

Research Article

Genetic Variability Analysis for Yield and Yield-Associated Traits of Finger Millet [*Eleusine coracana* (L.) Gaertn.] Accessions at Mechara, Eastern Ethiopia

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Abstract

The genetic enhancement of any crop, including finger millet, requires a certain degree of genetic variation for effective utilization in crop improvement programs. However, in Ethiopia, there is limited information on the extent and pattern of genetic variability of finger millet collections under diversified agro-climatic conditions. This makes it difficult for a population to adapt to changing environmental conditions. As a result, the population may be more vulnerable to extinction, exposure to new diseases, low productivity, and selection acting on any genes that may provide disease resistance. Therefore, knowledge of genetic variability is crucial for breeders in order to develop new cultivars with desired traits that are beneficial for both farmers and breeders. The present investigation was carried out to estimating the genetic variability, heritability, and genetic advance in sixty four finger millet accessions for yield and yield-related traits at Mechara agricultural research center. The experimental design was laid out in 8 x 8 simple lattice design. The analysis of variance for mean sum of squares due to genotypes revealed highly significant differences for all the 17 quantitative characters. The genotypes showed the highest mean performance for grain yield ranged from 1.38 ton per hectare for ACC#208448 to 4.35 ton per hectare for ACC#230255. Whereas, genotypic and phenotypic coefficients of variation were found high for biomass yield, harvest index, and grain yield. Broad-sense heritability ranged from 50.12% for the number of fingers per ear to 93.18% for days to heading. High heritability coupled with high genetic advance as percent of mean were observed for leaf number, finger length, ear weight, thousand grain weight, biomass yield, and harvest index. In general, the results demonstrated that the finger millet accessions exhibited a high degree of genetic variability for the traits studied, which can be helpful for genetic enhancement.

Keywords

Heritability, Finger Millet, Genetic Advance, Genetic Variability

1. Introduction

Finger millet [*Eleusine coracana* (L.) Gaertn.], is an important millet crop that belongs to the family: Poaceae, sub-

family: Chloridoideae is widely grown throughout the world's arid and semi-arid regions [26].

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The species of Eleusine Gaertn is an annual allotetraploid ($2n = 4X = 36$, AABB) that includes two distinct subspecies: *E. coracana* ssp. *coracana* (L) Gaertn and *E. coracana* ssp. *Africana* [16]. Eleusine coracana subspecies africana is the result of spontaneous hybridization between the diploid Eleusine indica (AA) and Eleusine floccifolia or Eleusine tristachya (BB) genomes [18].

It is relatively drought-tolerant and adapted to grow in harsh and marginal agro-ecologies [35]. Finger millet has resilience to adverse climatic conditions has the ability to withstand drought, high temperatures, and poor soil fertility, making it an important crop in areas with limited agricultural resources [28].

It has high nutritional values; it is non-glutinous, non-acidic, and easy to digest. The contents, like phytic acids and phytate, make it a versatile crop. It provides phosphorus, which plays a vital role in the structural development of body cells and bones. It is also well balanced with essential amino acids along with vitamins A and B [29].

Finger millet having the adaptability to diverse agro-ecological zones, including arid and semiarid regions, it is highly valued. Finger millet has resilience to adverse climatic conditions has the ability to withstand drought, high temperatures, and poor soil fertility, making it an important crop in areas with limited agricultural resources [28].

Ethiopia is the center of origin and diversity for finger millet [17]. Despite its immense benefits for the nation's production system, there are a number of factors that limit its potential. These include complex biotic and abiotic constraints, including the widespread use of farmers' varieties that yield low yields, a lack of improved varieties that are suitable for different production systems, the prevalence of diseases like blast, moisture stress in dry areas, and poor quality improved varieties [12].

Besides this, many scholars in Ethiopia study finger millet genetic variability with the primary goal of developing high-yielding genotypes with traits of importance [2, 5, 7, 33]. However, there are still a large number of finger millet genotypes whose genetic variability remains unexplored. Therefore, to improve the crop, more research and the identification of desirable genotypes are necessary.

