Biological Forum – An International Journal 14(2): 727-731(2022)

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Assessment of Genetic Divergence for Seed Yield and Its Component Traits in a New Set of Germplasm in Finger Millet (*Eleusine coracana* L. Gaertn)

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(Received 22 February 2022, Accepted 29 April, 2022)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: Investigation of germplasm accessions for genetic diversity is of immense importance in selection of choice of parents for hybridisation programme. An experiment was conducted to unravel the genetic diversity for seed yield and its contributing traits among a new set of 145 finger millet germplasm accessions obtained from IIMR, Hyderabad. Present study was conducted at Zonal Agriculture Research Station, V.C. Farm, Mandya in Randomized Complete Block Design with two replications. Accessions were organized into 10 clusters through Mahalanobis D^2 statistics and maximum inter cluster D^2 value (448.27) was observed between cluster II and VIII followed by D^2 value (436.08) among cluster II and IV. Significant difference was observed among cluster means for most of the traits. Maximum percentage of contribution to the genetic divergence was displayed by 1000-seed weight (34.39%). The findings revealed that accessions 3855 (cluster II) and 4866 (cluster VIII) were more genetically diverse suggesting that these could be used in future hybridization programme to get desirable segregants.

Keywords: Genetic divergence, finger millet, Mahalanobis D^2.

INTRODUCTION

Finger millet (*Eleusine coracana* L. Gaertn) is a tetraploid with chromosome number 2n=4x=36 belonging to family poaceae and commonly known as Ragi, Nagli, Nachani and Mandua. It is evolved from a cross between two diploid species, *E. indica* (L.) Gaertn. (AA) and *E. flocifolia* or *E. tristachya* (BB) as genome donors (Chennaveeraiah and Hiremath, 1973). It is native to Ethiopian highlands of central Africa and was domesticated into Indian subcontinent nearly 3000 years ago (Anon., 1995). The cultivation of finger millet in India under diverse agro-climatic conditions associated with natural and human selection has resulted in larger variability in crop, thus India became the secondary centre of diversity. In world, finger millet is a widely cultivated in the semi-arid areas of Eastern and Southern Africa and South Asia. It serves as staple food for a huge section of poor and farming community in many areas of India. It ranked as fourth millet in world after sorghum, pearl millet and foxtail millet, while in India it ranks third after sorghum and pearl millet in millets (Upadhaya *et al*., 2007). An enormous number of small farmers cultivate finger millet with limited water resources and in numerous nations this crop is frequently known as "poor people's crop".

In India, ragi is cultivated in an area of 1.15 million hectare with a production of 1.99 million tonne giving an average productivity of 1724 kg/ha majorly in Karnataka, Andhra Pradesh, Tamil Nadu, Maharashtra, Uttarakhand and Odisha (Anon., 2022). Karnataka is the leading producer of finger millet which contributes 68.26 % to the total area and 68.34 % to the total production of ragi cultivated in India (Anon., 2022). Ragi is acknowledged for its health advantageous effects, like antidiabetic, anti-diarrheal, antitumerogenic, anti-inflammatory, atherosclerogenic, antiulcer, antimicrobial, antioxidant propertiesand commonly known as "nutritious millet" as contains a high quantity of calcium (0.38%), protein (6%–13%), carbohydrates (65%–75%), minerals (2.5%–3.5%) and dietary fiber (18%) (Ulagnathan and Nirmalakumari, 2014). It provides 8-10 times more calcium than that of rice and wheat.

As concerned to global food security for growing population, it is mandatory to enhance the production and productivity of ragi crop. In plant breeding programme, genetic improvement through conventional breeding approaches like hybridisation, selection depends mainly on availability of diverse germplasm with presence of enormous genetic variability. The maximum utilization of any species for breeding and its adaptation to different environments depend on the level of genetic diversity it holds. Genetic distance among parents may be attributed to their differences for number of genes and their functional relations in a given environment (Nei, 1976). Evaluation of genetic divergence and relatedness among breeding materials has significant implications for the improvement of crop plants. Knowledge on genetic diversity in finger millet could help breeders and geneticists to understand the structure of germplasm, predict which combinations would produce the best offsprings and facilitate to widen the genetic basis of breeding material for selection (Singh *et al*., 2013). Progenies derived from diverse parents selected on basis of genetic divergence analysis are expected to show a broad spectrum of genetic variability, providing a greater scope for isolating transgressive segregant in advanced generation (Singh and Mishra, 1996) and promising heterotic effect may be observed in early generation. Mahalanobis D^2 statistics-based clustering is powerful tools in quantification of genetic divergence among germplasm accessions with respect to productive *per se* traits. Assessment of genetic diversity in finger millet using Mahalanobis D^2 statistics has previously been done by many researchers (Kadam, 2008; Karad and Patil, 2013; Mahanthesha *et al.*, 2017; Negi *et al.*, 2017). Therefore, the present study was undertaken to estimate the genetic divergence in a set of 145 finger milletgermplasm and explore potential to evaluate the relationship of these genotypes based on quantitative trait data.

