Assessment of Genetic Variability, Heritability, Genetic Advance, and Diversity Analysis for Morpho Physiological Traits in Finger Millet [*Eleusine coracana* (l.) Gaertn.]

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The study, conducted during the *Kharif* season of 2022, aimed to evaluate genetic variability, heritability, genetic advance, and diversity for morpho-physiological traits in finger millet (*Eleusine coracana* (L.) Gaertn.) using 39 genotypes. Significant genetic variation was identified for all studied traits through variance analysis. While moderate to high values of Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were observed for most traits, exceptions were noted for days to 50 percent flowering, days to maturity, relative water content in leaves, and chlorophyll stability index. The study revealed high heritability with moderate to high genetic advance as a percent of the mean for most traits, suggesting the prevalence of additive gene effects. However, chlorophyll stability index and relative water content exhibited lower values.

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D^2 analysis indicated the existence of sufficient genetic diversity among the genotypes. The genotypes were categorized into five distinct non-overlapping clusters. Cluster I, the largest cluster with 35 genotypes, displayed maximum intra-cluster distance. Clusters V and III had the highest inter-cluster distances, Days to maturity played a significant role in overall divergence. The findings suggest that a direct selection approach in finger millet landraces could lead to a substantial increase in yield response. This research provides valuable insights into the genetic characteristics of finger millet genotypes, offering a foundation for targeted breeding programs to enhance crop improvement.

1. INTRODUCTION

Finger millet *(Eleusine coracana* L. Gaertn.), also known as African millet or ragi, holds significant importance as a versatile member of the small millets group, particularly in the North Eastern region of India. Millets, including ragi, are predominantly cultivated in marginal areas where major cereal crops consistently fail to produce acceptable harvests. This crop adapts well to diverse environments and boasts extended storage capabilities [1]. It is highly nutritious and rich in minerals and constitutes an essential ingredient in the human diet [2]. Moreover, it is a source of antioxidants and anti-ageing compounds. The crop thrives in high-temperature, arid areas with poor soil fertility due to its excellent carbon-concentrating mechanism within the C4 pathway [1]. In the face of climate change and depleting natural resources, finger millet emerges as a valuable nutritional resource for less developed nations. Recognizing the economic significance of millets, the Indian government declared 2023 as the "International Year of Millets," receiving support from 72 countries and the United Nations General Assembly (UNGA) [3]. Ragi is grown in over twenty-five African and Asian nations, with India, Uganda, Nepal, and China being the top producers. India, holding the position of the world's largest producer, recorded 1.74 million tonnes produced on 0.99 million hectares with an average yield of 1761 kg per hectare in 2019-20 [4].

In Assam, finger millet cultivation is limited, with productivity trailing behind the national average. However, a survey by the Regional Agricultural Research Station (RARS) in Gossaigoan for 2019-20 indicates a gradual increase in production and productivity. Tribal and siaothali farmers in Assam primarily cultivate finger millet for local wine production, pithas (chapatti), and laddu. Even in the Muslim community in Assam's "char" areas, there's a growing emphasis on millet cultivation for both domestic consumption and commercial purposes, often replacing rice. In certain hilly areas of Assam, the crop is integrated into Jhum systems. Cultivation occurs during the *kharif* season, locally known as "Marubadhan," with one-month-old seedlings transplanted in the first week of September and harvested in November.

The available genetic variability in finger millet necessitates the characterization of these resources for genetic improvement [5]. A diverse Germplasm collection is crucial for both breeding and genomic research in any crop species. Beyond genetic variability, knowledge of heritability and genetic advance measures the extent to which a trait is passed on to offspring, aiding breeders in implementing suitable breeding strategies to achieve specific objectives. Assessing genetic diversity is crucial for understanding intra-species crop performance and crop improvement. Hence, the present investigation was aimed to assess the genetic variability, heritability and genetic advance with regard to morpho-physiological traits in a set of 39 diverse finger millet genotypes. The present study also attempts to assess the nature and magnitude of genetic divergence for yield and its component traits in finger millet and also to identify divergent parents from distantly related clusters for hybridization through genetic divergence analysis.