Variation is the occurrence of differences among individuals due to differences in their genetic composition and the environment in which they are raised [3, 13]. The knowledge of the nature and magnitude of variation in available breeding materials is essential for further crop improvement.

Phenotypic variability is the observable variation present in a character in a population due to both genotypic and environmental variation. Genotypic variability is the component of variation that is due to the genotypic differences among individuals' genotypes within a population [31].

A basic understanding of genetic diversity and variability in populations, as well as the relationships between various features, is required for crop improvement [36].

The estimation of genetic variability should be combined with heritability and genetic advance since it does not give a clear-cut indicator of potential progress by selection [6]. Ge-

netic variability, heritability, and genetic advance are prerequisites for a breeding program and provide opportunities for breeders to select high-yielding genotypes or to combine or transfer genes having desirable traits [23].

To take advantage of the genetic variability in particular traits of interest, it is necessary to estimate the relative amounts of the country has not been genetic and non-genetic variability exhibited by various traits using genotypic coefficient of variation, phenotypic coefficient of variation, heritability, and genetic advance [24].

Therefore, this study aimed with the objectives of estimating the genetic variability, heritability, and genetic advance; for yield and yield-related traits in finger millet accessions.

2. Materials and Methods

2.1. Description of the Study Area

The experiment was conducted at Mechara Agricultural Research Center during 2021 cropping season. The center is situated at $8^{\circ}.75''$ latitude and $40^{\circ}.37''$ longitude. The altitude of the center is 1796 m.a.s.l. and the average minimum and maximum temperature of 15°C and 28°C , respectively. The total average rainfall of the year of study was 1120mm. The soil type is dominantly clay and reddish brown, with a pH ranging from 5.3 to 6.3.

2.2. Experimental Materials and Design

The material for the study comprised 64 finger millet genotypes as described in Table 1. The experiment was laid out using 8×8 simple lattice design, and each genotype was planted in a plot with four rows that were 5m long and 1.2m wide, with inter and intra spacing of 40cm and 10 cm, respectively. Hand drilling was done to sow at a seed rate of 10kg per hectare. Every agronomic procedure has been conducted as recommended for finger millet.

2.3. Data Collection

The data were collected from two central rows for plot-based and on five randomly sampled plants for plant-based, following the descriptors for finger millet on the following traits [19]: days to 50% heading, days to 50% maturity, number of leaves per plant, plant height (cm), number of tillers per plant, number of productive tillers per plant, number of fingers per main ear, finger length (cm), finger width (cm), number of ear-heads per plant, ear-head length (cm), ear-head width (cm), ear-head weight (g), thousand grain weight (g), biomass yield (tons ha^{-1}), harvest index (%), and grain yield (tons ha^{-1}).

2.4. Data Analysis

An analysis of variance was performed using SAS software. The Duncan multiple range test (DMRT) was used to test for

variations between genotypes that were statistically significant at the 5% level of significance.

The phenotypic and genotypic variances and their coefficients of variation for each trait were estimated by the formula as follows [8]:

$$\sigma^2_g = \left(\frac{K+1}{Kr} \right) (Msg - Mse); \sigma^2_p = \sigma^2_g + \sigma^2_e;$$

$$GCV = \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100, \text{ and } PCV = \frac{\sqrt{\sigma^2_p}}{\bar{x}} \times 100$$

Where; σ^2_g = genotypic variance, σ^2_e = environmental variance, σ^2_p = phenotypic variance, Msg= mean square of genotype, Mse= mean square of error, k = block size, r = number of replications, and GCV and PCV=genotypic and phenotypic coefficients of variation, respectively.

The PCV and GCV values were categorized as low (0 – 10%), moderate (10% – 20%), and high (> 20%) [32].

Heritability in the broad sense was estimated as follows [30]:

$$H^2 \% = \frac{\sigma^2_g}{\sigma^2_p} \times 100.$$

Where; H^2 = heritability in broad sense, σ^2_g = genotypic variance, and, σ^2_p = phenotypic variance. The heritability estimates were classified as: low (0 – 30%), moderate (31 – 60%), and high (> 60%) [20].

