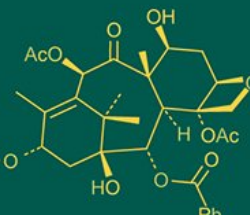


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Genetic variability and breeding potential of yield and yield-associated traits in white finger millet (*Eleusine coracana* (L.) Gaertn.)

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Abstract

The current investigation entitled “Genetic Variability and Breeding Potential of Yield and Yield-Associated Traits in White Finger Millet [*Eleusine coracana* (L.) Gaertn.]” was carried out at four locations viz., Hill Millet Research Station, Navsari Agricultural University, Waghai, The Dangs; Cotton Research Sub Station, Navsari Agricultural University, Achhalia; N. M. College of Agriculture, Navsari Agricultural University, Navsari and Krishi Vigyan Kendra, Dediapada during *kharif* 2023, using 40 finger millet genotypes in Randomized Complete Block Design (RCBD). Pooled analysis of variance indicated mean sum of squares for genotypes to be significant for all traits suggesting large amount of variability among different genotypes. The variation for environment and genotype × environment interaction was significant for all the morphological traits, indicating differential performance of genotypes across environments, whereas biochemical traits show non-significant genotype × environment interaction, suggesting relatively stable expression of these traits over environments. Promising genotypes according grain yield per plant based on per se performance viz., WVN 49, GN 5, CFMV 2, CFMV 3 and WVN 32. High estimates of heritability and genetic advance were found in all biochemical parameters as well as days to 50% flowering, ear head length, weight of matured panicle per plant, indicating additive gene action, thus simple selection would improve such traits. Moderate heritability along with high genetic advance as percent of mean was observed for grain yield per plant and fodder yield per plant. Combination of selective breeding and multi-location trials coupled with phenotypic selection would be effective for all such traits.

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

Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn.), popularly known as ragi or mandua, belongs to the family Poaceae, genus *Eleusine* and subfamily Chloridoideae. It is a highly self-pollinated allotetraploid species with a chromosome number of $2n = 36$. Finger millet is believed to have originated from its wild relative *Eleusine africana*, which evolved from the wild tetraploid ancestor *E. coracana* subsp. *africana*. After sorghum and pearl millet, finger millet is the third most important cereal crop among millets in India in terms of area and production. The annual herbaceous plant *E. coracana*, commonly known as finger millet, ragi, or nagli in Gujarat, is known by different names in various parts of India, including nagli, bavto, ragi, kezhvaragu, ragulu, nachani, and mandua. It is widely cultivated as a cereal crop in the arid and semi-arid regions of Africa and India.

Finger millet is recognized for its high nutritional value compared with many other cereals. It contains approximately 344 mg calcium per 100 g, 7-10% protein, 3.9 mg iron per 100 g and several other essential minerals. In India, the area under small millets during 2021-2022 was 1.45 million hectares, with finger millet occupying 1.004 million hectares, producing 1.76 million tonnes, and a productivity of 1747 kg/ha (Anonymous, 2023) [2]. The United States National Academies have recognized finger millet as one of the most nutrient-dense major cereals, making its potential as a “super cereal” (Manjunath *et al.*, 2013) [6]. Traditionally, brown-coloured grains are predominant and preferred by consumers. However, white-grained finger millet is preferred by the food-processing industry because of its higher protein content, lower tannin content and greater consumer acceptability (Sharathbabu *et al.*, 2008) [12]. In addition to its nutritional benefits, finger millet is an environmentally

sustainable crop. It has a relatively short growing season, requires comparatively low soil fertility and can easily endure extreme climatic conditions [Singamsetti *et al.*, 2018, Ulaganathan *et al.* 2014] ^[14, 15]. However, soil salinity is one of the important abiotic stresses limiting the growth and productivity of finger millet. This environmental stress can adversely affect crop growth and quality [Hema *et al.*, 2014] ^[5]. Considering its nutritional and environmental importance, greater attention is required for the improvement of finger millet through systematic breeding programmes aimed at increasing yield and productivity.