2. METHODOLOGY

The study was conducted at the experimental field and laboratory of Plant Breeding and Genetics, Biswanath College of Agriculture, AAU, Biswanath Chariali, during the *Kharif* season of 2022. The materials for this investigation comprised 39 diverse finger millet genotypes/ land races (Table 1), mainly collected from Regional Agricultural Research Station (RARS), AAU, Gossaigaon, Assam. These 39 finger millet genotypes were sown in a Completely Randomized Block Design (CRBD) with 3 replications. Each plot consisted of 3 rows, each

3.0 m in length, with a spacing of 10 cm between plants and 25 cm between rows. Seedlings were transplanted 30 days after sowing in the seedbed. Recommended cultural practices were followed for weeding, irrigation, and fertilization, and plant protection measures were implemented when necessary. Observations were taken on 13 metric traits *viz.* days to 50 percent flowering, days to maturity, plant height (cm), basal tillers per plant, panicle length (cm), ear per plant, 1000 grain weight (g), biological yield per plant (g), harvest index (%), grain yield per plant (g), total chlorophyll content (mg per g fw), chlorophyll stability index (%) and relative water content (%) of leaves. Observations for 13 quantitative traits were recorded based on five randomly selected plants in each replication for all the characters except days to 50 percent flowering and days to maturity which were recorded on a plot basis. The data were subjected to analysis of the variability parameters, heritability and genetic advance and were calculated with the help of standard statistical procedures given by Panse and Sukhatme [6]. Mahalanobis' [7] D^2 statistic was used for assessing the genetic divergence between the rice cultivars under study. D^2 analysis was done by using the programme INDOSTAT. Grouping of genotypes into different clusters was done by using Tocher's method as described by Rao [8]. The intra-cluster distances were calculated by the formula given by Singh and Chaudhary [9].

Table 1. List of 39 finger millet genotypes used in the investigation

Sl. No.	Genotypes	Source of collection
1	BR 14-28	RARS, Gossaigaon, Assam
2	CFMV 2 (i)	-do-
3	KMR 711	-do-
4	IIMR FM-7066	-do-
5	VR 1149	-do-
6	TNEc 1335	-do-
7	WN 572	-do-
8	GPU 67 (i)	-do-
9	DPLM 2	-do-
10	VL 410	-do-
11	KOPN 1056	-do-
12	DHFM-13-6	-do-
13	KMR 710	-do-
14	PR 202 (i)	-do-
15	WN 566	-do-
16	BR 9	-do-
17	DHFM-78-33	-do-
18	IIMR FM-7202	-do-
19	DPLM 3	-do-
20	IIMR FM-7835	-do-
21	KOPN 1055	-do-
22	CFMV 1 (i)	-do-
23	IIMR FM-7028	-do-
24	VR 1152	-do-
25	TNEc 1338	-do-
26	VL 391	-do-
27	VL 376 (i)	-do-
28	CFMV 1	-do-
29	VL-376	-do-
30	PR 1731	-do-
31	DPLN 2	-do-
32	OEB 610	-do-
33	PR 1506	-do-
34	CFMV 2	-do-
35	VL 408	-do-
36	GPU 67	-do-
37	VL 400	-do-
38	PR 202	-do-
39	Gossaigaon Maruadhan 1	-do-

3. RESULTS AND DISCUSSION

In the present investigation, significant genetic variation was observed for all the characters studied as revealed by the analysis of variance. The comparison of the mean performance (Table 2) of the different genotypes with respect to grain yield per plant revealed that the genotypes VL 408, VL 391, CFMV 1 (i), and CFMV 2 (i) exhibited high mean values. These four genotypes also recorded high mean values for a few other important yield-attributing morpho-physiological traits. VL 391 recorded the highest mean value for grain yield per plant and also exhibited high mean values for harvest index, 1000grain weight, and physiological traits like total chlorophyll content and chlorophyll stability index. Interestingly, the genotype CFMV 1 (i) which gave high grain yield matured early (about 98 days). It also recorded the highest mean value for basal tiller per plant and harvest index. The genotype VL 408 recorded the highest mean values for total 1000grain weight, biological yield per plant, and relative water content with high grain yield per plant. The genotype CFMV 2 (i) also accounted the high mean value for 1000grain weight, harvest index, and grain yield per plant. The low-yielding genotypes in general, were low performers for most of the yield-attributing traits under study. The four genotypes VL 408, VL 391, CFMV 1 (i), and CFMV 2 (i) could be considered potential genotypes for incorporation in finger millet breeding programme.

