Assessment of genetic divergence in white finger millet [*Eleusine coracana* (L.) Gaertn.] genotypes for yield and yield contributing traits

Abstract

The present investigation is carried out to study the genetic divergence among 55 finger millet genotypes for fourteen quantitative characters using Mahalanobis D^2 statistics during *kharif*, 2020. D^2 statistics indicated that the genotypes studied were genetically diverse. The 55 genotypes of finger millet were grouped into 6 clusters irrespective of geographical diversity, indicating no parallelism between geographic and genetic diversity. Clusters I had highest number of 50 genotypes and remaining all clusters had solitary. A wider genetic diversity was observed for the different traits studied among the genotypes as evidenced by the formation of six clusters. Out of fourteen quantitative traits studied grain yield per plant contributed majorly towards divergence with the value of 15.65% followed by productive tillers per plant contributes (12%), harvest index (10%) and other traits contribute minorly for divergence.

Keywords: Genetic divergence, D^2 statistics, white finger millet

Introduction

“Finger millet (*Eleusine coracana* L. Gaertn) is cultivated as a subsistence farming crop in Asian and African continents. Global area under finger millet is 4-4.5 million hectares with the production of 5 million tonnes" (Anonymous, 2012). “Finger millet seeds are consumed in variety of forms such as unleavened bread (roti), mudde, thin or thick porridge, fermented porridge and also used in brewing. Demand for finger millet grains has picked up in the urban areas and baking industry in the recent times due to high fibre and other health benefits associated with its consumption. However, the dark colour of grains has been the major hindrance for its acceptability in baking and food industry. Among both brown and white grain types, white grain types are preferred because of high protein, low fibre, low tannins and higher consumer acceptability" (Sharathbabu *et al.*, 2008). "However, the yield potentiality of all white grain types is significantly lower than the brown types Ragi is commonly called as "Nutritious millet" as the grain is nutritionally superior to many cereals providing fair amount of proteins, minerals, calcium and vitamins. It contains almost all the nutrients like protein (9.2 %), carbohydrates (76.32 %) and fat (1.29 %). It is very rich in minerals (2.70 %) such as calcium (452 mg/1000g), iron (3.90 mg/100g) and ash (3.90 %) which are the core ingredients of normal human diet. The protein of finger millet has been reported to possess a fairly high biological value, which is needed for the maintenance of nitrogen equilibrium of the body. It has crude fiber content (3-4 %) to supply energy for a long time after consumption and thus whole day sustenance, high cholesterol formation and intestinal cancer. Hence, people suffering from diabetics are advised to take finger millet and other small millets instead of rice" (Malleshi and Hadimani, 1993).

Genetic improvement through conventional breeding approaches depends mainly on the availability of the diverse germplasm and the amount of genetic variability present in the population. A method suggested by Mahalanobis (1936) knows as "Mahalanobis D^2 statistics" is "a powerful tool for quantifying the divergence between two populations. Therefore, the present study was undertaken 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 through genetic divergence analysis".

Material and methods

The preset investigation was consisted of evaluation of 55 white finger millet accessions for qualitative morphological descriptors at the Agricultural Research Station, Hagari, Ballari, Karnataka.The experiment was laid out in Randomized complete block design with one check variety (KMR 340) of white finger millet were obtained from the Indian Institute of Millets Research (IIMR), Hyderabad. Each entry was represented by two rows of 3-meter length. Present experiment consists of 11 blocks and one check which was randomly repeated in two replications. In each block, each genotype was sown in a single row with spacing of 30 cm between the rows and 10 cm between the plants within the rows. All recommended agronomical cultural practices were carried out to raise a good crop.

Observation were recorded based on five randomly selected plants in each genotype in each replication for fourteen important morphological characters *viz.*, days to 50 per cent flowering, days to maturity, plant height (cm), flag leaf blade length (cm), peduncle length (cm), productive tillers per plant, number of fingers per ear, finger width (cm), finger length (cm), ear head length (cm), harvest index (%), 1000 seed weight (g) and 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 fifty five genotypes. Based on genetic distance, all the genotypes were grouped in different clusters (Rao, 1952).

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.

Clustering of genotypes following the Tocher's method as described by Rao (1952). The fifty-five genotypes of finger millet were grouped into six different clusters (Table 1). Clusters I had highest number of 50 genotypes, clusters II, III, IV, V and cluster VI were solitary clusters. The formation of distinct solitary clusters may be due to the fact that geographic barriers hindering gene flow, intensive natural and human selection for diverse and adaptable gene complexes must be responsible for this genetic diversity (Arunachalam and Ram, 1967). The mutual relationship between clusters is represented by considering average intra and inter-cluster Mahalanobis's D^2 distances in Table 2. The present observations were concurring with the reports of earlier workers like Patel *et al*. (2017), Vara Prasad and Shivani (2017), Ponsiva *et al*. (2019).