The genetic advance as percent of the mean (GAM) for all traits was computed using the formula as follows [20]:

$$GA = kh^2\sigma_p;$$

$$GAM = \left(\frac{GA}{\bar{x}} \right) \times 100$$

Where; GA = expected genetic advance, GAM = Genetic advance as % of the mean, h^2 = heritability in broad sense, k = selection differential (at 5% selection intensity with value = 2.063), σ_p = phenotypic standard deviation on mean basis, \bar{x} = Grand mean.

The genetic advance as a percentage of the mean was categorized as low (0 – 10%), moderate (10–20%), and high (> 20%) [20].

Table 1. List of finger millet accessions with their passport data.

S/N	Accession number	Collection region	Alti.	Long	Lati.
1	ACC#244798	SNNPR	2169	37.9	7.3
2	ACC#243644	Amhara	1815	36.6	11
3	ACC#243638	Amhara	1870	37.3	12
4	Ikhulule	Released			
5	ACC#245088	Oromia	2060	37.2	9.8
6	ACC#243640	Amhara	1890	36.8	11
7	ACC#243637	Amhara	1870	37.3	12
8	ACC#245092	Oromia	1954	36.4	8.5
9	ACC#237969	Oromia	1930	37.6	9.8
10	ACC#237583	Oromia	1990	38.6	7.2
11	ACC#238303	Tigray	2020	39.6	13
12	ACC#238337	Tigray	1920	38.1	14
13	ACC#238320	Tigray	2020	38.1	14
14	ACC#238297	Tigray	2000	38.1	14
15	ACC#238333	Tigray	1110	38.2	14
16	ACC#238306	Tigray	2000	38.1	14
17	ACC#215908	Amhara	2250	36.9	11
18	ACC#215976	Amhara	1860	37.3	12
19	Meba	Released			
20	ACC#215968	Amhara	2500	37.5	13

S/N	Accession number	Collection region	Alti.	Long	Lati.
21	ACC#240506	Amhara	1880	37.7	11
22	ACC#216033	Oromia	1930	35.7	9.3
23	ACC#215994	Amhara	2050	37.7	12
24	ACC#215889	Amhara	2100	37.1	11
25	Kumsa	Released			
26	ACC#235141	Amhara	1870	37.4	12
27	ACC#234202	Tigray	2050	38.5	14
28	ACC#237468	Tigray	1940	38	14
29	ACC#234198	Tigray	1900	38.3	14
30	ACC#237463	Tigray	2080	38.8	14
31	ACC#237452	Tigray	1430	38.8	14
32	ACC#234208	Tigray	1950	37.7	14
33	ACC#216055	Oromia	1600	35.3	9
34	ACC#216035	Oromia	1900	35.7	9.3
35	ACC#219818	Tigray	2260	38.9	14
36	ACC#216048	Oromia	1640	35.2	9.7
37	ACC#219807	Tigray	1880	38.7	14.2
38	ACC#216049	Oromia	1600	35.1	9.8
39	ACC#216052	Oromia	1660	35.6	9.1
40	ACC#216037	Oromia	1950	35.6	9.4
41	ACC#228304	Amhara	NA	37.7	13
42	ACC#234187	Tigray	1850	38.2	14.1
43	ACC#229722	B- Gumuz	1750	36.7	11.2
44	ACC#219824	Tigray	1920	38.3	14.2
45	ACC#234175	Tigray	NA	38.1	14
46	ACC#229726	B-Gumuz	1600	36.2	10.7
47	ACC#230255	B-Gumuz	NA	36.7	11.2
48	ACC#228902	Oromia	NA	36.2	8.6
49	ACC#215869	Amhara	2260	37.4	11.4
50	ACC#208724	Oromia	1640	37.6	9.8
51	ACC#208448	Amhara	1880	36.4	11.1
52	ACC#212694	Amhara	2380	38	11.8
53	ACC#208726	Oromia	1880	36.8	8.5
54	ACC#215883	Amhara	2400	37.7	11.1
55	ACC#208446	Amhara	1920	37.4	12.4
56	ACC#215873	Amhara	2330	37.4	11.4
57	ACC#240506	SNNPR	NA	35.8	7.3
58	ACC#242131	Amhara	2350	37.4	12.5

