Received: 23 Sep 2023 | Revised: 15 Jun 2024 | Accepted: 21 Jun 2024

Electronic Journal of Plant Breeding

Research Note

Genetic variability, heritability and genetic advance in finger millet (*Eleusine coracana* L.) genotypes

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Abstract

An investigation was carried out with 101 finger millet genotypes for assessment of genetic variability and heritability in four environments during *Kharif* 2021. Variation due to genotypes for all the traits under study was found significant 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 seed yield and its component traits. Grain yield per plant (g) had moderate heritability estimates along with high genetic advance expressed as per cent of mean which implied that the character is controlled by genes having additive nature. High heritability combined with high genetic advance expressed as per cent of mean was noted for the characters *viz*., main ear head length, finger length, 1000-seed weight, protein content, calcium content, iron content and zinc content. Simple selection for such characters would be rewarding.

Keywords: Variability, Grain Yield, GCV, PCV, Heritability and Genetic advance

Millets have more nutritional value because of their high protein, fibre content, and vitamins and minerals like calcium, iron, and magnesium. Particularly for women and children, millet may safeguard against malnutrition and offer nutritional security. Small millets are more adaptable due to their agro-ecological diversity and capacity to adapt to a wide range of geographical environments (Patel *et al*., 2018). Millets are the recommended dietary supplements for those with diabetes and cardiovascular illnesses due to their high fibre and protein content (Patil *et al*., 2019). Finger millet, *Eleusine coracana* L., is among the three most cultivated millets, others being pearl millet and great millet. It grows best in dry farming conditions and is mostly cultivated as a rainfed crop (Vilas *et al*., 2015). Among all the small millets, finger millet assumes significance due to consumption in its natural state as well as after processing and is a good source of calcium and dietary fibre (Gopalan *et al.,* 1989; Rao and Murlikrishna, 2001). During 2021-2022, the area occupied by small millets in India was 1.45 million hectares of which finger millet alone occupied 1.004 million hectares with production of 1.76 million tonnes and productivity of 1747 kg/ha (Anonymous, 2023).

Poor productivity levels in finger millet are caused by the use of poor yielding cultivars and a lack of types tolerant to various stresses, both abiotic and biotic in nature (Madhavilatha *et al.,* 2019). Most breeding programmes continue to place a significant emphasis on improving yield (Yan *et al*., 2002). However, numerous morphological

https://doi.org/10.37992/2024.1502.058

characteristics or components affect yield and these yield components have a higher heritability than grain yield thus yield could be improved efficiently by selecting such characters. Selection based on the yield contributing characters would be more successful than selection based just on yield performance (Fisher, 1918). In pursuit to develop high yielding varieties, a breeder must know the heritability of traits to be enhanced and predict genetic gain under selection (Johnson *et al*., 1955b). To formulate and deploy appropriate breeding strategies for improving this crop, an attempt was made to study the yield and its attributing characters in 101 genotypes of finger millet by understanding key genetic parameters like Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), Heritability and Genetic Advance.

The current investigation was carried out at two location *viz*., Hill Millet Research Station, NAU, Waghai and College Farm, N. M. College of Agriculture, NAU, Navsari during *Kharif* 2021. In both the locations crop was raised in two different dates of sowing within a gap of one month essentially creating four environments. All the 101 genotypes were obtained from Hill Millet Research Station. The experiment was conducted in all four environments in a Randomized Block Design (RBD) with three replications. The genotypes were sown on raised bed for nursery and transplanted 30 days after sowing. Observation on 16 traits were recorded on five competitive plants which were selected randomly from each single row plot in each replication, excluding border. Days to 50 % flowering and days to maturity were the only characters which were recorded on whole plot basis.

The analysis of variance (ANOVA) technique suggested by Panse and Sukhatme (1978) was utilized to test the presence of significant difference among the genotypes for all the characters under study. Genotypic, phenotypic and environmental variances were determined using the formula proposed by Johnson *et al*. (1955a). Genotypic coefficient of variation (GCV) and Phenotypic Coefficient of Variation (PCV) was calculated using the formula provided by Burton (1952) and they were categorized as low, moderate and high as suggested by Burton and De-Vane (1953). The proportion of phenotypic variability due to genetic reason (Heritability) was computed in per cent utilizing the formula suggested by Allard (1960). Heritability (%) for all the characters was categorized as suggested by Robinson *et al.* (1949). The expected genetic advance (GA) was determined for every character by using the method recommended by Allard (1960). The genetic advance as per cent mean was calculated as suggested by Johnson *et al.* (1955b). Pooled analysis of variance for all 16 traits along with the various parameters like critical difference and coefficient of variation are presented in the **Table 1**.