MATERIALS AND METHODS

The current investigation on assessment of genetic divergence for yield and its contributing traits in finger millet germplasm accession was carried out during *kharif*, 2019 at Zonal Agricultural Research Station (ZARS), V. C. Farm, Mandya represents Southern Dry Zone of Karnataka (Zone 6) which is located at 12°32' N latitude and 76°53' E longitude and an altitude of 716 m above MSL. The material for present study was provided by ICAR- Indian Institute of Millets Research (IIMR) Rajendranagar, Hyderabad. The experiment was carried out in a randomized complete block design (RCBD) with two replications consisted of 145 germplasm accessions along with three checks *viz*. VL 352, GPU 67, and MR 6. The recommended package of practices was followed during crop growth period to raise a good crop. The observations on 11 quantitative traits viz., plant height (cm), productive tillers plant^{-1},days to 50% flowering, days to maturity, fingers ear^{-1}, finger length (cm), ear head length (cm), peduncle length (cm), seed yield plant^{-1} (g), straw yield plant^{-1}and 1000-seed weight (g) were recorded on five randomly selected plants from each germplasm accession in each replication. Estimation of genetic divergence was done by multivariate analysis using Mahalanobis (1936). All the D^2 values were calculated using Tocher's method as described by Rao (1952). The inter and intra cluster distances were calculated by the formula given by Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

Selection of parents based on the extent of genetic divergence has been successfully utilized in different crop species by different researchers (Sharma *et al.*, 2021). The investigated genotypes were organized into 10 clusters using Tocher's method (Rao, 1952). The clusters were constructed in such a way that the genotypes within a cluster had lower D^2 value than those of the other diverse clusters. The distribution pattern of genotypes into diverse clusters was furnished in Table 1. Out of 10 clusters, maximum number of accessions were organized into cluster I (135 accession including 3 checks) followed by cluster V with 5 accessions. The clusters II, III, IV, VI, VII, VIII, IX, X (*i.e.,* 8 clusters) were constituted by a single accession that revealed the presence of high degree of heterogeneity among accessions. Based on 11 quantitative traits, Euclidean genetic distances were estimated between different genotypes of finger millet. The average intra and inter cluster distances D^2 values were presented in Table 2 and Fig. 1. The maximum intra cluster D^2 values was recorded for cluster V (108.52) followed by cluster I (91.89). The intra cluster distances ranged from zero (solitary clusters) to 108.52 (Cluster V). Zero intra cluster distance was observed in cluster II, III, IV, VI, VII, VIII, IX and X represented by single accession. These results indicate that genotypes contributing to same clusters have a low diversity and the selection within a cluster is not considered as satisfactory.

Table 1: Distribution of finger millet accessions into 10 clusters obtained using D^2 statistics.

Sr. No.	Clusters	Number of accessions	Accessions
1.	I	135	3622, 4219, 6493, 3583, 4881, 4493, 4863, 5461, 3856, 3017, 4336, 3422, 2901, 3901, 3003, 5620, 5406, 4213, 5464, 5578, 2853, 5994, 2853, 5413, 6558, 3525, 5540, 6347, 5462, 3689, 3062, 2960, 3928, 4349, 3952, 4602, 2891, 3086, 4524, 3793, 5849, 5514, 3789, 3847, 3726, 5601, 3321, 4578, 5596, 6624, 3088, 4483, 5200, 5601, 5458, 4542, 5453, 4830, 3004, 3318, 3782, 5460, 4512, 3296, VL352, 3532, 4462, 6582, 5735, 6077, 5960, 5088, 3765, 4533, 6269, 6723, 4536, 3848, 6364, 6584, 6530, 3004, 3068, 4491, 3090, 6658, 3496, 5668, 2936, 3639, 6176, 6560, 4794, 4958, 4288, 5736, 4203, 6478, 3007, GPU67, 3376, 5341, 4482, 3883, 5562, 4331, 4260, 5732, 5599, 6188, 5717, 3871, 3608, 5893, 5301, 2899, 6546, 4957, 2872, 4874, 3022, 5731, 4527, 4961, 5337, 3026, 3538, 4498, 6525, 4644, 2998, 4303, 6563, 5425, MR6.
2.	II	1	3855
3.	III	1	4516
4.	IV	1	6526
5.	V	5	3336, 6423, 5154, 5158, 5160.
6.	VI	1	5433
7.	VII	1	6754
8.	VIII	1	4866
9.	IX	1	6772
10.	X	1	5412

Table 2: Average intra and inter cluster D^2 values of 10 clusters from finger millet accession.

