



Phenotypic Diversity of Finger Millet (*Eleusine coracana* (L.) Gaertn.) Genotypes for Grain Yield Characters

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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

Analysis of variance showed high significant differences among 40 finger millet genotypes for all the characters under study. High GCV and PCV was recorded for number of tillers per plant, biological yield and peduncle length respectively suggesting that there was predominance of additive gene action. Number of tillers per plant, biological yield, peduncle length, harvest index, grain yield per plant, finger length, ear head length, Number of fingers, days to 50 % flowering exhibited high estimates of heritability with high genetic advance, indicating that these characters are predominantly governed by additive gene action and selection on the basis of these characters would be more effective. Based on the relative magnitude of D^2 value, the genotypes were grouped into 4 clusters. The maximum inter cluster distance was observed between clusters II and IV (25.95) followed by cluster II and III (12.16) and crosses involving genotypes from these clusters can be selected to yield superior segregants and future genetic improvement. Peduncle length, biological yield, days to 50% flowering and grain yield per plant appeared to be the most important trait contributing 79.11% towards genetic divergence.

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1. INTRODUCTION

Despite the fact that they are staple in the diets of millions of people residing in the semi-arid and arid regions of the world, millets are sometimes referred to as Orphan Crops, or even Lost Crops. These crops are not actually lost but the term indicates their abundance by the developed countries and also their world production statistics indicate significantly low volumes compared to the other more popular food crops. However, these neglected crops are important by virtue of their contribution to biodiversity and the means of livelihood of the poor in various parts of the world" [1]. Millets are regarded as 'smart food' as they are good for you, good for the farmer and good for the planet. Realizing the significance of millets, the Government of India (GOI) had observed the year 2018 as 'National Year of Millets' in order to boost domestic production and achieve self-sufficiency.

"Among the small millets *Eleusine coracana* (L.) Gaertn, popularly known as Finger millet, ragi (derived from Sanskrit word Rajika means red) belongs to family Poaceae (Gramineae), subfamily Chloridoideae and tribe Eragrostidea . It is allopolyploid with chromosome number $2n=4x=36$ and evolved from a cross between two diploid species *Eleusine indica* (AA) and *Eleusine floccifolia* or *Eleusine tristachya* (BB) as genome contributors" [2].

"Eleusine, the generic name, which is a Greek word meaning 'Goddess of Cereals', is supposed to have originated in the Ethiopian highlands. It is domesticated about 5000 BC in eastern Africa (possibly Ethiopia) and introduced to India as a crop 3000 years ago" [3]. "In India it is extensively cultivated in Karnataka, Tamil Nadu, Orissa, Andhra Pradesh, Madhya Pradesh, Jharkhand and Bihar. Finger millet seeds are particularly rich in tryptophan, cystine, methionine, and total aromatic amino acids compared to other cereals" [4].

Now days because of its nutritional and health benefits awareness, Plant breeders give more attention for its research. The status of finger millet is now changing from neglected and underutilized crop to future smart crops for health food and functional food product with high value. To cater the needs of farming community, crop improvement over existing varieties is a continuous process in plant breeding. Crop

improvement depends on the amount of genetic variability and availability of diverse germplasm.

"Genetic variability refers to the presence of difference among the individual of plant population the existing variability is essential for improvement of genetic material" [5]. Besides genetic variability, knowledge on heritability and genetic advance measures the relative degree to which a character is transmitted to progeny, thereby assists the breeder to formulate a suitable selection breeding strategy in order to achieve the desired objective. Thus, estimation of genetic variability in conjunction with heritability and genetic advance gives an idea of the possible improvement of the character through selection.

Genetic diversity which is pre-requisite for any successful breeding programme is of paramount importance. Generally, plant breeders select the parents on the basis of phenotypic diversity. It is the breeding value which determines how much of the phenotype would be passed onto the next generation. Murthy and Arunachalam [6] stated that multivariate analysis with "Mahalanobis D^2 statistics" is a powerful tool in quantifying the degree of divergence among the populations.

Attempt has been made in this study to assess the nature and magnitude of genetic variability for yield and its component in finger millet and also to assess the extent and pattern of genetic diversity of finger millet germplasm based on phenotypic traits.

2. MATERIALS AND METHODS

The field work of the present study was carried out at field experimental center of Department of Genetics and Plant Breeding, Naini Agriculture Institute, SHUATS, Prayagraj during the academic session 2020-2022 (Fig.1). The experiment was conducted to evaluate 40 genotypes including 4 checks viz., GPU 48, GPU 67, PR 202 and VL 376 of Finger millet which were grown in Randomized block design (RBD) with three replications in *kharif* 2021. The experimental field was divided into 3 blocks of equal size each possessing single genotype (Fig. 2). The sowing was done on 23rd of July 2021 (Fig. 2). The experiment was conducted with a recommended package of practices.