The identification and development of superior genotypes with broad environmental adaptability require a comprehensive understanding of genetic variability, heritability, genetic advance and the direction and magnitude of association among yield and yield-contributing traits. Such information can facilitate the selection of promising genotypes and improve the efficiency of breeding programmes [Nandini *et al.*, 2010; Patil and Mane, 2013; Reddy *et al.*, 2013; Satish *et al.*, 2003; Shet *et al.*, 2010] ^[7, 9, 10, 11, 13]. The magnitude and nature of genetic variability in any crop are genetically controlled but are also influenced by environmental conditions and they determine the effectiveness of selection for yield and yield-contributing traits [Wright, 1921; Fisher, 1936] ^[16, 4]. Therefore, the assessment of genetic variability, heritability and genetic advance is essential for identifying traits and genotypes with greater potential for genetic improvement in finger millet.

Materials and Methods

The current study was carried out at four locations: College farm, N. M. College of Agriculture, Navsari Agricultural University in Navsari; Krishi Vigyan Kendra, Navsari Agricultural University in Dediapada; Cotton Research Sub Station, Navsari Agricultural University, Achhalia as well as the Hill Millet Research Station, Navsari Agricultural University, Waghai. In order to raise a superior crop, appropriate crop management techniques were used. Evaluation of forty distinct finger millet genotypes that were sown in Kharif 2023 using a Randomized Complete Block Design with three replications with four rows and a spacing of 22.5 × 7.5 cm² for each plot. The following biometric measurements were made on five randomly selected plants from each genotype in three replications, days to 50% flowering, days to maturity, plant height, productive tillers per plant, ear head length, finger per panicle, finger width, weight of matured panicle per plant, 1000 grain weight, harvest index, fodder yield per plant, grain yield per plant and four biochemical traits viz., protein content, calcium content, iron content and crude fiber content. To raise a successful crop, all the suggested set of procedures were performed, along with the mandatory preventative plant protection measures. Data was statistically analysed once observations were gathered. The variability was estimated in accordance with the procedure for analysis of variance recommended by Panse and Sukhame (1978), PCV and GCV were calculated by the formula by Burton (1952) ^[3], heritability in broad sense ($h^2_{(b)}$) by Allard and genetic advance *i.e.*, the expected genetic gain was calculated by using the procedure suggested by Allard (1960) ^[1].

Results and Discussion

Analysis of variance

Pooled analysis of variance for all sixteen traits along with the various parameters like critical difference and coefficient of variation presented in the Table 1. Total variance was partitioned into different sources of variation like replication, environment, genotypes, genotypes × environment interaction and pooled error.

Mean sum of squares for replication was found to be non-significant for all the traits indicate uniformity among replications within environments, suggesting minimal experimental error and experimental site used in the experiment was homogenous. Secondly, mean sum of squares for genotypes was found highly significant for all traits suggesting high amount of variability among different genotypes for different traits providing ample scope for selection and further evaluation as well as improvement in the grain yield and its component traits. Genotypes were found to interact significantly with the environments for all the traits except for protein content, calcium content iron content and crude fiber indicating the presence of appreciable influence of different environment on different genotypes as well as presence of significant interaction between genotype and environment meant that various genotypes performed differently across all the environments so, these traits were not considered for further stability analysis.

The mean sum of squares due to environment and genotype × environment interaction was significant for most of the morphological traits, indicating differential performance of genotypes across environments, whereas biochemical traits viz., protein content, calcium content, iron content and crude fiber show non-significant G × E interaction, suggesting relatively stable expression of these traits over environments.

The analyses of variance for all the sixteen traits in individual environments are presented in the Table 2. Mean sum of squares for replication under each environment was found non-significant for all traits under all environment which means that experimental sites were homogenous at all the locations. Mean sum of squares for genotypes was found highly significant all the characters across all the environments under study. This suggested that large amount of variability and diversity is present among all the genotypes in all the environments which can be further utilized by the plant breeders for selecting desired genotypes having all favourable traits in order to improve yield and its component traits. The range, mean, genotypic, phenotypic and environmental variance, phenotypic and genotypic coefficients of variation, heritability and expected genetic advance as percent of mean for sixteen characters are presented in Table 3 and 4.

