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Genetic diversity analysis in finger millet [*Eleusine coracana* (L.) Gaertn.]

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Abstract

The experimental material comprised 36 diverse genotypes of finger millet (*Eleusine coracana* L. Gaertn.). The data on 12 quantitative traits viz., days of 50% flowering, days to maturity, plant height, number of productive tillers per plant, number of fingers per earhead, main ear head length, finger length, finger width, grain yield per plant, straw yield per plant, 1000-grain weight and harvest index were collected from a random sample of five plants for each genotype. On the basis of Tocher's method, all the 36 genotypes of the present study were grouped into seven clusters. Maximum no. of genotypes (26) were included in cluster I followed by five genotypes in cluster IV, while cluster II, III, V, VI and VII were comprised by each single genotype. The inter-cluster distance varied from 115.74 between clusters VI and VII to 24.98 between clusters I and III. Analysis corroborated the absence of relationship between geographic origin and genetic diversity, as genotypes from the different area grouped into same clusters and the genotypes of same area were grouped in the different clusters. Therefore, breeder must evaluate their material for genetic diversity and should not merely depend on their geographical origin.

Keywords: Genetic, finger millet, *Eleusine coracana* (L.) Gaertn

Introduction

Finger millet [*Eleusine coracana* (L.) Gaertn.] subspecies coracana belongs to family Poaceae. It is an important cereal crop amongst the small millets and ranks third in importance among millets in the country in area and production after sorghum and pearl millet. Typically, a tropical, rainfed crop, it is one of the best suited for dry farming. Finger millet is very adaptable and thrives at higher elevations than most other tropical cereals and adapted for its valued food grains. Its adaptability to wide range of geographical areas and agro-ecological diversity makes it more versatile. The availability of diverse genetic resources is a prerequisite for genetic improvement of any crop including finger millet. Besides the availability of genetic resources, their characterization is essential for effective utilization in crop improvement programs especially for quality improvement (Patil *et al.*, 2018)^[6, 9]. Success of hybridization programme depends to a large extent upon the choice of suitable parents of diverse origin with the possibility of obtaining large frequency of transgressive segregants. The D² statistics is one of the powerful tools to assess the relative contribution of different component traits to the total diversity. Knowledge of genetic diversity among genotypes on the basis of divergence analysis usually helps a breeder in choosing diverse parents for breeding program. Therefore, the present investigation was undertaken to estimate the extent of genetic diversity in finger millet genotypes available in India.

Material and Methods

The experimental material consisted 36 finger millet genotypes collected from different location of country. The material was grown in simple randomized block design with three replications at Hill Millet Research Station, Navsari Agricultural University, Waghai, The Dangs, during *khariif*, 2017-18. All the recommended agronomic and cultural practices were followed for raising a healthy crop. Data were recorded on five randomly taken plants per replication of each genotype for twelve characters viz., days of 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, number of fingers per earhead, main ear head length (cm), finger length (cm), finger width (cm), grain yield per plant (g), straw yield per plant (g), 1000-grain weight (g) and harvest index (%). Genetic diversity was studied following Mahalanobis's (1936)^[1] D² statistics as extended by Rao (1952)^[2]. On the basis of D² values genotypes were grouped into different clusters according to Tocher's method given by Rao (1952)^[2].

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Result and Discussion

Distribution of genotypes into clusters

With the help of Tocher's method seven clusters were formed from thirty-six genotypes of finger millet given in table 1. The results indicated that a maximum number of diverse genotypes fall in cluster I (26 genotypes) followed by cluster IV (5 genotypes), cluster II, III, V, VI and VII were comprised by each single genotype. Genotypes of different geographical areas were fall in one group and also the genotypes of the same geographical area were clubbed into different groups indicating there is no formed relationship between geographical diversity and genetic diversity (Satish *et al.* 2007, Kumar *et al.* 2010, Suryanarayana *et al.*, 2014; Devaliya *et al.*, 2017 and Patel *et al.*, 2018) ^[10, 5, 13, 4, 6, 9].

A study of the data revealed that the inter-cluster distance (D) ranged from 24.98 to 115.74. The maximum inter-cluster distance (D=115.74) was observed between cluster VI and VII followed by those between cluster V and VII (D=93.04). The minimum inter-cluster distance (D=24.98) was observed between cluster I and III followed by the cluster I and II (D=26.07). Intra-cluster distance (D) ranged from 0.00 to 18.3. At intra-cluster level, cluster IV had the highest intra cluster distance (D=18.30) followed by cluster I (D=16.92) which involve 5 and 26 genotypes, respectively. The intra-cluster distance within cluster II, III, V, VI and VII was zero (0)

because these clusters were composed of only single genotype.