Observation were recorded based on five randomly selected plants in each genotype in each replication for fourteen important morphological characters viz., Days to 50% Flowering, Plant Height (cm), Number of productive tillers per plant, Days to Maturity, Finger Length (cm), Finger number per ear, Flag Leaf Length (cm), Flag Leaf Width (cm), Peduncle Length (cm), Ear Head Length (cm), Biological Yield (g), Harvest Index (%), Test Weight (g), Grain yield per plant (g). The mean data of these five plants were utilized for the statistical analysis. Analysis of variance was carried out as per standard procedure [7]. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) [8], heritability [9], genetic advance [10], were estimated. The genetic divergence was computed using Mahalanobis [11] D^2 statistics as described by [12] among all the forty genotypes. Based on D^2 values, all the genotypes were grouped in different clusters [12].

3. RESULTS AND DISCUSSION

“Analysis of variance revealed significant differences for all the characters indicating sufficient variability among the genotypes and

can be used for selection. The data revealed that the mean sum of squares due to genotype showed highly significant for all the 14 quantitative characters. Significant genetic variation in various component characters exhibited by the genotype indicated these characters might be effective. Similar results in finger millet have also been reported by Ganapathy et al. [13] and Suryanarayana et al. [14]. The results from analysis of variance among 40 finger millet germplasm for 14 quantitative characters are presented in Table 1.

The estimates of both genotypic and phenotypic coefficient of variation were presented in Table 2. High magnitude of PCV and GCV were recorded for number of tillers per plant (58.136% and 56.563%), biological yield per plant (48.78% and 46.11%), harvest index (43.284% and 39.707%), peduncle length (41.22% and 40.637%) and grain yield per plant (38.958% and 35.3%). The similar results of high PCV and GCV were reported by Ganapathy et al. [13] for productive tillers/plant. Similar results were reported for biological yield, number of tillers and grain yield per plant by Satish [15], John [16], Subramanian et al. [17] and Kadam [18]. These characters were more suitable for direct selection.



Fig. 1. An overview of finger millet in experimental field at Field Experimentation Center, department of genetics and plant breeding, SHUATS, Prayagraj (Allahabad) during transplanting stage