Among the six clusters formed Cluster I (21.21) has the highest intra cluster distance however, all other 5 clusters had the value of 0.00 with no intra cluster Mahalanobis's D^2 distance due to solitary clusters.

Cluster I is found to have nearest value with cluster II (30.45), cluster III (31.22), cluster IV (34.54), cluster V (44.6) and cluster VI (47.41). Cluster II is found to have nearest value with cluster I (30.45), cluster IV (34.66), cluster VI (57.88), cluster III (62.66) and cluster V (91.51). Cluster III is found to have nearest distance value with cluster V (20.98), cluster I (31.22), cluster IV (32.2), cluster VI (62.44) and cluster II (62.66).

Cluster IV is found to have nearest distance value with cluster III (32.2), cluster I (34.54), cluster II (34.66), cluster V (45.85) and cluster VI (82.58). Cluster V is found to have nearest distance value with cluster III (20.98), cluster I (44.6), cluster IV (45.85), cluster II (91.51), cluster VI (99.09). Cluster VI is found to have value of nearest distance with cluster I (47.41), cluster II (57.88), cluster III (62.44), cluster IV (82.58) and V (99.09). The present results were in confirmative with the report of earlier workers like Negi *et al*. (2017b), Geethanjali and Jagadeeswar (2016) and Kaluthantri and Dasanayak (2016).

Cluster group means for 14 characters are presented Table 3. Cluster I having 50 genotypes showed highest cluster mean for test weight. Cluster II having 1 genotype, exhibited highest cluster mean for harvest index and days to 50 per cent flowering. The monogenotypic cluster III resulting highest cluster mean for plant height, finger length, fingers per ear head, flag leaf blade length and ear head length. The monogenotypic cluster IV not recorded higher cluster mean for any of the characters. Cluster V, which was represented by 1 entry possessed highest cluster mean for productive tillers per plant, flag leaf blade length and grain yield per plant. Cluster IV had 1 genotype, exhibited highest cluster means for days to maturity, peduncle length and finger width. On the basis of above results it is evident that cluster III had maximum cluster means for most of desirable characters *viz.,* plant height, finger length, fingers per ear head, flag leaf blade length and ear head length. Therefore, genotypes improvement of a large number of seed yield and yield contributing characters, simultaneously. Earlier worker Bedis *et al.,* 2007 and Sahu *et al.,* 2012 also reported wide variability among clusters for yield and most of the yield contributing characters.

Contribution of individual traits towards divergence

The per cent contribution of all the studied fourteen traits towards divergence is computed in Table 4. The knowledge of how the character's influence divergence is the pivotal aspect to a plant breeder. The total contribution of various traits towards genetic divergence follows, grain yield (15.67 %) showed maximum contribution towards genetic diversity followed by the other characters *viz.*, productive tillers per plant (12 %), harvest index (10 %), fingers per ear head (9.63 %), 1000 seed weight (8 %), finger width (8 %), finger length (7 %), peduncle length (7 %), ear head length (5.72 %), flag leaf blade length (5 %), flag leaf blade width (4 %), days to 50 per cent flowering (3 %), days to maturity (3 %) and plant height (2 %) contributed towards genetic divergence. The present findings were on par with the report of earlier workers like Shinde *et al*. (2013), Jadhav *et al.* (2014) for plant height, Ulaganathan and Nirmala kumari (2015) and Babu *et al.* (2017) for days to maturity in ragi, Brunda *et al*. (2015b) for days to maturity, Gangurde *et al*. (2016) for grain yield per plant towards the maximum contribution to the divergence.

Table.1 Clustering pattern of 55 genotypes of finger millet on the basis of genetic divergence

Clusters	No. of genotypes	Genotypes
I	50	E 319, E 325, IC0473986, IC0473924, IC0474226, E331, IC0474231, GPU67, IC0473978, IC0473970, IC0621996, IC0473987, IC0473948, IC0473957, IC0474219, OUAT 2, IC0473874, IC0473959, IC0473996, IC0474228, KMR 340, IC0474183, IC0473971, IC0474232, IC0474233, IC0473993, IC0473984, IC0473980, VL 352, IC0621993, ER 97, IC0474038, IC0474215, IC0473947, IC0473950, IC04022775, IC0474356, IC0473983, PR202,IC0474045, IC0474037, IC0474227, IC0474222, IC0473992, IC0474206, IC0475624, IC0473990, IC0474207,IC0065595, IC0474433.
II	1	IC0473972
III	1	IC0474065
IV	1	IC0473989
V	1	IC0474226
VI	1	IC0474044

Table.2 Intra and inter cluster distance D^2 values among 55 genotypes of finger millet.