As far as inter-cluster distance is concerned cluster VI and VII showed the maximum distance. High value of inter-cluster distance points out towards high amount of diversity between the clusters involved.

Hence, from the above discussion we can concluded that the genotypes from the cluster VI and VII are more divergent than any other cluster. As we discuss above magnitude of heterosis largely depends on the degree of genetic diversity in the parental lines. Hence, the genotypes belonging to the distinct cluster (VI and VII) could be used in hybridization programme for obtaining a wide spectrum of variability among the segregants.

From the results of this investigation, it was found that number of clusters contained at least one genotype with the desirable traits, which ruled out the possibility of selecting directly one genotype for immediate use. (Suryanarayana *et al.*, 2014; Devaliya *et al.*, 2017 and Patel *et al.*, 2018) ^[13, 4, 6, 9]. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits. From the results, it could be concluded that inter-crossing genotypes from cluster II, III, V, VI and VII might result in wide array of variability for exercising effective selection (Sheriff *et al.* 1992 and Patel *et al.* 2018) ^[6, 9].

Table 1: The distribution of thirty-six genotypes of finger millet into seven different clusters on the basis of Mahalanobis's D² statistics

Cluster	No. of genotypes	Genotypes
Cluster I	26	GN 4, GN 5, GNN 6, GN 3, ML 322, GN 2, KOPN 1059, KMR 623, OEB 601, GN 1, WN 595, PR 1511, VR 1101, GPU 45, GPU 47, TNEC 1294, GPU 96, GPU 97, PR 1507, ML 181, KWFM 49, GNN 7, TNEC 1292, RAuF 13, PRS 38, PR 202
Cluster II	1	OEB 602
Cluster III	1	WN 550
Cluster IV	5	WN 585, IIMR 6655, VL 389, VL 352, RAuF 15,
Cluster V	1	KMR 632
Cluster VI	1	VL 390
Cluster VII	1	Gossigoan Marubadhan

Table 2: Average Intra and Inter-cluster distance for thirty-six genotypes of finger millet.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	16.92	26.07	24.98	38.22	28.67	42.93	54.71
Cluster II		0.00	40.15	30.44	63.33	46.41	41.33
Cluster III			0.00	34.10	54.13	65.43	47.83
Cluster IV				18.30	76.26	42.57	68.31
Cluster V					0.00	53.43	93.04
Cluster VI						0.00	115.74
Cluster VII							0.00

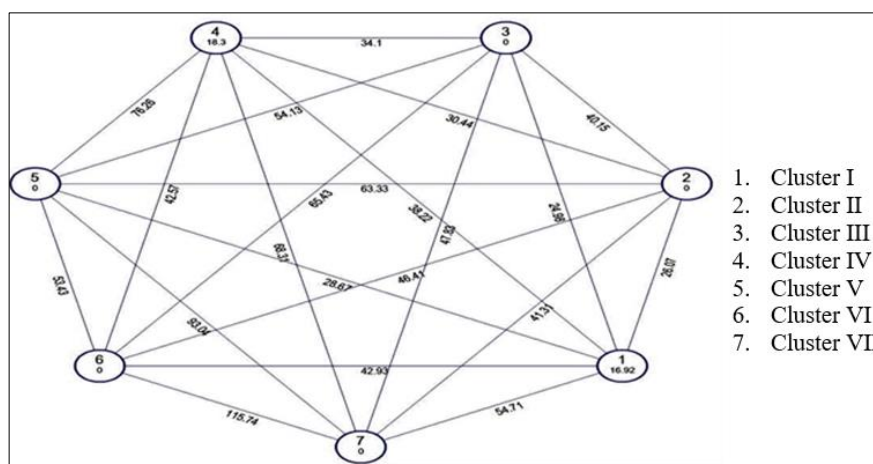


Fig 1: Clustering pattern in finger millet genotypes based on morphological character

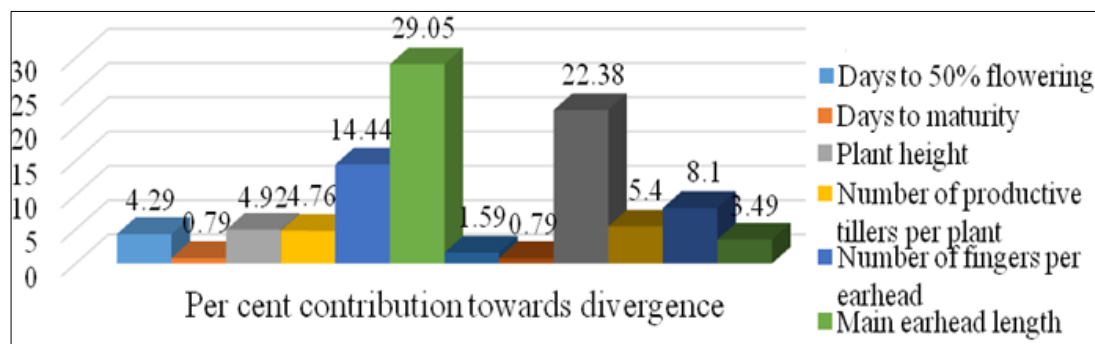


Fig 2: Contribution (%) of various traits of finger millet towards divergence.