The estimates of the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability in a broad sense, and genetic advance as per cent of mean (GAM) were computed for the 13 traits. These results are presented in Table 3, Fig. 1, and Fig. 2. The variance components revealed that the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV), with a narrow difference observed for all traits. This implies that a significant portion of the variability in these traits is attributed to genetic factors, as the influence of the environment is minimal. In the present study, high, moderate as well as low GCV and PCV were exhibited by the characters. High magnitude of PCV and GCV were recorded for ear per plant, panicle length, grain yield per plant, and harvest index. These results indicated that a sufficient amount of variation existed for these characters and offered greater scope for selection for improvement programmes. These results are in accordance with the findings of Saundaryakumari and Singh

[10] for harvest index, and grain yield per plant; Suryanarayana et al. [11] for grain yield per plant and panicle length; Karad and Patil [12] for ear per plant.

Moderate PCV and GCV were observed for plant height, basal tiller per plant, 1000grain weight, biological yield per plant, and total chlorophyll content in leaves. Similar results were observed by Lule et al.[13] for plant height, basal tiller per plant, and 1000grain weight in finger millet. Contrary to the above, low estimates of PCV and GCV were recorded for days to 50 per cent flowering, days to maturity, the relative water content in leaves, and chlorophyll stability index. This indicated that the selection of these characters might not be effective. Similar works were reported by Ulaganathan and Nirmalakumari [14], and Lule et al. [13], and Reddy et al. [15] for days to 50 percent and days to maturity in finger millet. Johnson et al. [16] Proposed that combining the calculations of heritability and genetic advance is more valuable for predicting the success of selecting superior individuals compared to relying on information from heritability and genetic advance alone. Consequently, for selection to be efficacious, a character with high heritability should ideally be associated with a substantial genetic advance.

In the present study, characters such as 1000 grain weight, panicle length, biological yield per plant, grain yield per plant, ear per plant, number of basal tillers per plant, total chlorophyll content, plant height, and harvest index exhibited high heritability along with a substantial genetic advance as a percentage of the mean. This suggests that these traits are more influenced by additive gene action, and their expression is less influenced by the environment. Consequently, these traits are highly conducive for selection, and using simple methods like mass selection based on phenotypic value will be effective for their improvement. Moreover, the investigation revealed high heritability coupled with a moderate genetic advance as a percentage of the mean for characters like days to 50 percent flowering and days to maturity. This indicates that selection for these traits will also be effective. Similar results were reported by Saundaryakumari and Singh [10] for panicle length, harvest index, basal tiller per plant, 1000-grain weight, and grain yield per plant; Selvi et al. [17] for plant height and biological yield per plant; Priyadharshini et al. [18] for harvest index, grain yield per plant, basal tiller per plant, and plant height; Karad and Patil [12] for days to 50 percent flowering and days to maturity. In the