To more precisely determine the degree of genetic variability, genetic metrics such as variance components, genotypic and phenotypic coefficients of variation, heritability, and genetic advance are crucial. In order to determine the percentage of inherent variability present for each character, the phenotypic variance was divided into its genotype and environment components. This was done because the breeding potential of experimental material depends on the amount of genetic variability, which is a prerequisite for the selection.

Variability parameter

For several characters such as calcium content, protein content, iron content, crude fiber content, days to 50% flowering, days to maturity, plant height, fingers per panicle, finger width and weight of matured panicle per plant. the genotypic variance constituted a major proportion of the phenotypic variance, indicating that these traits were predominantly governed by genetic factors with relatively less influence of the environment and hence direct phenotypic selection for these characters would be effective. In contrast, for characters like ear head length, productive tillers per plant, 1000 grain weight, harvest index, fodder yield per plant and grain yield per plant. The environmental variance exceeded the genotypic variance, suggesting that these traits were highly influenced by environmental factors and therefore selection based solely on phenotypic performance may not be reliable, making evaluation over multiple environments and progeny testing essential to achieve stable genetic improvement. Thus, characters exhibiting high genotypic variance coupled with high heritability can be effectively improved through simple phenotypic selection, whereas traits dominated by environmental variance require multi-environment testing and appropriate breeding strategies to exploit their genetic potential efficiently.

Low genotypic and phenotypic co-efficient of variation values were found in the traits fingers per panicle, while low GCV coupled with moderate PCV was property of characters viz., days to maturity, plant height and finger width. Moderate genotypic and moderate to high phenotypic co-efficient of variation was recorded in days to 50% flowering, productive tillers per plant, weight of matured panicle per plant, 1000 grain weight, harvest index, fodder yield per plant, grain yield per plant, protein content, calcium content and crude fiber content. while both genotypic and phenotypic co-efficient of variation were high for ear head length and iron content. Characters having high GCV had very high amount inherent variation i.e. backed by genetic makeup of plants. It is not possible to determine the amount of variability, which is heritable, with the help of genotypic coefficient of variation alone. Burton (1952) [3] also suggested that GCV together with a heritability estimates would provide better insight for amount of genetic gain expected through phenotypic selection.

Among 40 genotypes evaluated d GPU 45, WWN 45, WWN 47 and WWN 55 were most promising genotypes in respect to days to 50% flowering. Conferring days to maturity, genotypes viz., WWN 55, WWN 45, GPU 45, WWN 47 and WWN 57 were outstanding performer. According to grain yield per plant were WWN 49, GN 5, CFMV 2, CFMV 3 and WWN 32. Genotypes with highest per se performance in fodder yield per plant were GN 2, GN 3, WWN 56, WWN 32 and GN 4 as best genotypes. Among the biochemical parameters, protein content was found highest in WWN 46 followed by WWN 49, WWN 56, WWN 15 and WWN 41. While, calcium content was highest in WWN 38 followed by WWN 40, WWN 44,

WWN 43 and WWN 45. Maximum iron content was found in genotypes viz., WWN 37, WWN 47, VL 352, WWN 44 and WWN 42 while, crude fiber content was found maximum in WWN 43, WWN 38, WWN 39, WWN 47 and GN 4.

Heritability and Genetic advance

In the present study, high heritability coupled with high genetic advance as percent of mean was observed for the traits viz., days to 50% flowering, ear head length, weight of matured panicle per plant, protein content, calcium content iron content and crude fiber content. Grain yield per plant and fodder yield per plant had estimates of moderate heritability along with high genetic advance as percent of mean which implied that trait is governed by genes with additive nature but are influenced by environment upto some extent thus mass selection along with progeny testing is recommended and coupled with pedigree selection can improve trait great extent.