Variation occurring due to replication was found to be non-substantial for all the traits except for the character finger width (cm) suggesting that experimental site used in the experiment was homogenous. Variance due to genotypes was found significant for all the 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 seed yield and its component traits.

Variation for environment and genotype × environment was found to be substantial for all the morphological traits and non-significant for all the biochemical parameters like protein content (%), calcium, iron and zinc content (mg/100g) 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 indicating further studies are required for these traits.

Environmental variance was found to be higher than genotypic variance for many of the characters like days to 50 % flowering and maturity, plant height (cm), productive tillers per plant, fingers per ear head, grain yield per plant (g), fodder yield per plant (g) and harvest index (%) indicating high influence of environment in expression of characters. Genotypic variance was found higher than environment for the characters *viz*., main ear head length (cm), finger width (cm), finger length (cm), 1000 seed weight (g), protein content (%), calcium content (mg/100g), iron content (mg/100g) and zinc content (mg/100g) showing extremely small role of external factors in expression of characters (**Table 2 and 3**). Direct phenotypic selection would be ineffective for improvement of such characters but combination of selective breeding and multi-location trials coupled with intense phenotypic selection would be effective.

Low GCV and PCV values were found in the traits days to 50 % flowering (4.28 % and 6.48 %) and days to maturity (3.53 % and 5.90 %). Low GCV and PCV for flowering and maturity were also reported by John (2006), Ulaganathan and Nirmalakumari (2011) and Suryanarayana *et al.* (2014). Low GCV coupled with moderate to high PCV was observed for characters *viz*., plant height (8.39 % and 15.11 %) and fingers per ear head (7.15 % and 20.75 %), which was consistent with the findings of John (2006), Ulaganathan and Nirmalakumari (2011), Patel *et al*. (2020), Anuradha *et al*. (2017) and Soe *et al*. (2022) .

Moderate GCV and moderate to high PCV was recorded in productive tillers per plant (10.40 % and 39.46 %), main ear head length (15.34 % and 18.62 %), finger width (10.66 % and 13.29 %), 1000 seed weight (14.61 % and 15.18 %), fodder yield per plant (15.72 % and 27.78 %) and harvest index (15.13 % and 24.52 %). These results were in congruence with Mahanthesha *et al.* (2017), Anuradha *et al*. (2017), Devaliya *et al.* (2018), Keerthana *et al.* (2019), Madhavilatha *et al*. (2021), Bharathi *et al*.

Table 1. Pooled analysis of variance for 16 traits under study in finger millet

Source of variation	Degree of freedom	Mean sum of square							
		Days to 50% flowering	Days to maturity	Plant height (cm)	Productive tillers per plant	Fingers per ear head	Main ear head length (cm)	Finger Width (cm)	Finger length (cm)
Replications	2	0.49	2.74	62.72*	0.03	0.07	0.23	0.04**	0.06
Environment	3	1936.97**	2176.95**	1049.3**	33.55**	168.44**	1.81**	0.32**	8.73**
Genotypes	100	147.55**	256.65**	1528.85**	1.38**	8.7**	17.14**	0.15**	11.96**
G × E	300	14.36**	78.29**	398.72**	0.73**	4.97**	0.65**	0.01**	0.56**
Pooled Error	806	1.11	3.26	15.14	0.01	0.11	0.13	0.002	0.05
SEm±		0.61	1.04	2.25	0.06	0.19	0.21	0.02	0.13
CD at 5%		1.69	2.89	6.25	0.17	0.53	0.58	0.06	0.36
CV (%)		1.35	1.64	3.5	4.5	4.63	4.69	4.23	4.89

Source of variation	Degree of freedom	Mean sum of square							
		1000-Seed weight (g)	Grain yield per plant (g)	Fodder yield per plant (g)	Harvest index (%)	Protein content (%)	Calcium content (mg/100g)	Iron content (mg/100g)	Zinc content (mg/100g)
Replications	2	0.001	0.34	0.35	4.11	0.01	243.11	0.004	0.002
Environment	3	0.13**	81**	361.67**	578.78**	0.02	86.64	0.003	0.006
Genotypes	100	1.35**	27.37**	122.18**	199.06**	27.12**	32704.96**	10.48**	8.17**
G × E	300	0.01**	4.05**	18.37**	23.74**	0.02	391.95	0.002	0.002
Pooled Error	806	0.001	0.22	1.02	2.85	0.05	444.42	0.003	0.004
SEm±		0.02	0.27	0.58	0.97	0.13	3.56	0.03	0.04
CD at 5%		0.06	0.75	1.61	2.69	0.36	9.88	0.08	0.11
CV (%)		1.25	7.48	5.4	6.68	3.08	2.08	2.92	3.52