Table 2. Variation in morpho-physiological traits in finger millet genotypes

Sl.No.	Genotypes	DF	DM	PH	BT	PL	EP	1000 GW	BYP	HI	TC	CSI	RWC	GY/P
1	BR 14-28	73.67	107.67	112.00	4.77	5.75	4.50	2.73	23.79	35.76	2.34	60.23	83.90	8.53
2	CFMV 2 (i)	73.67	108.67	116.60	3.97	9.84	8.17	3.45	30.01	37.07	2.29	58.77	81.65	11.11
3	KMR 711	85.33	119.33	124.73	3.40	8.24	8.57	2.36	27.62	24.75	2.14	60.32	81.87	6.88
4	IIMR FM-7066	71.00	103.67	99.33	2.83	5.06	5.00	3.04	25.45	38.64	2.13	61.05	75.81	9.83
5	VR 1149	75.33	107.33	97.00	3.30	6.36	6.13	2.76	23.33	35.46	2.26	61.02	82.16	8.29
6	TNEc 1335	64.00	96.00	81.37	2.10	4.87	2.77	2.90	16.79	25.14	1.92	54.23	73.89	4.22
7	WN 572	76.67	119.33	120.63	3.40	7.41	7.23	2.55	25.16	29.66	1.95	58.89	78.00	7.40
8	GPU 67 (i)	76.00	105.33	118.17	3.60	7.68	5.47	2.24	24.84	23.71	1.87	58.86	81.33	5.89
9	DPLM 2	74.00	105.67	106.80	4.53	11.03	7.30	2.09	31.41	19.78	2.23	62.66	80.40	6.22
10	VL 410	78.00	112.00	107.83	3.50	9.05	6.20	2.21	25.79	20.87	2.17	58.65	77.22	5.41
11	KOPN 1056	75.00	109.33	126.50	3.80	10.91	8.83	2.37	32.78	21.38	1.99	58.18	80.91	7.03
12	DHFM-13-6	73.33	102.00	111.50	4.60	7.78	5.30	2.53	24.78	29.66	2.18	63.73	76.46	7.27
13	KMR 710	73.33	112.33	128.73	4.10	8.60	6.90	2.24	25.30	20.80	2.70	60.61	80.83	5.27
14	PR 202 (i)	78.67	117.33	148.33	4.07	6.13	6.40	2.34	22.12	26.31	1.96	58.17	82.49	5.80
15	WN 566	73.33	116.33	135.17	4.87	10.10	7.80	2.76	28.53	30.49	3.00	65.55	77.65	8.66
16	BR 9	70.33	97.00	107.93	4.93	9.81	5.40	2.31	21.75	27.21	2.54	57.57	85.03	5.77
17	DHFM-78-33	78.33	120.33	128.33	4.73	5.43	4.47	2.65	22.09	35.22	2.06	57.74	70.72	7.72
18	IIMR FM-7202	73.67	103.67	123.00	3.60	8.01	5.47	2.72	25.92	33.24	1.93	59.32	80.44	8.55
19	DPLM 3	75.33	107.00	119.67	4.03	10.98	8.07	2.24	33.81	19.06	1.86	57.18	79.08	6.44
20	IIMR FM-7835	80.00	120.67	134.00	3.73	8.96	6.47	2.64	32.31	24.90	2.49	62.09	81.65	8.01
21	KOPN 1055	78.67	119.33	135.40	3.47	8.80	9.33	2.67	31.55	26.05	2.88	66.08	83.69	8.14
22	CFMV 1 (i)	72.00	98.33	122.67	5.47	6.43	4.30	3.30	28.42	36.70	2.34	60.99	81.76	10.38
23	IIMR FM-7028	73.00	104.00	123.00	4.10	13.36	11.33	2.26	32.07	19.55	2.10	59.27	76.42	6.22
24	VR 1152	74.00	106.67	125.33	4.43	8.83	8.00	2.45	27.52	23.87	1.86	62.72	84.26	6.52
25	TNEc 1338	82	114	128.17	3.90	12.13	7.6	2.78	30.50	28.22	2.13	59.66	83.14	8.63
26	VL 391	73.00	103.67	101.40	3.43	6.86	7.07	3.42	26.85	41.77	2.46	62.81	79.53	11.24
27	VL 376 (i)	69.33	99.00	80.00	3.87	5.04	3.93	2.72	20.78	36.80	2.26	63.79	77.41	7.61
28	CFMV 1	84.00	119.33	130.00	3.30	10.36	5.67	2.25	25.73	24.29	1.87	57.71	83.94	6.17
29	VL-376	74.33	108.00	120.00	3.50	8.33	6.27	2.46	23.18	23.60	2.26	62.95	76.94	5.43
30	PR 1731	74.00	105.00	111.00	5.20	8.88	4.80	1.90	21.32	19.18	2.14	57.46	78.93	4.09
31	DPLN 2	72.67	101.67	103.17	3.37	6.13	4.47	2.46	22.18	30.72	2.17	58.07	79.05	6.83
32	OEB 610	82.67	118.00	115.00	3.37	9.29	6.33	2.64	34.43	23.52	2.26	60.17	80.58	8.11
33	PR 1506	78.33	114.33	126.00	3.77	7.31	5.20	2.64	31.09	26.59	2.02	57.07	78.99	8.24
34	CFMV 2	72.33	100.33	113.67	3.47	9.35	6.93	2.50	28.73	24.29	2.31	56.50	77.85	6.94
35	VL 408	75.33	103.00	119.00	4.10	6.98	7.93	2.48	27.60	24.73	2.32	60.89	82.24	6.83
36	GPU 67	73.67	104.00	140.33	3.63	9.48	9.20	2.43	31.00	26.84	2.38	60.28	78.59	8.29
37	VL 408	71.67	100.33	141.07	3.17	6.32	6.67	3.49	26.82	39.46	1.80	60.60	86.46	10.58
38	PR 202	78.33	120.33	146.33	4.87	7.98	7.07	3.09	26.54	37.68	2.36	61.69	82.45	9.89
39	Gossaigaon Maruadhan 1	81.33	123.00	135.67	3.53	8.53	7.07	3.00	28.01	25.74	1.90	60.27	80.31	8.17
Mean		75.38	109.06	119.61	3.89	8.27	6.55	2.62	26.87	28.17	2.20	60.10	80.10	7.50
C.V		2.32	1.95	4.97	11.57	9.35	11.05	7.88	8.83	14.15	7.60	3.30	3.39	12.68