High heritability along with moderate genetic advance as percent of mean was present in days to maturity indicating that the genotypes under study were diverse with immense genetic potential and further improvement in these traits would possible by practicing simple selection technique.

Moderate heritability coupled with moderate genetic advance (% of mean) was observed for the character plant height and 1000 grain weight while, moderate heritability combined with low genetic advance as percent of mean was found in finger width. It showed the involvement of both additive and non-additive gene actions in the inheritance of these traits. Hence, breeder should use suitable methodology to use additive gene action like developing transgressive segregants and combination breeding simultaneously for significant improvement.

Low heritability coupled with moderate genetic advance as percent of mean was observed for productive tillers per plant and harvest index, indicating that these traits are predominantly influenced by non-additive gene action with a limited proportion of additive effects. Fingers per panicle having low heritability along with low genetic advance as percent of mean which, indicated that the non-additive gene action being responsible for the expression of these characters.

High estimates of heritability and high genetic advance indicated the additive gene action and possibility for improvement of that character by selection. High heritability with low genetic advance suggests that these characters cannot be improved by direct selection. Low estimate of heritability with low genetic advance indicated that the non-additive gene action being responsible for the expression of these characters. Moderate value of heritability with low genetic advance was observed for some traits indicated that non-additive gene action may be playing a role in the expression of these traits and improvement may be limited by adopting selection procedures.

Table 1: Pooled analysis of variance for different traits under study in finger millet

Source of variation	DF	Mean sum of square							
		Days to 50% flowering	Days to maturity	Plant height (cm)	Productive tillers per plant	Ear head length (cm)	Fingers per panicle	Finger width (cm)	Weight of matured panicle per plant (g)
Replications	2	3.85	5.46	163.57	0.56	0.44	0.01	0.0006	1.76
Environments	3	614.64**	689.74**	2770.88**	101.02**	4.75**	16.27**	0.09**	133.09**
Genotypes	39	1323.59**	1278.51**	1531.6**	11.13**	45.96**	1.07**	0.06**	90.29**
G × E	117	28.26**	28.05**	135.64**	2.01**	0.73**	0.19**	0.01**	1.56**
Pooled Error	318	3.05	6.05	77.04	2.00	0.19	0.04	0.0008	0.68
SEm±		1.01	1.42	5.07	0.26	0.25	0.11	0.02	0.48
CD at 5%		2.81	3.95	14.11	0.72	0.7	0.31	0.06	1.34
CV (%)		2.32	2.17	7.4	6.64	5.51	3.6	3.42	5.55

Source of variation	DF	Mean sum of square							
		1000 Grain weight (g)	Harvest index (%)	Fodder yield per plant (g)	Grain yield per plant (g)	Protein content (%)	Calcium content (mg/100 g)	Iron content (mg/100 g)	Crude fiber content (%)
Replications	2	0.1	2.33	6.59	1.46	0.04	7.5	0.002	0.01
Environments	3	0.91**	180.65**	352.32**	108.03**	0.01	13.33	0.0013	0.0017
Genotypes	39	1.22**	153.69**	158.13**	17.31**	19.7**	9829.85**	4.92**	7.42**
G × E	117	0.09**	31.87**	11.27**	1.94**	0.02	19.49	0.0013	0.003
Pooled Error	318	0.05	7.00	2.39	0.61	0.04	31.71	0.0026	0.01
SEm±		0.13	1.53	0.89	0.45	0.12	3.25	0.03	0.05
CD at 5%		0.36	4.26	2.48	1.25	0.33	9.04	0.08	0.14
CV (%)		8.65	9.47	8.46	11.23	2.92	2.02	1.63	1.76

Table 2: Analysis of Variance (environment wise) for different traits under study in finger millet

Source of Variation	DF	Days to 50 % flowering				Days to maturity				Plant height (cm)			
		E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄
Replications	2	1.97	2.408	0.075	8.23	1.11	1.658	2.8	4.93	114.15	16.986	87.329	25.45
Genotypes	39	346.58**	340.25**	329.25**	392.3**	339.94**	336.35**	361.36**	325.02**	602.48**	550.33**	321.37**	464.32**
Error	78	2.86	2.74	3.05	3.56	4.68	7.73	6.46	5.68	70.71	84.94	72.64	83.72