Clusters \ Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	91.89									
II	163.93	0								
III	158.42	97.04	0							
IV	168.36	**436.08**	320.19	0						
V	177.66	277.90	177.44	176.43	**108.52**					
VI	157.01	369.79	249.04	**37.95**	205.74	0				
VII	155.67	213.92	324.80	291.28	334.96	249.26	0			
VIII	187.34	**448.27**	328.00	169.30	195.99	223.94	300.29	0		
IX	170.27	345.72	308.27	69.20	255.27	68.09	206.66	317.93	0	
X	216.76	114.79	153.80	392.99	203.53	415.29	343.00	425.73	368.20	0

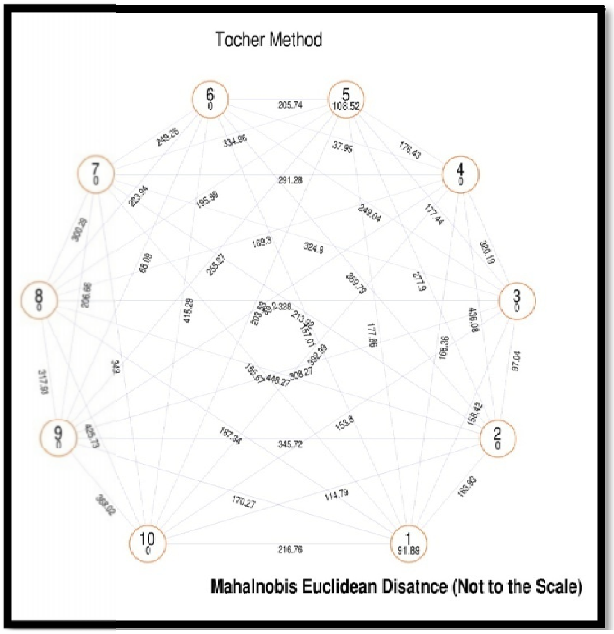

Fig. 1. Intra and inter cluster distance of 145 finger millet accession into 10 clusters based on Euclidean D^2 value.

A broad range of inter cluster distance were recorded from 37.95 (among cluster IV and VI) to 448.27 (among cluster II and VIII). The maximum inter cluster D^2 value (448.27) was observed between cluster II (accession 3855) and VIII (accession 4866) followed by D^2 value (436.08) among cluster II and IV, revealed that maximum heterosis can be anticipated from the crosses with parents belonging to theses most diverse clusters i.e., cross among 3855 × 4866 and 3855× 6526 accessions as parents could be used further in hybridization programme for enhancing the productivity of finger millet. Similar results were reported by Kadam (2008); Kumar *et al*. (2010) ; Devaliya *et al.* (2017). Therefore, the accessions from diverse clusters mentioned above can be used as parent in future breeding programme to develop desirable segregates.

Cluster means of the traits: The cluster mean for all quantitative traits under investigation were illustrated in Table 3. Cluster III was recorded the highest mean values of seed yield plant^{-1} (18.75), straw yield plot^{-1} (0.89), earhead length (15.80), peduncle length (34.80), productive tillers plant^{-1} (5.30) and plant height (107.00). Accession from cluster VII *i.e.,* 6754 was found the lowest mean values for seed yield plant^{-1} (9.06), straw yield plot^{-1} (0.26), earhead length (6.30), peduncle length (20.20), days to 50% flowering (58.50), finger length (4.55), finger number ear^{-1} (4.90) and plant height (59.70). Genotype of cluster III revealed the possibility of selecting directly one genotype that can be used for yield enhancement as it showed highest cluster mean for yield and important contributing traits. The present findings were in agreement with the findings of Kadam (2008); Kumar *et al.* (2010); Mahanthesha *et al.* (2017); Devaliya *et al.* (2017).