Sl.No.	Genotypes	DF	DM	PH	BT	PL	EP	1000 GW	BYP	HI	TC	CSI	RWC	GY/P
S.E		1.01	1.23	3.43	0.26	0.45	0.42	0.12	1.37	2.30	0.10	1.14	1.57	0.55
C.V 5%		2.84	3.46	9.67	0.73	1.26	1.18	0.34	3.86	6.48	0.27	3.22	4.42	1.55

*Chlorophyll stability index (%)(CSI), Total chlorophyll content (TC), Ear per plant (EP), Grain yield per plant (GY/P), Relative water content in leaves (%)(RWC), Panicle length (PL), Number of basal tillers per plant (BT), plant height (PH), Biological yield per plant (BY/P), Days to 50% flowering (DF), Days to maturity (DM), 1000 grains weight (1000GW), and harvest index (HI). Coefficient of Variance (CV), Standard Error(SE).

Table 3. Genetic variance and other related parameters for grain yield and component characters

Sl.No.	TRAITS	Mean	SE	Range		GV	PV	EV	GCV (%)	PCV (%)	Hbs (%)	GA	GAM (%)
				Min.	Max.								
1	DF	75.38	1.01	64	85.33	16.85	19.89	3.04	5.45	5.92	84.675	7.78	10.32
2	DM	109.06	1.23	96	123	59.03	63.56	4.53	7.05	7.31	92.873	15.25	13.99
3	PH	119.61	3.43	80	148.33	229.45	264.84	35.39	12.66	13.61	86.636	29.04	24.28
4	BT	3.89	0.26	2.1	5.47	0.40	0.60	0.20	16.33	20.02	66.584	1.07	27.46
5	PL	8.27	0.45	4.87	13.36	3.85	4.45	0.59	23.74	25.52	86.573	3.76	45.51
6	E/P	6.55	0.42	2.77	11.33	2.81	3.34	0.52	25.59	27.87	84.289	3.17	48.39
7	1000GW	2.62	0.12	1.9	3.49	0.12	0.17	0.04	13.63	15.75	74.932	0.64	24.31
8	BY/P	26.87	1.37	16.79	34.43	14.61	20.25	5.63	14.23	16.75	72.168	6.69	24.90
9	HI	28.17	2.3	19.06	41.77	36.20	52.10	15.89	21.36	25.62	69.49	10.33	36.68
10	TC	2.2	0.1	1.8	3	0.06	0.09	0.02	11.73	13.98	70.42	0.45	20.28
11	CSI	60.1	1.14	54.23	66.08	5.03	8.96	3.92	3.73	4.98	56.186	3.47	5.77
12	RWC	80.1	1.57	70.72	86.46	7.73	15.12	7.39	3.47	4.86	51.121	4.10	5.11
13	GY/P	7.5	0.55	4.09	11.24	2.79	3.69	0.90	22.27	25.62	75.515	2.99	39.86

