FOR MORPHOLOGICAL AND NUTRITIONAL TRAITS IN FINGER MILLET (*ELEUSINE CORACANA* L. GAERTN.)

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ABSTRACT

The study was conducted with 50 finger millet genotypes to evaluate 12 morphological and seven nutraceutical traits at the Agricultural Research Station, AAU, Muvaliya farm, Dahod during the *kharif*, 2023. The objective was to evaluate different genetic variability parameters. High genotypic and phenotypic coefficient of variation along with high heritability and high genetic advance as a percent of mean was observed for the number of productive tillers per plant, grain yield per plant, harvest index, protein content, total carbohydrate content, total phenol content, antioxidant activity and iron content. These traits will be improved in further generations by direct phenotypic selection. High heritability was found for all traits except the main earhead length showing the influence of environmental factors on this trait while nutraceutical traits show maximum heritability showing very little influence of environment.

Key words : Finger millet, Genetic variability, Broad sense heritability, Genetic advance, Nutraceutical traits.

Introduction

Finger millet is the most interesting miracle crop from the genus *Eleusine* in the family Poaceae. *Eleusine coracana* (L.) Gaertn consists of chromosome 2n = 4x = 36 and is an allotetraploid. It is an important small millet crop coming under the cereal group and ranks fourth in the country after sorghum, pearl millet and foxtail millet. Globally India, Ethiopia, Nepal, Uganda and Malawi are the top countries in terms of area (99.4%) and production (99.6%). During the last decade finger millet was grown in 28.1 lakh hectares area and produced 38.3 lakh tonnes of grain with 1362 kg/ha productivity worldwide. India is top on the table with 11.63 lakh hectares area and 16.91 lakh tonnes of grain production with productivity 1454 kg/ha higher than the global productivity in the year 2022-23(Bhat *et al.*, 2023). Karnataka is the leading state in acreage and production followed by Uttarakhand, Tamil Nadu, Maharashtra and Odisha (Anonymous, 2023).

Finger millet's wider adaptation in different environments even in drought-prone areas, low levels of input requirement and acclimatization in hilly agroecosystems make it a "crop of the future" (Li and Siddique, 2020). It is alsoconsidered a food security crop because of its excellent nutritional quality and exceptional storage qualities without any damage. Calcium - one of the main supplements of the human body is the highest (310-370 mg/100g) in finger millet among all cereals. It also contains vitamin B complex (specifically niacin, B_6 and folic acid), iron, potassium, magnesium and zinc. Grain with a low glycemic index releases glucose slowly in the bloodstream making it an excellent choice for diabetic patients. Good source of protein, carbohydrates, fat minerals and other vitamins making it a powerful tool for combating malnutrition in Asian and African countries. Also, it contains high levels of amino acids (methionine, lysine and tryptophan) with high fiber are preferred by people with cardiovascular and constipation problems (Mirza and Marla, 2019).

Yield is regulated by many genes (polygenes) and a complex quantitative trait. In the selection programme selecting yield alone is not effective. Therefore, selecting traits with high heritability and which are interrelated with yield is effective. For that genetic variability should be present within the crop population. Thus, understanding genetic variability within a population is most important for any crop through selection. The selection of parents with highly diverse backgrounds is an important criterion for the success of any hybridization programme and the effective selection of hybrids. Therefore, this study was conducted to examinethe variability for yield contributing traits in fifty finger millet genotypes by evaluating different genetic parameters *viz*., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability $\left(h_{bs}^2\right)$ and genetic advance as a percent of mean (GAM).

Materials and Methods

For this study, 50 finger millet genotypeswere collected from the Agricultural Research Station, AAU, Muvaliya farm, Dahod. The crop was sown at Agricultural Research Station, AAU, Dahod during the *kharif* 2023. This station is located at 22° 83' N latitude, 74° 26' E longitude and 286 m above sea level. All 50 diverse genotypes were arranged in Randomized Complete Block Design (RCBD) in three replications with 22.5 cm inter-row and 10 cm between plant spacing.

For 12 morphological and seven nutraceutical parameters, data were taken. Days to 50% flowering and days to maturity were observed on a plot basis while traits like plant height (cm), number of productive tillers per plant, finger length (cm), finger width (cm), number of fingers per earhead, main earhead length (cm), grain yield per plant (g), straw yield per plant (g), harvest index (%) data were taken by selecting five random plants from each replication. 1000 grain weight (g) and quality parameters analysis were done by taking a required quantity of seed needed for a particular parameter from bulk produce of the plot.Seven nutraceutical parameters estimated using different methods: protein content (%) was determined by micro-kjeldhal distillation method (A.O.A.C., 1990), total carbohydrate content was calculated using anthrone method (Hedge and Hofreiter,1962), total phenol content (%) was determined by folin-ciocalteau method (Malik and Singh, 1980), antioxidant activity (%) was determined by method developed by Sreemalu *et al.* (2009) and micronutrients *viz.*, Ca (ppm), Fe (ppm) and Zn (ppm) were analyzed by atomic absorption spectroscopy (AAS) method suggested by Sen Gupta *et al.* (2020).

