Original Research Article

Phenotypic diversity of finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes for grain yield characters

ABSTRACT

The aim of present experiment was to estimate variability, heritability, genetic advance and genetic diversity of 14 quantitative traits in 40 genotypes, during *kharif* – 2021 in randomised block design. Analysis of variance showed significant differences among 40 finger millet genotypes for all the characters under study at 1% level of significance. High GCV and PCV was recorded for no. of tillers per plant, biological yield and peduncle length respectively suggesting that there was predominance of additive gene action. Based on the relative magnitude of D^2 value, the genotypes were grouped into 4 clusters. The maximum inter cluster distance was observed between cluster 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 maximum towards genetic divergence.

Comment [A1]: it is better if the purpose of the abstract is adjusted to the introduction

Comment [A2]: explain with numbers

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Keywords: Variability, Genetic advance, Heritability, Genetic divergence, Finger millet.

INTRODUCTION:

Millets refers to a group of annual grasses, belonging to the family Poaceae with tiny edible seeds that do not shatter readily at maturity. Often termed as coarse cereals, they thrive predominantly in the arid and semi-arid tracts globally as 'rainfed crops', under marginal conditions of soil fertility and moisture owing to their hardy nature and yield stability. 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.

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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 **(Hiremat and Salimath, 1992**).

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 **(Hilu *et al.*, 1979)**. In India it is extensively cultivated in Karnataka, Tamil Nadu, Orissa, Andhra Pradesh, Madhya Pradesh, Jharkhand and Bihar. Finger millet is highly nutritious as its grain contains the high quality protein (7-10%). It is the richest source of calcium (344 mg/100 g), iron (3.9 mg/100 g) and other minerals. It is also rich in phosphorus (283 mg/100 g) and potassium (408 mg/100 g). Finger millet seeds are particularly rich in tryptophan, cystine, methionine, and total aromatic amino acids compared to other cereals **(Kurien *et al.*, 1959***)*.

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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 (1966)** stated that multivariate analysis with "Mahalanobis D 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 divergence for yield and its component in finger millet and also to identify divergent parents from distantly related clusters for suitable hybridization.

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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. 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. The sowing was done on 23rd of July 2021.The experiment was conducted with a recommended package of practices.

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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.

The genetic divergence was computed using **Mahalanobis (1936)** D^2 statistics among all the fourty genotypes. Based on genetic distance, all the genotypes were grouped in different clusters **(Rao, 1952).**

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RESULTS AND DISCUSSION

D^2 statistics, a concept developed by **Mahalnobis (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 D^2 Values 40 genotypes were grouped into four clusters (Table 1). Cluster I had the maximum of 37 genotypes, while the remaining three clusters were solitary. The genotypes FINM 7393, FINM 7391, FINM 4979 formed single stocked cluster indicating wide diversity from set, as well as from each other. In finger millet, similar results was found by **Karad and Patil (2013), Anantharaju and Meenakshiganesan (2008) and Suryanarayana *et al.*, (2014).**

Intra and inter cluster D^2 values were worked out using D^2 values from divergence analysis (Table 2). 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 (**Anand and Murthy, 1968**). 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.* (2003) and Chaturvedi and Maurya (2005)** recommended that parents should be selected from two clusters having wider inter-cluster distance.

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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.

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Cluster group means for 14 characters are presented Table 3. cluster I has highest mean value of no. of fingers and test weight. Custer 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, no. 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.*, 2012** also reported wide variability among clusters for yield and most of the yield contributing characters.

The relative contribution of different quantitative characters (Table 4) 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.

CONCLUSION

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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 no. 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 DISCLAIMER:

Authors have declared that no competing interests exist. The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

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Comment [A16]: all theory must be included

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Table 1. 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	FINM 6432, FINM 7611, FINM 7617, FINM 7659, FINM 7666, FINM 7673, FINM 7681, FINM 7772, FINM 7046, FINM 7056, FINM 7062, FINM 4981, FINM 4985, FINM 5110, FINM 5118, FINM 5124, FINM 5133, GPU 48, VL 376, FINM 6436, FINM 7614, FINM 7650, FINM 7665, FINM 7668, FINM 7680, FINM 7753, FINM 7390, FINM 7050, FINM 7059, FINM 4983, FINM 5114, FINM 4986, FINM 5122, FINM 5127, FINM 8214, GPU 67, PR 202.
2	II	1	FINM 7393
3	III	1	FINM 7391
4	IV	1	FINM 4979

Table 2. 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 3. 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 4. Contribution of different plant growth and grain yield characters to total divergence in 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%