*Chlorophyll stability index (%)(CSI), Total chlorophyll content (TC), Ear per plant (EP), Grain yield per plant (GY/P), Relative water content in leaves (%)(RWC), Panicle length (PL), Number of basal tillers per plant (BT), plant height (PH), Biological yield per plant (BY/P), Days to 50% flowering (DF), Days to maturity (DM), 1000 grains weight (1000GW), and harvest index (HI), Standard Error(SE), Genotypic Coefficient of Variability (GCV), Phenotypic Coefficient of Variability(PCV), Coefficient of Variance (CV), Broad Sense Heritability(Hbs), Genetic Advance over Mean (GAM).
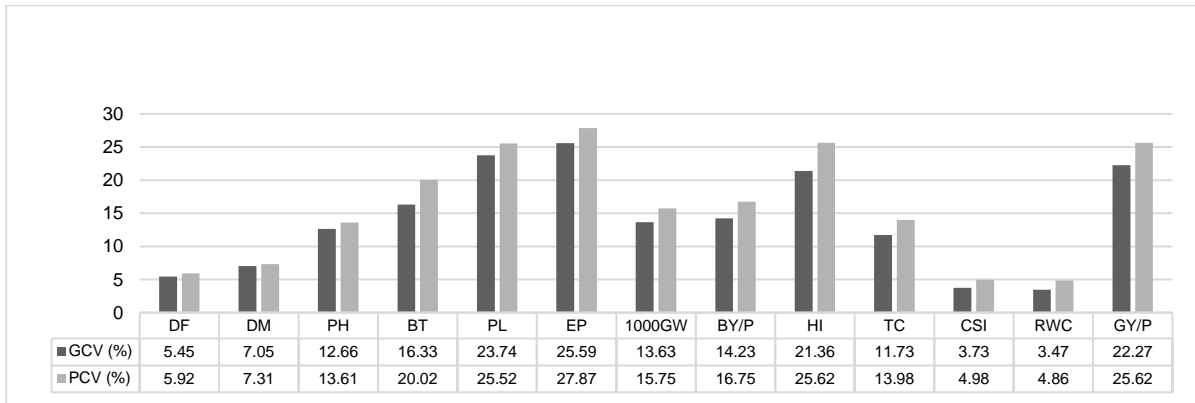
Fig. 1. Genotypic Coefficient of Variability (GCV) and Phenotypic Coefficient of Variability(PCV)for various characters of Finger millet
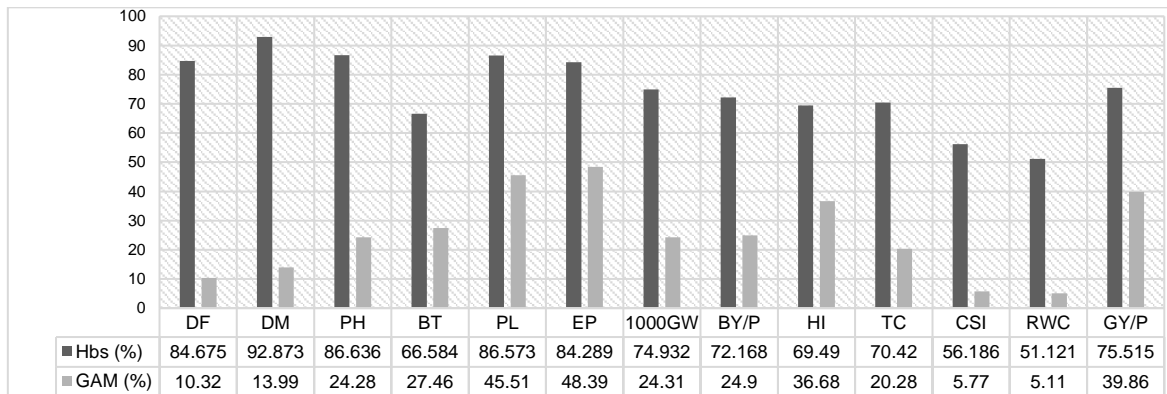
	DF	DM	PH	BT	PL	EP	1000GW	BY/P	HI	TC	CSI	RWC	GY/P
GCV (%)	5.45	7.05	12.66	16.33	23.74	25.59	13.63	14.23	21.36	11.73	3.73	3.47	22.27
PCV (%)	5.92	7.31	13.61	20.02	25.52	27.87	15.75	16.75	25.62	13.98	4.98	4.86	25.62