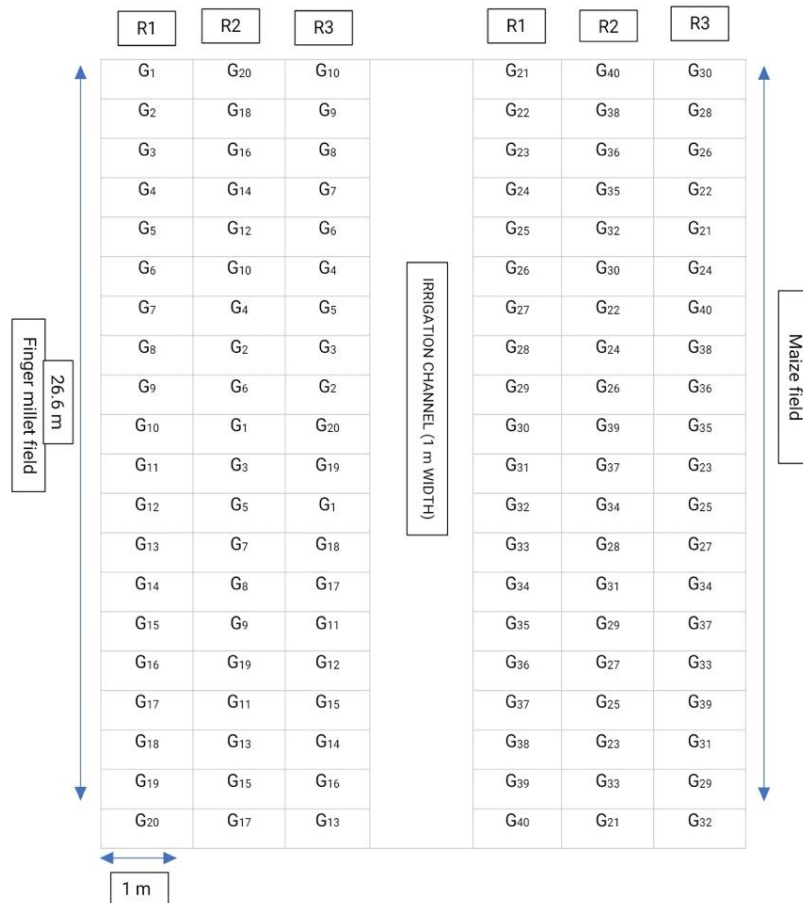


Fig. 2. Layout of experimental plot

“Moderate estimates of PCV and GCV were recorded for number of fingers (19.051% and 16.458%), finger length (18.93% and 18.044%), ear head length (16.872% and 15.841%), test weight (11.863% and 10.038%), plant height (11.23% and 10.224%) and days to 50% flowering (10.515% and 10.272%). Similar results were reported by” Shinde et al. [19]. “Low estimates of PCV and GCV were recorded for flag leaf width (9.973% and 7.685%) followed by flag leaf length (9.528% and 7.902%) and days to maturity (7.63% and 7.471%). Similar findings were also reported by” Patil [20], Reddy et al. [21], Sreeja et al. [22] and Ulaganathan and Nirmalakumari [23]. Moderate to low PCV and GCV restrict the scope of selection of genotypes based on characters.

“The magnitude of the Phenotypic Coefficient of Variation (PCV) was higher than the Genotypic Coefficient of Variation (GCV) for all the characters. These results were in conformity with the findings” of Ganapathy et al. [13] and Sahu et al. [24].

In the present study, high heritability values were recorded for all the characters except flag leaf width. High heritability was recorded for peduncle length (97.2%), days to maturity (95.9%), days to 50% flowering (95.4%), number of tillers (94.7%), finger length (90.9%), biological yield per plant (89.35%), ear head length (88.1%), harvest index (84.2%), plant height (82.9%), grain yield per plant (82.1%), number of fingers (74.6%), test weight (71.6%), flag leaf length (68.8%) and moderate for flag leaf width (59.4%). Ganapathy et al. [13] also reported such high heritability for the traits viz., days to 50% flowering, days to maturity, productive tillers/ plant, plant height and grain yield/plant. Jayashree and Nagarajaiah [25] reported “high heritability for plant height, finger length and days to 50% flowering. Such characters are predominantly governed by additive gene action and can be improved through individual plant selection”.

Heritability is the measure of the extent of phenotypic variance caused by the actions of genes. It is the proportion of genetic variability,

which is transmitted from parent to offspring. The estimates of heritability are more advantageous when expressed in terms of the genetic advance. High heritability coupled with high genetic advance as per cent mean were recorded for number of tillers per plant (94.7% and 98.67%), biological yield (89.35% and 89.8%), peduncle length (97.2% and 82.529%), harvest index (84.2% and 75.036%), grain yield per plant (82.1% and 65.891%), finger length (90.9% and 35.429%), ear head length (88.1% and 30.637%), number of fingers (74.6% and 29.29%), days to 50% flowering (95.4% and 20.672%), indicating a predominance of additive gene effects and the possibilities of effective selection for the improvement of these characters. Similar findings were reported by Salini et al. [26], Ulaganathan and Kumari, [23] and Haradari and Ugalat, [27] for number of productive tillers and grain yield per plant. Similar findings were reported for days to 50% flowering, plant height, number of productive tillers, number of fingers, finger length and grain yield per plant by Ganapathy et al. [13].

High heritability coupled with moderate genetic advance (>10 to 20) was recorded for plant height (82.9% and 19.174%), test weight (71.6% and 17.499%), days to maturity (95.9% and 15.07%), flag leaf length (68.8% and 13.501%), suggesting the greater role of both additive and

non-additive gene action in their inheritance. Similar findings were reported by Ulaganathan and Nirmalakumari [23].

Moderate heritability coupled with moderate genetic advance (<10) was recorded for flag leaf width (59.4% and 12.199%). It is indicative of non-additive gene action. The low heritability is being exhibited due to the favorable influence of environment rather than genotype and selection for such traits may not be rewarding.

D² statistics, a concept developed by Mahalanobis (1936) is important tool to plant breeder to classify the genotypes into different groups based on genetic divergence between them. The basic idea behind formation of clusters is to get the intra and inter-cluster distances. The serves as index for selection of parents with diverse origin.

“In the present study magnitude of D² Values 40 genotypes were grouped into four clusters (Table 3). Cluster I had the maximum of 37 genotypes, while the remaining three clusters were solitary. The genotypes IC0403282, IC0403280, IC0473931 formed single stocked cluster indicating wide diversity from set, as well as from each other. In finger millet, similar results was found by” Anantharaju and Meenakshiganesan [28] and Suryanarayana et al. [14].