Cluster distances						
Clusters	**I**	**II**	**III**	**IV**	**V**	**VI**
I	**21.21**	30.45	31.22	34.54	44.6	47.41
II	30.45	**0**	62.66	34.66	91.51	57.88
III	31.22	62.66	**0**	32.2	20.98	62.44
IV	34.54	34.66	32.2	**0**	45.85	82.58
V	44.6	91.51	20.98	45.85	**0**	99.09
VI	47.41	57.88	62.44	82.58	99.09	**0**

Table.3 Intra cluster group means for various components of 55 finger millet genotypes

Clusters	N	DFF	DM	PH	PTP	FL	FPE	1000SW	HI	FLBL	FLBW	PL	EHL	FW	GYP	Overal Score	Rank
I	50	72.03 (4)	104.72 (4)	65.5 (5)	2.26 (3)	7.23 (4)	6.71 (4)	**3.23** **(1)**	29.39 (5)	35.67 (4)	0.79 (4)	16.21 (3)	9.95 (3)	0.78 (2)	21.17 (3)	49	3
II	1	**79** **(1)**	102 (5)	67.2 (3)	2 (5)	**5.9** **(6)**	6.5 (5)	3.03 (4)	**32.1** **(1)**	33.8 (5)	**0.67** **(6)**	16.4 (2)	9.8 (4)	0.72 (5)	**17.7** **(6)**	58	2
III	1	74.5 (3)	112 (2)	**74.9** **(1)**	2.6 (2)	**9.5** **(1)**	**9** **(1)**	3.2 (2)	29.6 (4)	36.5 (3)	**0.87** **(1)**	15.2 (4)	**10.7** **(1)**	0.75 (4)	**22.7** **(2)**	31	6
IV	1	**60** **(6)**	108 (3)	67.15 (4)	2.1 (4)	9 (3)	**6.5** **(6)**	**2.62** **(6)**	31.5 (2)	**33.5** **(6)**	0.71 (5)	**12.9** **(6)**	9.2 (5)	**0.68** **(6)**	20.2 (4)	66	1
V	1	76.5 (2)	**99** **(6)**	**55.7** **(6)**	**2.9** **(1)**	9.1 (2)	7.6 (2)	2.98 (5)	**24.4** **(6)**	**39.6** **(1)**	0.82 (3)	15 (5)	**9.1** **(6)**	0.77 (3)	**25.9** **(1)**	49	4
VI	1	65 (5)	**118.5** **(1)**	71.4 (2)	**2** **(6)**	7.2 (5)	7.6 (3)	3.19 (3)	31.3 (3)	36.8 (2)	0.85 (2)	**16.7** **(1)**	10.3 (2)	**1.59** **(1)**	18.9 (5)	41	5

Table.4 Contribution of different plant growth and grain yield characters to total divergence in 55 finger millet genotypes

Sl. No	Source	No. of first rank	Contribution %	Cumulative
1	Days to 50% flowering	45	3	3
2	Days to maturity	45	3	6
3	Plant height (cm)	30	2	8
4	Productive tillers per plant	179	12	20
5	Finger length (cm)	104	7	27
6	Fingers per ear head	144	9.63	36.63
7	1000 seed weight (g)	119	8	44.63
8	Harvest index (%)	149	10	54.63
9	Flag leaf blade length (cm)	75	5	59.63
10	Flag leaf blade width (cm)	60	4	63.63
11	Peduncle length (cm)	104	7	70.63
12	Ear head length (cm)	85	5.72	76.35
13	Finger width (cm)	119	8	84.35
14	Grain yield/plant (g)	234	15.65	100

Conclusion : There is acute need of improve of yield in Finger millet as it is one of the main subsistence cereal crop in Africa and India. Finding out the variation for the trait, among the different genotypes is most important and use of different statistical tools like Mahalanobis D^2 is also impartment for selecting proper geneotypes. In addition to yield trait the yield contributing traits like productive tillers per plant, harvest index, fingers per ear head, finger width, finger length, peduncle length, ear head length, flag leaf blade length and flag leaf blade width also contribute the yield. The results of the current study showed that ample genetic diversity existed among finger millet genotypes to be used in future breeding program through selection and hybridization.

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