Fig. 2. Heritability (Hbs %) and genetic advance as percent mean (GAM %) for various characters of Finger millet genotypes

	DF	DM	PH	BT	PL	EP	1000GW	BY/P	HI	TC	CSI	RWC	GY/P
Hbs (%)	84.675	92.873	86.636	66.584	86.573	84.289	74.932	72.168	69.49	70.42	56.186	51.121	75.515
GAM (%)	10.32	13.99	24.28	27.46	45.51	48.39	24.31	24.9	36.68	20.28	5.77	5.11	39.86

present investigation, both chlorophyll stability index and relative water content displayed moderate heritability along with a low genetic advance as a percentage of the mean. This suggests the presence of non-additive gene action for these traits. The heritability of grain yield per plant in the present study was moderately high, approximately 75.5 %. However, when compared to most other characters, it appeared comparatively lower. This discrepancy can be attributed to the complexity of yield as a character, heavily influenced by environmental factors. Nevertheless, the substantial heritability coupled with a high genetic advance as a percentage of the mean implies that selection can be effectively employed in this crop for improving grain yield per plant.

Using Mahalanobis D² statistics and the Tocher method for estimating Genetic divergence, the 39 finger millet genotypes were categorized into five distinct clusters (Table 4). Cluster I, with 35

genotypes, showed substantial intra-cluster diversity (Fig. 3). Notably, significant inter-cluster distances, especially between Clusters V and III, II, and III, and I and V.

The intra-cluster D² values varied from 0 to 32.29. The highest intra-cluster distance was exhibited by cluster I (32.29) which is an indication that some amount of genetic divergence existed among the genotypes within the cluster. The clusters II, III, IV, and V being monogenotypic/ solitary clusters had no intra-cluster distance, Similar findings were reported by Jaylal and Haider [19] and Karad and Patil, [12]. Based on the per se performance and inter-cluster distances for different traits, the genotypes viz., PR 202 (i), CFMV 1 (i), VL 408, VL 391, OEB 610, WN 566, KOPN 1055 belonging to Cluster I and TNEc 1335 belonging to Cluster V are expected to produce desirable segregants for grain yield, earliness and other important yield attributing traits after hybridization. Also, IIMR FM-7028 belonging to

cluster III and TNEC 1335 belonging to cluster V may be selected for undertaking a hybridization programme to exploit heterosis and recovery of productive recombinants.

The relative contribution of the 13 characters towards genetic divergence and the number of times that each of the characters appeared in the first rank are presented in Table 5. The contribution of days to maturity was found to be highest (25.25%) towards divergence having ranked 189 times 1st, it was followed by plant height (15.25%) ranked 113 times, panicle length (15.11%) ranked 112times, ear per plant (10.12%) ranked 75 times, total chlorophyll content and days to 50 *per cent* flowering (8.23%)each ranked 61 times, 1000grain weight(7.69%) ranked 57times, number of basal tillers (3.1%)ranked 23 times, biological yield per plant (2.97%) ranked 22 times, relative water content (1.48%) ranked 11 times, harvest index (1.08%) ranked 8 times, grain yield per plant (0.67%) ranked 5times and finally chlorophyll stability index (0.54%) ranked 4 times 1st, The high contribution of days to maturity followed by panicle length towards divergence was reported by Jaylal and Haider [19]; a similar finding was reported by Shinde et al. [20] for the high contribution of plant height and days to maturity towards divergence.