S/N	Accession number	Collection region	Alti.	Long	Lati.
59	ACC#242105	Amhara	1860	37.6	11.2
60	ACC#243617	Amhara	1780	39.8	11
61	ACC#242628	Tigray	1740	39.6	14.1
62	ACC#241769	SNNPR	1500	37.5	5.5
63	ACC#242618	Tigray	1950	39.6	14.6
64	ACC#242620	Tigray	1770	38.4	14.8

Where: ACC# = Accession number; S/N = Serial number; B-Gumuz = Benishangul-Gumuz; SNNPR = Southern Nations, Nationalities, and People's Region; Alti. = altitude (m.a.s.l.), Long. = longitude, and Lati. = latitude.

3. Results and Discussion

3.1. Analysis of Variance

Table 2. Mean squares from analysis of variance for 17 traits of 64 finger millet accessions.

Traits	Rep (1)	Genotype (63)	Blocks with in rep (Adj) (14)	Error		Total (127)	RE to RCBD	R ²	CV%
				Intra (49)	RCBD (63)				
DH	27.2*	166.57**	7.52	5.41	5.88	85.76	102.28	0.98	2.52
DM	63.28ns	131.94**	18.83	16.47	17.00	74.38	100.39	0.91	2.79
NL	5.24ns	12.11**	2.11	1.43	1.58	6.83	103.20	0.92	9.62
NT	3.063*	2.41**	0.35	0.69	0.61	1.52	89.11	0.83	9.89
NPT	6.71**	0.44**	0.15	0.13	0.13	0.34	100.49	0.85	6.53
PH	1320**	319.21**	129.63	81.67	92.33	214.55	104.46	0.85	12.10
NFPE	0.79ns	3.90**	1.42	1.26	1.30	2.58	100.34	0.81	16.00
FL	3.45ns	3.72**	1.05	0.82	0.87	2.30	101.35	0.86	9.36
Fwd	0.269*	0.25**	0.07	0.06	0.07	0.16	100.05	0.84	11.6
NEPP	1.14ns	2.05**	0.63	0.60	0.62	1.33	99.86	0.82	17.1
EL	7.01**	4.11**	1.03	0.89	0.92	2.55	100.49	0.87	9.04
Ewd	0.08ns	1.09**	0.30	0.25	0.26	0.67	100.57	0.85	9.46
EW	0.02ns	3.47**	0.18	0.23	0.22	1.83	94.86	0.95	5.74
TSW	0.03ns	0.65**	0.07	0.12	0.11	0.38	90.69	0.87	11.6
BMV	0.01ns	22.00**	4.72	4.07	4.21	13.90	100.48	0.88	17.8
HI	72.86*	117.75**	17.25	10.97	12.36	37.16	104.28	0.89	16.56
GY	1.82*	1.23**	0.58	0.34	0.39	0.81	106.02	0.84	20.14

Where: ns = non-significant, * = significant, and ** = indicate highly significant, RE = Relative Efficiency to RCBD, R² = Coefficient of determination, CV = Coefficient of Variation, DH = Days to 50% heading, DM = Days to 50% maturity, LN = Leaf Numbers per Plant, NT = number of tillers per plant, NPT = number of productive tillers per plant, PH = Plant height (cm), NFPE = number of fingers per main ear FL = finger length (cm), Fwd = finger width (cm), NEPP = number of ear-heads per plant, EL = ear-head length (cm), Ewd = ear-head width (cm), EW = ear-head weight (g), TGW = 1000-grain weight (g), BMV = biomass yield (ton ha⁻¹), HI = harvest index (%), and GY = grain yield (ton ha⁻¹).

The analysis of variance indicated highly significant ($P \leq 0.01$) among the genotypes for all traits (Table 2). This implied that selection of superior genotypes with important could promote genetic improvement of the crop [2, 5, 7, 33].