Table 1. Analysis of variance for different quantitative parameters of finger millet genotypes during Kharif -2021

S. No.	Parameters	Mean sum of squares		
		Replications (d.f = 2)	Treatment (d.f = 39)	Error (d.f = 78)
1	Days to 50% flowering	1.408	184.526**	8.434
2	Plant height	43.983	342.75**	58.627
3	Days to maturity	6.475	183.046**	7.543
4	Flag leaf length	20.742	34.135**	10.665
5	Flag leaf width	0.099	0.032**	0.013
6	Number of fingers	2.153	6.392**	1.4
7	Finger length	1.727	5.29**	0.484
8	Ear head length	0.478	7.366**	0.873
9	Peduncle length	11.821	140.194**	3.937
10	Number of tillers	0.197	4.346**	0.232
11	Biological yield	13.65	14440.85**	55.058
12	Harvest index	124.367	298.52**	47.304
13	Test weight	0.792	0.201**	0.057
14	Grain yield	22.422	42.016**	7.519

Table 2. Genetic parameters for 14 quantitative characters of 40 finger millet genotypes

S. No.	Characters	Var Genotypical	Var Phenotypical	GCV	PCV	h ² (Broad Sense)	Genetic Advancement 5%	Gen. Adv as % of Mean 5%
1	Days to 50% flowering	58.697	61.509	10.272	10.515	95.4	15.418	20.672
2	Days to maturity	58.501	61.015	7.471	7.63	95.9	15.428	15.07
3	Plant height	94.71	114.27	10.224	11.23	82.9	18.251	19.174
4	Flag leaf length	7.821	11.37	7.902	9.528	68.8	4.778	13.501
5	Flag leaf width	0.006	0.011	7.685	9.973	59.4	0.126	12.199
6	Ear head length	2.164	2.455	15.841	16.872	88.1	2.845	30.637
7	Number of fingers	1.76	2.358	16.458	19.051	74.6	2.361	29.29
8	Finger length	1.602	1.763	18.044	18.93	90.9	2.485	35.429
9	Peduncle length	45.419	46.731	40.637	41.22	97.2	13.687	82.529
10	Number of tillers	1.371	1.449	56.563	58.136	94.7	2.347	98.67
11	Biological yield per plant	0.987	1.678	46.11	48.78	89.35	41.85	89.8
12	Harvest index	83.741	99.509	39.707	43.284	84.2	17.293	75.036
13	Test weight	0.048	0.067	10.038	11.863	71.6	0.382	17.499
14	Grain yield per plant	11.499	14.005	35.3	38.958	82.1	6.33	65.891

** Significant at 1% Level of Significance

Intra and inter cluster D^2 values were worked out using D^2 values from divergence analysis (Table 4). Highest intra cluster distance was recorded for cluster I (9.19) followed by cluster II, III and IV showing no intra cluster distance. Hybridization programme involving genetically diverse parents belonging to different distant clusters would provide analysis opportunity for bringing together diverse gene combinations, promising hybrid derivatives probably due to complementary interaction of divergent genes in parents [29]. The inter cluster distance ranged from 12.26 cm (cluster I and II) to 25.95 cm (cluster III and IV) respectively. The highest inter cluster distance was observed between cluster III and IV (25.95 cm) followed by 17.8 cm (cluster II and III), 17.13 cm (cluster III and IV) and 15.94 cm (cluster II and IV). To realize much variability and high heterotic effect, Mishra et al. [30] and Chaturvedi and Maurya [31] recommended that parents should be selected from two clusters having wider inter-cluster distance.

Hence, from the above discussion we can conclude that the genotypes from the cluster VIII and III were more divergent than any other cluster. Hence, the genotypes belonging to the distinct cluster (VIII and III) could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants.

Cluster group means for 14 characters are presented Table 5. cluster I has highest mean value of number of fingers and test weight.

Cluster II has highest mean value of flag leaf length, flag leaf width, ear head length, finger length, peduncle length, no. of tillers, biological yield per plant and grain yield per plant. Cluster III has highest mean value of harvest index. Cluster IV has highest mean value of days to 50% flowering, days to maturity and plant height. On the basis of above results it is evident that cluster II had maximum cluster means for most of desirable characters viz., flag leaf length, flag leaf width, ear head length, finger length, peduncle length, number of tillers, biological yield per plant and grain yield per plant. Therefore, genotypes including in this cluster can be used for improvement of a large number of seed yield and yield contributing characters, simultaneously. Earlier worker Sahu et al. [24] also reported "wide variability among clusters for yield and most of the yield contributing characters".