Source of Variation	DF	Productive tillers per plant				Ear head length (cm)				Fingers per panicle			
		E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄
Replications	2	0.18	0.208	0.365	0.52	0.51	0.432	0.164	0.29	0.01	0.042	0.033	0.01
Genotypes	39	5.69**	3.99**	4.46**	3**	12.71**	12.24**	11.86**	11.35**	0.33**	0.32**	0.46**	0.53**
Error	78	0.21	0.12	0.25	0.21	0.2	0.17	0.13	0.24	0.03	0.04	0.02	0.06

Source of Variation	DF	Finger width (cm)				Weight of matured panicle per plant (g)				1000 Grain weight (g)			
		E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄
Replications	2	0.0017	0.0003	0.001	0.0044	1.02	1.319	0.487	0.11	0.02	0.018	0.063	0.04
Genotypes	39	0.02**	0.02**	0.02**	0.02**	28.87**	24.84**	21.58**	19.7**	0.5**	0.32**	0.33**	0.34**
Error	78	0.001	0.0003	0.0003	0.0017	0.66	0.81	0.68	0.6	0.05	0.06	0.05	0.06

Source of Variation	DF	Harvest Index (%)				Fodder yield per plant (g)				Grain yield per plant (g)			
		E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄
Replications	2	1.7	1.926	1.776	12.69	2.52	2.907	2.675	1.25	0.52	1.184	0.041	0.88
Genotypes	39	85.32**	54.94**	56.85**	52.18**	61.82**	47.88**	43.02**	39.23**	8.15**	6.83**	4.52**	3.63**
Error	78	6.53	6.18	10.28	5.13	3	2.52	2.03	2.1	0.73	0.55	0.78	0.41

Source of Variation	DF	Protein content (%)				Calcium content (mg/100 g)			
		E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄
Replications	2	0.01	0.03	0.037	0.05	24.08	9.034	23.345	0.46
Genotypes	39	4.86**	5.02**	4.82**	5.06**	2473.38**	2470.01**	2489.74**	2455.18**
Error	78	0.03	0.03	0.04	0.06	40.43	34.53	23.79	29.25

Source of Variation	DF	Iron content (mg/100 g)				Crude fiber content (%)			
		E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄
Replications	2	0.0019	0.001	0.001	0.0013	0.02	0.014	0.003	0.01
Genotypes	39	1.21**	1.22**	1.26**	1.23**	1.88**	1.84**	1.86**	1.85**
Error	78	0.0032	0.0033	0.0031	0.0009	0.01	0.01	0.01	0.0047

* and ** significant at 5 and 1 per cent levels, respectively.

E₁: Waghai-2023, E₂: Navsari-2023, E₃: Dediapada-2023 and E₄: Achhalia-2023

Table 3: Descriptive statistics for different traits under study along with respective phenotypic, genotypic and environmental variances in finger millet

Sr. No.	Characters	Range		Mean	Variance		
		Minimum	Maximum		Phenotypic	Genotypic	Environmental
1.	Days to 50 % flowering	51.33	95.67	75.27	136.21	107.94	28.26
2.	Days to maturity	86.33	136.33	113.44	132.26	104.20	28.05
3.	Plant height (cm)	84.71	151.79	118.61	251.97	116.33	135.64
4.	Productive tillers per plant	2.87	10.43	6.68	2.76	0.76	2.00
5.	Ear head length (cm)	4.06	13.59	7.87	4.50	3.77	0.73
6.	Fingers per panicle	4.19	6.69	5.28	0.26	0.07	0.19
7.	Finger width (cm)	0.66	1.08	0.85	0.011	0.004	0.0067
8.	Weight of matured panicle per plant (g)	9.15	23.19	14.87	8.96	7.39	1.56
9.	1000 Grain weight (g)	1.97	3.52	2.65	0.19	0.09	0.092
10.	Harvest index (%)	17.80	44.00	27.92	42.02	10.15	31.87
11.	Fodder yield per plant (g)	10.20	28.84	18.26	23.51	12.24	11.27
12.	Grain yield per plant (g)	4.20	12.59	6.97	3.22	1.28	1.94
13.	Protein content (%)	3.58	10.03	6.87	1.66	1.64	0.02
14.	Calcium content (mg/100 g)	204.20	338.46	279.03	837.02	817.53	19.49
15.	Iron content (mg/100 g)	2.03	4.88	3.15	0.41	0.41	0.0013
16.	Crude fiber content (%)	3.45	6.75	5.24	0.62	0.62	0.0030