Relative contribution of characters towards genetic divergence: The numbers of times that each one of the 11 characters showed up 1st rank and their corresponding per cent contribution to genetic divergence were furnished in Table 4. Among all traits under investigation, 1000 seed test weight (34.39%), straw yield plot^{-1}(17.09%), finger length (12.21%), days to maturity (9.28%), days to 50% flowering and seed yield plant^{-1} (8.08%) were reported the higher contribution towards the genetic divergence. Similar results were observed by Negi *et al.* (2017) for days to 50% flowering, straw yield plot^{-1} and peduncle length. The findings for plant height and productive tillers plant^{-1} were in accordance with Mahanthesha *et al.* (2017).

Table 3: Estimates of mean values of clusters for 11 traits in finger millet accession (Tocher's method).

Traits Clusters	PH	PT	FN	FL	PL	EL	DFF	DM	GY	SY	TW
I	87.17	4.25	7.03	7.23	25.26	9.18	68.47	102.36	15.45	0.53	2.54
II	95.30	4.30	5.90	7.40	28.20	9.20	66.50	101.50	17.79	0.82	**3.51**
III	**107.00**	**5.30**	6.65	9.45	**34.80**	**15.80**	72.50	106.00	**18.75**	**0.89**	2.87
IV	75.10	3.45	9.30	9.85	23.20	12.80	74.00	106.00	12.64	0.32	1.76
V	86.96	3.60	8.30	9.06	25.98	11.64	**78.10**	**113.10**	17.71	0.80	2.24
VI	85.65	4.10	7.15	**10.45**	26.10	15.40	73.00	106.00	10.75	0.29	1.87
VII	**59.70**	2.80	**4.90**	**4.55**	**20.20**	**6.30**	**58.50**	100.50	**9.06**	**0.26**	2.61
VIII	93.60	3.30	7.50	5.25	23.20	7.20	74.00	105.50	15.99	0.56	**1.54**
IX	82.10	**2.40**	9.40	10.35	25.60	13.80	59.00	**99.00**	9.99	**0.26**	2.22
X	96.40	4.15	**10.30**	7.40	29.20	9.20	78.00	111.00	17.80	0.85	3.40

PH - Plant height (cm) FL – Finger length (cm) DFF – Days to 50% flowering SY – Straw yield plot^{-1} (kg) FN – Finger number ear^{-1}
PL – Peduncle length (cm) PT – Productive tillers plant^{-1} EL – Ear head length (cm) DM – Days to maturity GY – seed yield plant^{-1} (g)
TW – 1000 seed weight (g)

Table 4: Contribution of seed yield and its contributing traits to total divergence in 145 finger millet genotypes

Sr. No.	Characters	Number of times appearing 1st in ranking	Per cent contribution
1.	Plant height (cm)	111	1.02
2.	Productive tillers plant^{-1}	50	0.46
3.	Fingersear^{-1}	566	5.2
4.	Finger length (cm)	1328	12.21
5.	Peduncle length (cm)	450	4.14
6.	Ear head length (cm)	5	0.05
7.	Days to 50% flowering	879	8.08
8.	Days to maturity	1010	9.28
9.	Seed yield plant^{-1}(g)	879	8.08
10.	Straw yield plot^{-1} (kg)	1859	17.09
11.	1000 seedweight (g)	3741	34.39

CONCLUSION

The assessment of genetic diversity is not only important for crop improvement efforts but also for efficient management and protection of germplasm resources. Genetic divergence studies using D^2 statistic showed the presence of substantial diversity. The germplasm accessions were organized into 10 diverse clusters. The maximum inter cluster D^2 value (448.27) was observed between cluster II and VIII followed by D^2 value (436.08) among cluster II and IV. It was observed that Cluster III i.*e*., accession 4516 was registered the highest seed yield plant^{-1}, straw yield plot^{-1}, earhead length, peduncle length, productive tillers plant^{-1} and plant height which revealed the possibility for immediate or further use in breeding programme. Accession 3855 (cluster II) and 4866 (cluster VIII) were found genetically more diverse indicating that these accessions could be used in future hybridization programmes to get desirable segregates.

Acknowledgement. The first author is thankful to Indian Council Agricultural Research, New Delhi for providing him financial assistance in the form of junior research fellowship, also grateful to the Department of Genetics and Plant Breeding, College of Agriculture, UAS, GKVK, Bangalore for giving best of knowledge and resources for conducting this research required for partial fulfilment of M.Sc. (Agri.) programme.
Conflict of Interest. None.

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How to cite this article: Mohit Sharma, K. Madhusudan, Prashant Vasisth, Parul Gupta and V. Balar (2022). Assessment of Genetic Divergence for Seed Yield and its Component Traits in a New Set of Germplasm in Finger Millet (*Eleusine coracana* L. Gaertn). *Biological Forum – An International Journal*, *14*(2): 727-731.