Analysis of variance estimated using the method given by Panse and Sukhatme (1978). For each trait, genetic variability analysis was done using various variability parameters. Genotypic, phenotypic and environmental variance was computed using the method given by Johnson *et al.* (1955a). Genotypic and phenotypic coefficient of variation was calculated using formulae given by Burton (1952). Broad sense heritabilityand genetic advance as a percent of mean were measured using a formula proposed by Allard (1960) and Johnson *et al.* (1955b), respectively.

Results and Discussion

For all 19 traits studied, analysis of variance indicated significant genetic differences among all genotypes, which are summarised in Table 1. A considerable amount of genetic variability presented among genotypes suggested a wide range for improvement in yield and other traits. Table 2 showed the genetic variability parameters like GCV (%), PCV (%), (%) and GAM (%) for all traits studied.

The phenotypic coefficient of variation value is higher than the genotypic coefficient of variation for all the traits showing the influence of environmental factors in a study of the variation of traits. High genotypic and phenotypic coefficient variation was recorded for the number of productive tillers per plant, grain yield per plant, harvest index, protein content, total carbohydrate content, total phenol content, antioxidant activity and iron content, suggesting high scope for improvement of traits by selection programme because of ample variability present in the studied material. High genotypic and phenotypic coefficients of variation for such traits were also examined by researchers including Charitha and Lal (2023) for the number of productive tillers per plant and harvest index; Hema *et al.* (2022) for grain yield per plant; Gopal *et al.* (2021) for protein content, antioxidant activity and iron content; Thakre *et al.* (2023) for total carbohydrate content in foxtail millet and Sahithi Reddy (2022) for total phenol content in sorghum. Moderate phenotypic and genotypic coefficients of variation were observed for finger length, number of fingers per earhead, 1000 grain weight and zinc content. This result indicates a chance of further improvement by selecting individual traits based on the observed wide range of variation. For these traits Keerthana *et al.* (2019) also observed similar variations in finger length; Divya *et al.* (2022) for the number of fingers per earhead; Sharma *et al.* (2023) for 1000 grain weight and Nagargoje (2015) for zinc content. Moderate GCV and High PCV were found for straw yield per plant indicating a moderate to high degree of variability in the studied population. This result is similar

Table 1 : Analysis of variance (mean sum of squares) for different characters under study in finger millet.

Characters	**Mean Sum of Squares**		
	Replications (df: 02)	**Genotypes (df: 49)**	**Error (df: 98)**
Days to 50% flowering	18.32	80.29**	7.98
Days to maturity	6.50	173.60**	8.37
Plant height	112.91	376.70**	51.95
Number of productive tillers per plant	0.12	1.39**	0.10
Finger length	2.22*	5.71**	0.62
Finger width	0.003	0.022**	0.003
Number of fingers per earhead	0.02	2.95**	0.41
Main earhead length	3.63*	2.04**	1.11
1000 grain weight	0.04	0.62**	0.02
Grain yield per plant	15.73*	52.17**	3.96
Straw yield per plant	59.71	192.80**	25.19
Harvest index	150.96	549.25**	56.62
Protein content	0.34*	8.83**	0.10
Total carbohydrate content	4.99	315.18**	2.35
Total phenol content	0.00010	0.00186**	0.00004
Antioxidant activity	0.00025	0.05105**	0.00033
Calcium content	304.12	312427.97**	10836.50
Iron content	0.41	25.33**	0.14
Zinc content	0.42	2.18**	0.14

to the study done by Yadav *et al.* (2023). Low GCV and Moderate PCV were found for plant height, finger width and main earhead length, suggesting a moderate level of variability present in the population. Similar results were examined earlier by researchers; Divya *et al.* (2022) for plant height; Patel *et al.* (2020) for finger width and Hema *et al.* (2022) for main earhead length. Low genotypic and phenotypic coefficients of variations were observed for days to 50% flowering, days to maturity and calcium content indicated genotypes under study had a limited variability among them. For these traits, Anand *et al.* (2024) also observed similar variation in days to 50% flowering and days to maturity while Devaliya *et al.* (2018) for calcium content.