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

(2022), Madhusri *et al*. (2022) and Udamala *et al*. (2022). Both GCV and PCV were high for finger length (20.92 % and 26.39 %), grain yield per plant (21.99 % and 38.62 %), protein content (21.07 % and 21.17 %), calcium content (24.14 % and 25.84 %), iron content (46.53 % and 46.58 %) and zinc content (43.91 % and 43.98 %). Mahanthesha *et al.* (2017), Devaliya *et al.* (2018), Keerthana *et al.* (2019), Bharathi *et al*. (2022) and Madhusri *et al*. (2022) observed high GCV and PCV for the trait grain yield while Mahanthesha *et al.* (2017) for finger length and Udamala *et al*. (2022) for biochemical parameters.

High estimates of heritability was found for iron content (99.81%) followed by zinc content (99.68%), protein content (99.05%), 1000-seed weight (92.60%), calcium content (87.29%), main ear head length (67.94%), finger width (64.34%) and finger length (62.87%). Moderate amount of heritability was found for days to 50% flowering (43.60%), harvest index (38.10%), days to maturity (35.75%), grain yield per plant (g) (32.42%), fodder yield per plant (32.01%) and plant height (30.83%) while low amount of heritability was recorded in the characters like fingers per ear head (11.88%) and productive tillers per plant (6.95%) (**Tables 2 and 3**).

High estimates of genetic advance as per cent of mean were observed for the character calcium content (99.97%) followed by iron content (95.77%), zinc content (90.31%), protein content (43.19%), finger length (34.18%), 1000-seed weight (28.96%), main ear head length (26.05%) and grain yield per plant (25.79%). Moderate estimates of genetic advance expressed as per cent of mean was recorded for the traits *viz*., harvest index (19.24%), fodder yield per plant (18.32%) and finger width (17.61 %) while low estimates were obtained in the attributes plant height (9.60%) followed by days to 50% flowering (5.82%), productive tillers per plant (5.65%), fingers per ear head (5.08%) and days to maturity (4.34%).

In the present study, high heritability in combination with high genetic advance expressed as per cent of mean was observed for the traits *viz*., main ear head length (cm), finger length (cm), 1000 seed weight (g), protein content (%), calcium content (mg/100g), iron content (mg/100g) and zinc content (mg/100g). These observations led to conclusions that these traits were largely controlled by genes of additive nature and selection would be rewarding. Similar findings were earlier reported by Priyadharshini *et al*. (2011), Karad and Patil (2013), Mahanthesha *et al.*

Table 2. Mean, minimum and maximum values for all 16 characters along with respective phenotypic, genotypic and environmental variances

S. No.	Characters	Range		Mean	Variance		
		Minimum	Maximum		Phenotypic	Genotypic	Environmental
1	Days to 50 % flowering	67.33	98.33	77.82	25.46	11.10	14.36
2	Days to maturity	98.33	128.33	110.56	42.52	15.20	27.32
3	Plant height (cm)	70.6	141.20	110.49	278.87	85.97	192.90
4	Productive tillers per plant	1.00	4.60	2.24	0.78	0.05	0.73
5	Fingers per ear head	4.80	10.80	7.20	2.23	0.27	1.97
6	Main ear head length (cm)	4.89	11.70	7.64	2.02	1.37	0.65
7	Finger width (cm)	0.68	1.58	1.02	0.02	0.01	0.01
8	Finger length (cm)	2.60	8.40	4.66	1.51	0.95	0.56
9	1000-Seed weight (g)	1.40	3.20	2.29	0.12	0.11	0.01
10	Grain yield per plant (g)	2.80	12.6	6.34	6.00	1.94	4.05
11	Fodder yield per plant (g)	7.40	29.85	18.71	27.03	8.65	18.37
12	Harvest index (%)	13.15	38.45	25.26	38.35	14.61	23.74
13	Protein content (%)	1.61	13.84	7.13	2.28	2.26	0.02
14	Calcium content (mg/100g)	103.83	344.60	214.93	3084.68	2692.73	391.95
15	Iron content (mg/100g)	0.77	4.99	2.01	0.872	0.870	0.002
16	Zinc content (mg/100g)	0.71	4.83	1.88	0.682	0.680	0.002

Table 3. Genotypic and Phenotypic Coefficient of Variation (GCV and PCV) for all sixteen characters along with respective heritability, genetic advance and genetic advance (% of mean)