Table 4. Clustering pattering among 39 genotypes of finger millet by Tocher's method

Cluster	No. of entries	Genotypes
I	35	BR 14-28 , CFMV 2 (i) ,KMR 711, IIMR FM-7066, VR 1149 , WN 572,GPU 67 (i), DPLM 2,VL 410, KOPN 1056, DHFM-13-6, KMR 710,PR 202 (i),WN 566, DHFM-78-33, IIMR FM-7202, CFMV 1,VL-376,PR 1731,DPLN 2,OEB 610,PR 1506,CFMV 2,VL 408,GPU 67,VL 408,PR 202,Gossaigaon Maruadhan 1, DPLM 3,IIMR FM-7835,KOPN 1055,CFMV 1 (i), VR1152,TNEc 1338,VL 391.
I	1	VL 376 (i)
III	1	IIMR FM-7028
IV	1	BR 9
V	1	TNEc 1335

Table 5. Relative Contribution of different characters to Genetic Diversity in finger millet

| Sl.no.	Characters	Times ranked 1st	Contribution (%)
1	Days to 50% flowering	61	8.23
2	Days to maturity	189	25.51
3	Plant height	113	15.25
4	Number of basal tillers per plant	23	3.1
5	Panicle length	112	15.11
6	Ear per plant	75	10.12
7	1000 grain weight	57	7.69
8	Biological yield per plant	22	2.97
9	Harvest index (%)	8	1.08
10	Total chlorophyll content	61	8.23
11	Chlorophyll stability index (%)	4	0.54
12	Relative water content in leaves (%)	11	1.48
13	Grain yield per plant	5	0.67
Total contribution			**100.00**
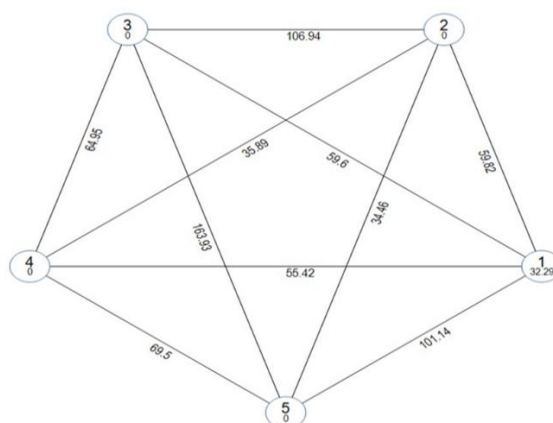
Fig. 3. Mahalanobis' euclidean distance

4. CONCLUSION

The analysis of variance in the 39 genotypes of finger millet revealed the presence of significant variation for all the characters studied. Hence, there is ample scope for selection with respect to all these traits for further improvement of finger millet. Based on the per se performances, the genotypes, viz., CFMV 2 (i), CFMV1 (i), VL 391, and VL 408 were found promising for higher yield. Moderate to high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for all the traits except for the days to 50 per cent flowering, days to maturity, relative water content in leaves, and chlorophyll stability index. This indicated the presence of considerable heritable variation among the genotypes justifying the utility of the genotypes in future crop improvement programme. However, the relative water content in leaves, chlorophyll stability index, days to 50 per cent flowering, and days to maturity exhibited low estimates of PCV and GCV. In the present study, a high estimate of heritability (broad sense) coupled with moderate to high genetic advance as per cent of mean was recorded for 1000grain weight, plant height, number of basal tillers per plant, panicle length, biological yield per plant, ear per plant, harvest index, grain yield per plant, total chlorophyll content, days to 50 percent flowering and days to maturity which demonstrated the presence of additive gene action indicating the effectiveness of selection for improvement of these traits. Using Mahalanobis D^2 statistics and the Tocher method, the 39 finger millet genotypes were categorized into five distinct clusters. Cluster I, with 35 genotypes, showed substantial intra-cluster diversity. The presence of significant inter-cluster distances, especially between Clusters V and III, II, and III, and I and V, indicated the potential for obtaining genetically diverse genotypes with desirable traits through hybridization.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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