Table 3: Cluster means for twelve characters in thirty-six genotypes of finger millet

Cluster	DF	DM	PH	PTP	FPE	MEL	FL	FW	TW	GY	SY	HI
Cluster I	94.18	128.54	122.39	2.85	6.30	9.27	7.37	0.84	2.69	8.30	23.88	25.89
Cluster II	84.00	115.67	120.67	3.57	5.17	6.77	5.40	0.77	2.53	6.55	24.02	21.45
Cluster III	97.00	135.33	119.20	2.83	8.13	8.97	7.27	0.73	3.04	10.85	24.52	30.80
Cluster IV	77.13	112.13	114.19	2.63	9.33	8.24	6.45	0.85	2.71	8.45	19.62	30.49
Cluster V	99.00	137.33	119.07	2.97	6.10	11.43	10.27	0.87	2.55	8.80	27.27	24.38
Cluster VI	87.00	119.67	92.00	2.33	8.17	8.77	6.07	0.67	2.38	5.20	15.45	25.29
Cluster VII	112.00	145.00	120.73	2.87	6.47	6.90	6.13	0.93	2.75	8.87	33.22	21.15

DF	Days to 50 % flowering	PTP	No. of productive tillers per plant	FL	Finger length (cm)	GY/P	Grain yield per plant (g)
DM	Days to maturity	FPE	Number of fingers per earhead	FW	Finger width (cm)	SY/P	Straw yield per plant (g)
PH	Plant height (cm)	MEL	Main ear head length (cm)	TW	1000-Grain weight (g)	HI	Harvest index (%)

Table 4: Contribution of twelve characters under study towards total divergence

Sr. No.	Characters	No. of time ranked first	Per cent contribution towards divergence
1	Days to 50% flowering	27	4.29
2	Days to maturity	5	0.79
3	Plant height (cm)	31	4.92
4	Number of productive tillers per plant	30	4.76
5	Number of fingers per earhead	91	14.44
6	Main earhead length (cm)	183	29.05
7	Finger length (cm)	10	1.59
8	Finger width (cm)	5	0.79
9	1000-Grain weight (g)	141	22.38
10	Grain yield per plant (g)	34	5.4
11	Straw yield per plant (g)	51	8.1
12	Harvest index (%)	22	3.49
	Total	630	100

Cluster means for different characters

Cluster mean for all the sixteen characters are presented in Table 3. The results clearly indicated appreciable difference among cluster means for most of the characters.

As far as cluster means are concerned, cluster I had the highest mean values for the character plant height (122.39). Cluster II had the highest mean values for the character number of productive tillers per plant (3.57) while, it had minimum cluster mean for characters viz., number of fingers per earhead (5.17), main earhead length (6.77) and finger length (5.40). Cluster III had the highest mean values for the characters viz., 1000 grain weight (3.04), grain yield per plant (10.85) and harvest index (30.80). Cluster IV had the highest mean values for number of fingers per earhead (9.33) while, it had minimum cluster mean for traits viz., days to 50% flowering (77.13) and days to maturity (112.13). Cluster V had the highest mean values for the traits viz., main earhead length (11.43) and finger length (10.27). Cluster VI had the minimum cluster mean values for traits viz., plant height (92.00), number of productive tillers per plant (2.33), finger width (0.67), 1000 grain weight (2.38), grain yield per plant (5.20) and straw yield per plant (15.45). Cluster VII had the highest mean values for the traits viz., days to 50% flowering

(112.00), days to maturity (145.00), finger width (0.93) and straw yield per plant (33.22) while, it had minimum cluster mean for harvest index (21.15).

Contribution of various characters towards genetic divergence

In the present study, main earhead length, 1000 grain weight, number of fingers per earhead, straw yield per plant, grain yield per plant contributed much more towards total genetic divergence (Table 4). Similar results were earlier obtained in this regard by Das *et al.* (2013^b)^[3] for main earhead length, number of fingers per earhead and grain yield per plant; Suryanarayana *et al.* (2014)^[13] for main earhead length and straw yield per plant and Patil *et al.* (2017)^[7, 8] as well as Saundarya Kumari and Singh (2015)^[11] for grain yield per plant. Therefore, these characters should be given due importance. Inter cluster distances indicated that the accessions included in the diverse clusters would be used in further crop improvement programme.

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