S. No.	Characters	GCV (%)	PCV (%)	Heritability (Broad sense %)	Genetic advance	Genetic advance (% of mean)
1	Days to 50 % flowering	4.28	6.48	43.60	4.53	5.82
2	Days to maturity	3.53	5.90	35.75	4.80	4.34
3	Plant height (cm)	8.39	15.11	30.83	10.61	9.6
4	Productive tillers per plant	10.40	39.46	6.95	0.13	5.65
5	Fingers per ear head	7.15	20.75	11.88	0.37	5.08
6	Main ear head length (cm)	15.34	18.62	67.94	1.99	26.05
7	Finger width (cm)	10.66	13.29	64.34	0.18	17.61
8	Finger length (cm)	20.92	26.39	62.87	1.59	34.18
9	1000-Seed weight (g)	14.61	15.18	92.60	0.66	28.96
10	Grain yield per plant (g)	21.99	38.62	32.42	1.64	25.79
11	Fodder yield per plant (g)	15.72	27.78	32.01	3.43	18.32
12	Harvest index (%)	15.13	24.52	38.10	4.86	19.24
13	Protein content (%)	21.07	21.17	99.05	3.08	43.19
14	Calcium content (mg/100g)	24.14	25.84	87.29	99.87	46.47
15	Iron content (mg/100g)	46.53	46.58	99.81	1.92	95.77
16	Zinc content (mg/100g)	43.91	43.98	99.68	1.70	90.31

(2017), Devaliya *et al.* (2018), Keerthana *et al.* (2019), Madhavilatha *et al.* (2021), Bharathi *et al.* (2022), Madhusri *et al.* (2022) and Udamala *et al.* (2022) for various traits in finger millet.

Grain yield per plant (g) had estimates of moderate heritability along with high GAM which implied that trait is controlled by additive nature genes but are influenced by environment upto some extent thus mass selection along with progeny testing, coupled with pedigree selection can improve trait to a great extent. These results are in congruence with earlier reports of Reddy *et al.* (2013) who reported moderate heritability for grain yield in finger millet, John (2006), Ulaganathan and Nirmalakumari

(2011), Karad and Patil (2013), Mahanthesha *et al.* (2017), Anuradha *et al.* (2017), Devaliya *et al.* (2018), Anuradha *et al*. (2020), Patil *et al*. (2018) in little millet.

The trait finger width (cm) was observed to record high heritability in combination with moderate genetic advance as per cent of mean showing that improvement in such a trait would be further possible by practicing simple selection technique. Similar results were also obtained by Ulaganathan and Nirmalakumari (2011) and Anuradha *et al*. (2020).

Moderate heritability in combination with moderate genetic advance as per cent of mean was recorded for the characters *viz*., fodder yield per plant (g) and harvest index (%) while moderate heritability combined with little genetic advance as per cent of mean was found in the traits days to 50 % flowering, days to maturity and plant height (cm). It demonstrated the pre-dominance of additive gene effect in the expression of these traits and also presence of dominance variance. Breeder should use suitable methodology like developing transgressive segregants and combination breeding simultaneously in order to utilize additive gene action for significant improvement of such traits.

Characters days to 50 % flowering, days to maturity, plant height (cm), productive tillers per plant and fingers per ear head had low to moderate estimates of GCV and PCV thus there is little or no scope for improvement for such characters. Heritability and genetic advance estimates in those characters were also low to moderate. So there is absence of any room for improvement for such characters utilizing the current population.

If the heritability estimates, in broad sense, are caused by non-additive gene effects, there would be little expected gain; but if it is due to additive gene effects, a high genetic advance may be anticipated. Genetic gain gives a clear picture of expected progress for a particular trait under suitable selection procedure. High values 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 suggest 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 theses trait and improvement may be limited by adopting selection procedures.

Characters like days to 50 % flowering and maturity had low GCV, PCV as well as low to moderate heritability and genetic advance. Therefore such traits are non-responsive to selection and there is no scope for further improvement from current population. Characters like plant height (cm) and fingers per ear head had low GCV but moderate to high PCV coupled with low heritability and genetic advance. Such characters could be improved by focusing on increasing the genetic control over the trait expression by reducing the influence of environmental factors. Moderate GCV, PCV coupled with medium to high heritability and genetic advance was found for traits like main ear head length (cm), finger length (cm), finger width (cm), 1000 seed weight (g), grain yield per plant and fodder yield per plant. To improve such characters, genetic variability among the population needs to be increased by introducing new genetic material into breeding programme and stringent selection by choosing individuals with the highest phenotypic values for the target traits would help to concentrate favorable alleles and increase the frequency of desired genetic variants in subsequent generations.

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