3.2. Mean Performance of the Genotypes

The range and mean performances of 64 genotypes for 17 traits are summarized in Table 3, indicating that there is enough genetic variation among genotypes to provide a broad range for selection. With a mean of 92.3 days, the days to heading ranged from 73.5 for ACC#242628 to 107 for ACC#208448. The range of days to maturity was 129 for Ikhulule to 164.5 for ACC#208448, with a mean of 145.6 days. The ranges and the mean values of leaf number, number of tillers, and number of productive tillers ranged from 7.25 for ACC#208448 to 18.25 for ACC#216033, 6.9 for ACC#215873 to 10.8 for ACC#238306, and 4.6 for ACC#215873 to 6.95 for ACC#230255, with means of 12.43, 9.89, and 5.52, respectively.

The range observed for number of fingers was 3.4 for ACC#237468 to 10.3 for ACC#237583, with a mean of 7.02. The maximum 1000-grain weight (3.89g) was for ACC#229726 whereas the minimum (1.53g) was for ACC#215968, with a mean of 3.04g. The tallest genotype (102.3cm) was ACC#208726 whereas the shortest (46.3cm) was ACC#219824. The mean ear length, and finger length ranged from 5.95cm for Meba to 12.45cm for ACC#242131 and 5.3cm for Meba to 11.8cm for ACC#208446, with a mean of 10.41 cm, and 9.65cm, respectively (Table 3).

The range for finger width and ear width were 1.69cm for ACC#215887, 3.43cm for ACC#216048, 3.55cm for ACC#241769, and 6.35cm for Ikhulule, with a mean of 2.2cm and 8.34 cm, respectively (Table 3).

The mean ear length, and finger length ranged from 5.95cm for Meba to 12.45cm for ACC#242131 and 5.3cm for Meba to 11.8cm for ACC#208446, with a mean of 10.41 cm, and 9.65cm, respectively. The range for finger width and ear width were 1.69cm for ACC#215887, 3.43cm for ACC#216048, 3.55cm for ACC#241769, and 6.35cm for Ikhulule, with a mean of 2.2cm and 8.34 cm, respectively.

Biomass yield and harvest index varied from 4.62 for ACC#234208 to 18.1 tons ha^{-1} for ACC#208724 and 14.86 for Meba to 44.44% for ACC#234208, respectively. The highest yielder genotype was ACC#230255 (4.35tons ha^{-1}), the lowest yielder was ACC#208448 (1.38tons ha^{-1}) with a mean of 2.88 tons ha^{-1} . A varied range of variability was reported in finger millet [33, 21, 38].

3.3. Genotypic and Phenotypic Variability and Coefficient of Variation

Estimates of genotypic and phenotypic variances, genotypic coefficient of variation, and phenotypic coefficient of variation

are presented in Table 3. For all of the traits, the phenotypic variance exceeded the genotypic variance, demonstrating the impact of environmental influences on the expression of these traits. The GCV values ranged from 5.21% for days to maturity to 26.39% for biomass yield. Biomass yield (26.39%), grain yield (22.5%), and harvest index (25.1%) recorded high GCV values (Table 3), indicating that these traits are more influenced by the genotype [11, 33]. Plant height (14.26), finger width (13.84), finger length (12.37), ear head length (12.14), ear width (12.08), the number of ears (18.64), leaf numbers (18.46), 1000-grain weight (17.07), number of fingers (16.25), and ear weight (15.3) all displayed moderate GCV values. The moderate GCV values reported in earlier studies [11, 25, 34, 37].

The PCV values ranged from 5.93% for days to maturity to 32.04% for biomass yield. Grain yield (31.23%), harvest index (31.54%), leaf number (21.05%), number of fingers (22.95%), number of ears (25.43%), 1000-grain weight (20.33%), and grain yield (31.23%) had high PCV values (Table 3). Similarly, high PCV values were reported [4, 5, 37].

Plant height (19.21), finger width (18.07), ear weight (16.29), ear width (15.46), ear head length (15.23), number of tillers (12.43), and days to heading (10.06) all had moderate PCV levels [14, 34].

3.4. Estimation of Broad Sense Heritability

The broad-sense heritability ranged from 50.12% for the number of fingers to 93.18% for the number of days to heading (Table 3). The days to heading (93.18%), ear weight (88.2%), and days to maturity (77.18%), leaf number (76.89%), 1000-grain weight (70.5%), biomass yield (67.87%), ear length (63.48%), harvest index (63.36%), finger length (62.17%), and ear width (61.07%) were all found to have high heritability in the broad sense. This suggests that the manifestation of the traits under study was less impacted by their environment [9, 25, 27, 33, 34].