The relative contribution of different quantitative characters (Table 6) depicted that peduncle length (38.85%) towards genetic divergence followed biological yield per plant (19.23%), days to 50% flowering (10.90%), grain yield per plant (10.13%), ear head length (4.62%), finger length (4.36%) and days to maturity (4.32%), number of finger (1.79%), plant height (1.03%) while remaining 5 characters played negligently role less (<1%) in contributing genetic diversity. Earlier workers Shinde et al. [19], Muduli et al. [32], Ravikanth and Sarma, [33] and Anuradha et al. [34] also reported days to 50% flowering and days to maturity contributed more to genetic

Table 3. Clustering pattern of 40 genotypes of finger millet on the basis of genetic divergence

S. No.	Cluster number	Number of genotypes	Genotypes included
1	I	37	IC0266942, IC0402831, IC0402837, IC0402884, IC0402891, IC0402898, IC0402906, IC0402977, IC0403295, IC0403306, IC0403312, IC0473933, IC0473937, IC0474150, IC0474158, IC0474164, IC0474173, GPU 48, VL 376, IC0279376, IC0402837, IC0402874, IC0402890, IC0402893, IC0402905, IC0402956, IC0403279, IC0403300, IC0403309, IC0473935, IC0474154, IC0474150, IC0474162, IC0474167, IC0372819, GPU 67, PR 202.
2	II	1	IC0403282
3	III	1	IC0403280
4	IV	1	IC0473931

Table 4. Intra and inter cluster distance $\sqrt{D^2}$ values among 40 genotypes of finger millet

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	9.19	12.16	15.66	15.94
Cluster II		0	17.8	17.13
Cluster III			0	25.95
Cluster IV				0

Table 5. Intra cluster group means for various components of 40 finger millet genotypes

S. No.	Character	Cluster 1	Cluster 2	Cluster 3	Cluster 4
1	Days to 50% flowering	74.3	70.33	54.67	109.88
2	Days to maturity	99.06	101	81.67	136
3	Plant height	95.49	91.73	75.53	99.26
4	Flag leaf length	35.42	37.76	30.42	37.07
5	Flag leaf width	1.04	1.1	0.75	1.04
6	Ear head length	9.43	10.04	5.13	7.54
7	Number of fingers	8.17	8.1	5.6	6.43
8	Finger length	7.06	8.12	4.66	6.71
9	Peduncle length	16.39	25.9	11.9	19
10	Number of tillers	1.94	4.7	2.17	4.3
11	Biological yield per plant	45.68	49.67	42.89	49.45
12	Harvest index	22.89	18.47	50.49	5.9
13	Test weight	2.2	2.13	2.17	1.7
14	Grain yield per plant	9.67	11.87	7.12	7.39

Table 6. Contribution of different plant growth and grain yield characters to total divergence of finger millet

S. No.	Source	Times Ranked 1st	Contribution %
1	Days to 50% flowering	85	10.90%
2	Days to maturity	33	4.23%
3	Plant height	8	1.03%
4	Flag leaf length	5	0.64%
5	Flag leaf width	1	0.13%
6	Ear head length	36	4.62%
7	Number of fingers	14	1.79%
8	Finger length	34	4.36%
9	Peduncle length	303	38.85%
10	Number of tillers	0	0.00%
11	Biological yield per plant	150	19.23%
12	Harvest index	26	3.33%
13	Test weight	6	0.77%
14	Grain yield per plant	79	10.13%

divergence. Suryanarayana et al. [14] reported highest contribution for grain yield per plant and ear head length.

4. CONCLUSION

The present investigation is concluded that the genotype FINM 7056 was found to be superior for grain yield per plant among 40 finger millet genotypes followed by FINM 7059, FINM 4983, VL 376 and GPU 48. It is concluded from

experimental results that significant variation can be exploited further for improvement of finger millet. High GCV, PCV, heritability and genetic advance for number of tillers per plant, biological yield and peduncle length will be effective in this studied population. The present investigation further revealed that genotypes belonging to cluster I have maximum intra cluster distance and can improve the yield potential. As maximum inter cluster distance was notice between cluster III and cluster IV and cluster II and cluster III crosses involving genotypes from these clusters

would give wider and desirable recombination's. Therefore, genotypes present in these clusters are suggested to provide a broad spectrum of variability and may be used as parent for future hybridization programme to develop desirable genotypes.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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