High heritability with high genetic advance as a percent of mean was found for most traits like the number of productive tillers per plant, finger length, number of fingers per earhead, 1000 grain weight, grain yield per plant, straw yield per plant, harvest index, protein content, total carbohydrate content, total phenol content, antioxidant activity and iron content,suggesting that all above traits were primarily influenced by the additive gene action so direct phenotypic selection will be useful to improve these traits. Similarly high heritability with high genetic advance as a percent of mean for such traits were also examined by researchers including Divya *et al.* (2022) for the number of productive tillers per plant, finger length, number of fingers per earhead, grain yield per plant and straw yield per plant; Gopal *et al.* (2021) for 1000 grain weight, protein content, antioxidant activity and iron content; Patil *et al.* (2023) for harvest index; Thakre *et al.* (2023) for total carbohydrate content in foxtail millet and Sahithi Reddy (2022) for phenol content in sorghum. Traits like days to maturity, plantheight, finger width, calcium content and zinc content showed high heritability with moderate genetic advance as a percent of mean. The prevalence of additive gene action for these traits indicates that direct phenotype selection will lead to improvement. High heritability with moderate genetic advance as a percent of mean for these traits was also examined by Das *et al.* (2016); Keerthana *et al.* (2019); Patil *et al.* (2019) and Anand *et al.* (2024). High heritability with low genetic advance as a percent of mean was observed for only days to 50% flowering, suggesting the trait was primarily influenced by non-additive gene action then selection will be less effective so alternative breeding strategies, such as utilizing hybrid vigour to exploit non-additive gene action.Anjana *et al.* (2023) also observed similar result for days to 50% flowering. Low heritability with low genetic advance as a percent of mean was found for the main earhead length which indicated phenotypic variability seen for this trait is mainly due to environmental factors rather than genetic factors so improvements achieved through selection would be less effective. This result was in accordance with Anuradha *et al.* (2020).

Findings from this study showed that significant genetic variability was present among 50 genotypes of the finger millet study. A wide range of variation was observed across all 19 traits studied. Moderate to high genotypic and phenotypic coefficient of variation along with high heritability and high genetic advance as a percent of mean observed for most of the traits viz., number of productive tillers per plant,finger length,number of fingers per earhead, 1000 grain weight, grain yield per plant,harvest index,protein content, total carbohydrate

Table 2: Genetic variability parameters for different morphological and nutraceutical traits in finger millet.

Characters	σ^2_g	σ^2_p	**Variance**	**GCV(%)**	**PCV(%)**	**GAM(%)**
Days to 50% flowering	24.10	32.08	5.50	6.34	75.13	9.81
Days to maturity	55.07	63.45	5.91	6.35	86.81	11.35
Plant height	108.25	160.20	8.90	10.83	67.57	15.07
Number of productive tillers per plant	0.43	0.53	23.85	26.36	81.84	44.44
Finger length	1.70	2.32	16.98	19.83	73.32	29.95
Finger width	0.006	0.009	8.86	10.73	68.16	15.07
Number of fingers per earhead	0.85	1.26	13.22	16.11	67.33	22.34
Main earhead length	0.31	1.42	5.78	12.34	21.94	5.58
1000 grain weight	0.20	0.22	13.17	13.69	92.55	26.11
Grain yield per plant	16.07	20.03	31.55	35.22	80.23	58.21
Straw yield per plant	55.87	81.06	18.73	22.57	68.93	32.04
Harvest index	164.21	220.83	38.36	44.49	74.36	68.15
Protein content	2.91	3.01	23.46	23.88	96.56	47.50
Total carbohydrate content	104.28	106.62	24.57	24.84	97.80	50.05
Total phenol content	0.00061	0.00065	22.57	23.30	93.75	45.01
Antioxidant activity	0.0169	0.0172	33.03	33.35	98.09	67.38
Calcium content	100530.49	111366.99	9.36	9.85	90.27	18.32
Iron content	8.39	8.54	28.92	29.16	98.34	59.07
Zinc content	0.68	0.82	10.26	11.25	83.21	19.28

σ^2_g : Genotypic variance, σ^2_p : Phenotypic variance, **GCV:** Genotypic coefficient of variation, **PCV:**Phenotypic coefficient of variation, h^2_{bs} **:** Broad sense heritability, **GAM:** Genetic advance as apercent of mean.

content, total phenol content, antioxidant activity and iron content. Moderate to high GCV and PCV values suggest a high scope for improvement of these traits through selection programmes because a wide range of variability is present in the studied material while High heritability with high genetic advance as a percent of mean suggests that traits were primarily influenced by additive gene action making a direct phenotypic selection effective.

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