Number of tillers per plant (59.31%), finger width (58.67%), plant height (55.13%), number of ears (53.72%), number of productive tillers (53.18%), grain yield (51.9%), and number of fingers (50.12%) all showed moderate estimates of heritability [11, 27].

3.5. Estimation of Genetic Advance

The genetic gain that could be expected from selecting the top 5% of the genotypes as a percent of the mean varied from 9.44% for days to maturity to 44.86% for biomass yield, as expressed in Table 3.

With regard to GAM, the traits with the highest values are biomass yield (44.86%), harvest index (41.22%), grain yield (33.44%), leaf number (33.39%), ear width (29.64%), 1000-grain weight (29.57%), and number of ears per plant (28.18%), number of fingers per main ear (23.73%), finger

width (21.87%), plant height (21.85%), and finger length (20.13%) [4, 9, 33]. This showed that the environment effect had very little influence on most of the investigated traits, but the gene effect had a greater influence.

Moderate GAM was observed for ear length (19.95%), ear width (19.48%), days to heading (19.34%), number of tillers (15.21%), and productive tillers (10.66%). The GAM for days to maturity was low (9.44%). Low GAM was reported for days to maturity [4, 5], and for ear length [1], while moderate GAM for days to heading, number of tillers and number of productive tillers was reported [9].

High broad-sense heritability alone does not always guarantee a high forecast of genetic gain to ensure efficient selection for improvement, rather, higher heritability combined with a higher estimate of GCV and GAM is reliable [20]. For leaf number, finger length, ear weight, 1000-grain weight, biomass yield, and harvest index, high heritability together with high genetic progress as a percentage of the mean were noted in this study. This indicates that selection based on these

traits will enhance the performance of the genotypes because these traits are heritable owing to gene effects [10, 15].

For plant height, finger number per plant, finger width, ear number per plant, and grain yield, moderate heritability and high genetic progress were observed [10, 25], it indicated that selection for these traits may thus be successful.

Days to heading, ear length, and ear width all showed high heritability paired with moderate genetic progress as a percentage of the mean. This revealed that the interplay of genetic and environmental factors largely controls how these traits manifest. Accordingly, high heritability with moderate GAM has been documented for the days to heading [10, 22], the ear length [1], and the ear width [25].

The number of tillers per plant and the number of productive tillers showed moderate heritability coupled with moderate genetic advance as a percent of the mean [10]. This indicates both additive and non-additive gene actions, and much reliance cannot be placed on expected genetic advancement.

Table 3. Estimates of range-mean and genetic parameters of finger millet accessions for 17 quantitative traits at Mechara.

Traits	Min	Max	SE	Mean	MSg	σ^2_e	σ^2_g	σ^2_p	GCV%	PCV%	H ² %	GA	GAM
DH	73.50	107.00	1.71	92.30	166.57	5.88	80.34	86.22	9.71	10.06	93.18	17.85	19.34
DM	129.00	164.50	2.92	145.60	131.94	17.00	57.47	74.47	5.21	5.93	77.18	13.74	9.44
LN	7.25	18.25	0.89	12.43	12.11	1.58	5.26	6.85	18.46	21.05	76.89	4.15	33.39
NT	6.90	10.80	0.55	9.89	2.41	0.61	0.90	1.51	9.57	12.43	59.31	1.50	15.21
NPT	4.60	6.95	0.26	5.52	0.44	0.13	0.15	0.29	7.08	9.71	53.18	0.59	10.66
PH	46.30	102.30	6.79	74.68	319.21	92.33	113.44	205.77	14.26	19.21	55.13	16.31	21.85
NFPE	3.40	10.30	0.80	7.02	3.90	1.30	1.30	2.60	16.25	22.95	50.12	1.67	23.73
FL	5.30	11.80	0.66	9.65	3.72	0.87	1.43	2.29	12.37	15.69	62.17	1.94	20.13
Fwd	1.69	3.43	0.18	2.20	0.25	0.07	0.09	0.16	13.84	18.07	58.67	0.48	21.87
NEPP	1.90	6.90	0.56	4.54	2.05	0.62	0.72	1.33	18.64	25.43	53.72	1.28	28.18
EL	5.95	12.45	0.68	10.41	4.11	0.92	1.60	2.51	12.14	15.23	63.48	2.08	19.95
Ewd	3.55	6.35	0.36	5.33	1.09	0.26	0.41	0.68	12.08	15.46	61.07	1.04	19.48
EW	5.90	11.80	0.33	8.34	3.47	0.22	1.63	1.85	15.30	16.29	88.21	2.47	29.64
TSW	1.53	3.89	0.24	3.04	0.65	0.11	0.27	0.38	17.07	20.33	70.50	0.90	29.57
BMV	4.62	18.10	1.45	11.30	22.00	4.21	8.90	13.11	26.39	32.04	67.87	5.07	44.86
HI	14.86	44.44	3.63	26.92	117.75	26.41	45.67	72.08	25.10	31.54	63.36	11.10	41.22
GY	1.430	4.36	0.44	2.88	1.23	0.39	0.42	0.81	22.50	31.23	51.90	0.96	33.44