Table 4: Genetic parameters for different traits under study along with respective heritability, genetic advance and genetic advance (% of mean) in finger millet

Sr. No.	Characters	(in %)					
		GCV	PCV	ECV	Heritability (Broad sense)	Genetic advance (% of mean)	Genetic advance
1.	Days to 50 % flowering	13.80	15.51	7.06	79.25	25.31	19.05
2.	Days to maturity	9.00	10.14	4.67	78.79	16.45	18.67
3.	Plant height (cm)	9.09	13.38	9.82	46.17	12.73	15.10
4.	Productive tillers per plant	13.06	24.89	21.18	27.55	14.13	0.94
5.	Ear head length (cm)	24.66	26.95	10.87	83.72	46.49	3.66
6.	Fingers per panicle	5.13	9.71	8.24	27.94	5.59	0.29
7.	Finger width (cm)	7.60	12.24	9.59	38.56	9.72	0.08
8.	Weight of matured panicle per plant (g)	18.29	20.13	8.41	82.53	34.23	5.09
9.	1000 Grain weight (g)	11.57	16.25	11.41	50.67	16.96	0.45
10.	Harvest index (%)	11.41	23.22	20.22	24.16	11.56	3.23
11.	Fodder yield per plant (g)	19.15	26.55	18.38	52.05	28.47	5.20
12.	Grain yield per plant (g)	16.24	25.74	19.97	39.80	21.10	1.47
13.	Protein content (%)	18.64	18.75	2.09	98.75	38.15	2.62
14.	Calcium content (mg/100 g)	10.25	10.37	1.58	97.67	20.86	58.21
15.	Iron content (mg/100 g)	20.33	20.36	1.14	99.69	41.81	1.32
16.	Crude fiber content (%)	15.00	15.04	1.05	99.51	30.82	1.62

Conclusion

The pooled and individual environment analyses of variance revealed significant genetic variability among the 40 genotypes for all sixteen traits, indicating ample scope for selection and genetic improvement. Significant genotype $\times$ environment interaction was observed for most morphological traits, indicating differential genotype performance across environments and the need for multi-environment evaluation. In contrast, protein, calcium, iron and crude fibre contents showed non-significant $G \times E$ interaction, suggesting relatively stable expression across environments.

High heritability with high genetic advance was observed for days to 50% flowering, ear head length, weight of matured panicle per plant, protein, calcium, iron and crude fibre content, indicating that these traits can be effectively improved through selection. Grain yield and fodder yield showed moderate heritability with high genetic advance, suggesting combination of selective breeding and multi-location trials coupled with phenotypic selection would be

effective for all such traits.

Among the genotypes, WVN 49, GN 5, CFMV 2, CFMV 3 and WVN 32 were promising for grain yield, while GN 2, GN 3, WVN 56, WVN 32 and GN 4 were promising for fodder yield. GPU 45, WVN 45, WVN 47 and WVN 55 showed good performance for early flowering and maturity. For nutritional traits, WVN 46, WVN 38, WVN 37 and WVN 43 were superior for protein, calcium, iron and crude fibre content, respectively.

Overall, the identified genotypes with desirable yield, maturity and nutritional traits can be used as potential parents in future pearl millet breeding programmes. The results also suggest that selection based on traits with high heritability and genetic advance can be effective for developing improved genotypes with higher yield and better nutritional quality.

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