Where: SE = the standard error of the mean, σ^2_g = genotypic variance, σ^2_e = environmental variance, σ^2_p = phenotypic variance, MSg = mean square of genotype, Mse = mean square error; PCV = phenotypic coefficient of variation; GCV = genotypic coefficient of variation; H² = heritability in the broad sense; GA = genetic advance; GAM = genetic advance as a percentage of the mean. DH = days to 50% heading; DM = days to 50% maturity. LN = leaf numbers plant⁻¹, NT = number of tillers per plant, NPT = number of productive tillers per plant, PH = plant height (cm), NFPE = number of fingers per main ear-head, FL = finger length (cm), Fwd = finger width (cm), NEPP = number of ear-heads per plant, EL = ear-head length (cm), Ewd = ear-head width (cm), EW = ear-head weight (g), TGW = 1000-grain weight (g), BMV = biomass yield (ton ha⁻¹), HI = harvest index (%), GY = grain yield (ton ha⁻¹)

4. Conclusion

Information on genetic variability is crucial for development and for the effective use of the available genetic resources. The study has revealed crucial details about the variation among finger millet accessions. For all examined traits, the analysis of variance revealed highly significant results. The grain yield varied from 1.38 tons ha⁻¹ for ACC#208448 to 4.35 tons ha⁻¹ for ACC#230255, with a mean of 2.88 tons ha⁻¹.

The accession numbers ACC#229726, ACC#242628, ACC#208724, ACC#242618, and Ikhulule showed the earliest days to maturity. High genotypic and phenotypic coefficients of variation were found for biomass yield, harvest index, grain yield, thousand grain weights, number of fingers per ear, and number of ears per plant. The estimate of high heritability coupled with high genetic advance was observed for number of leaves per plant, finger length, ear-head weight, thousand grain weight, biomass yield, and harvest index.

Grain yield had highly significant and positive genotypic and phenotypic correlations with traits such as leaf numbers, number of productive tillers, number of ears per plant, ear weight, 1000 grain weight, biomass yield, and harvest index. At both the genotypic and phenotypic levels, biomass yield and harvest index showed a strong positive direct effect on grain yield, whereas leaf numbers, the number of productive tillers, ear weight, the number of fingers per ear, 1000-grain weight, ear width, finger width, and ear length showed a high positive indirect effect on grain yield. These traits ought to be taken into consideration as selection criteria since they are employed in the genetic modification of finger millet to increase grain yield.

Generally, high grain yield accessions are ACC#230255 (4.35), ACC#245092 (4.28), ACC#229726 (4.25), ACC#240506 (4.24), and Ikhulule (4.17 check) and could be selected for superior genotypes. According to the findings of this study, it showed that the presence of genetic variations among the studied genotypes for yield and yield-related traits could be used in future breeding work. However, it is important to evaluate the genotypes across locations and years to confirm the present results because the data were from one year and one location.

Conflicts of Interest

The authors declare no conflicts of interest.

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