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Genetic Diversity among Finger Millet [*Eleusine coracana* (L.) Gaertn] Genotypes for Yield and Its Contributing Traits

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A B S T R A C T

The present investigation is carried out to study the genetic divergence among 35 finger millet genotypes for fourteen morphological characters using Mahalanobis D^2 statistics during *kharif*, 2014. D^2 statistics indicated that the genotypes studied were genetically diverse. The 35 genotypes of finger millet were grouped into 6 clusters irrespective of geographical diversity, indicating no parallelism between geographic and genetic diversity. Clusters I and VI were highest number of 8 genotypes, followed by cluster II and V with 7 genotypes and cluster III with 4 genotypes. Cluster IV was monogenotypic. The highest inter-cluster distances was observed between cluster IV and V followed by cluster IV and VI, cluster II and IV, cluster I and IV, cluster III and V and cluster III and IV suggesting the use of genotypes from these clusters to serve as potential parents for hybridization. Considering cluster mean and genetic distance the crossing of entry of clusters IV with entries of cluster V and those genotypes of cluster VI would be fruitful for obtaining transgressive segregants for developing high yielding and better quality finger millet varieties.

Keywords

Finger millet, Genetic divergence, D^2 statistic.

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Introduction

Finger millet (*Eleusine coracana* L. Gaertn., 2n=4x=36) belongs to the family *Poaceae*. Among millets it ranks third in importance after sorghum and pearl millets. Its wide adaptability to diverse environments and cultural conditions makes it a potential food crop. The term *Eleusine* is derived from Eleusis, an old epic city sacred to Demater, the Greek deity presiding over agriculture. The term coracana is derived from kurukkan, the singhali name of the grain. The word Ragi is derived from Sanskrit word "Rajika" means red. 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 per cent), carbohydrates (76.32 per cent) and fat (1.29 per cent). It is very rich in minerals (2.70 per cent) such as calcium (452mg/1000g), iron (3.90 mg/100g) and ash (3.90 per cent) which are the core ingredients of normal human diet (Pandey and Kumar, 2005). 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 per cent) 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 (Arun *et al.,* 2008). 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.

Materials and Methods

The experimental material for the present investigation was conducted during *Kharif*, 2014 at Research Block, Department of Crop Improvement, V. C. S. G. Uttarakhand University of Horticulture and Forestry, College of Forestry, Ranichauri Campus with thirty-five diverse genotypes of finger millets including three checks *viz*., PRM-1, PRM-2 and VL-149. The experiment was laid out in Randomized Complete Block Design with three replications. Each entry was represented by two rows of 3 meter length. The spacing of 22.5 cm within rows and 10 cm between the plants was followed. 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 area (cm^2), peduncle length (cm), number of leaves on main culm, number of productive tillers per plant, number of fingers per ear, finger length (cm), ear length (cm), biological yield per plant (g), harvest index (%), 1000 seed 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 thirty-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 thirty-five genotypes of finger millet were grouped into six different non-overlapping clusters (Table 1). Clusters I and VI were highest number of 8 genotypes, followed by cluster II and V with 7 genotypes and cluster III with 4 genotypes. Cluster IV had only one genotype IC-308771 formed single stocked cluster indicating wide diversity from set, as well as from each other. Kumar *et al.,* (2010) grouped 140 genotypes in 10 clusters.

Intra and inter cluster D^2 values were worked out using D^2 values from divergence analysis

(Table 2, Fig 1). Cluster III had maximum intra cluster distance (511.68) followed by cluster V (436.29), cluster I (349.92), cluster VI (203.72) and cluster II (162.95). This implies that these clusters have the genotypes with varied genetic architecture. The cluster VI (IC-308771) showed zero intra cluster distance due to monogenotypic nature. High intra-cluster genetic distance in cluster III was because of heterogeneous composition of that cluster. Collaborative results have also been given by Bedis *et al.*, 2007, Das *et al.*, (2013) and Wolie *et al.*, (2013).

Maximum inter-cluster genetic distance was observed between cluster IV and V (2297.81) followed by cluster IV and VI (2251.55). The inter cluster between cluster II and cluster IV (1969.80), cluster I and IV (1554.258), cluster III and cluster V (1458.44) and cluster III and cluster IV (1321.21) were also high. The clusters with higher inter-cluster distances indicated that the genotypes included in those clusters had high genetic variation and hybridization between genotypes of these cluster may result heterotic hybrids because of convergence of diverse genes scattered in parents to progeny. The minimum estimate for inter cluster distance was recorded between cluster I and II (375.69), followed by cluster V and VI (487.21) and cluster I and VI (509.76). The clusters with lowest inter-cluster distances indicated that genotypes present in these cluster pairs were genetically close to each other. The crosses between genotypes belonging to clusters separated by low inter cluster distance were likely to throw promising recombinants in the segregating generations. Similar results have also been obtained by Vidyadhar and Devi (2007), Kumar *et al.*, (2010), Sahu *et al.*, (2012), Harti *et al.*, (2013) and Shinde *et al.*, (2013).

Fig.1 A statistical distance ($\sqrt{D^2}$) among thirty-five genotypes of finger millet

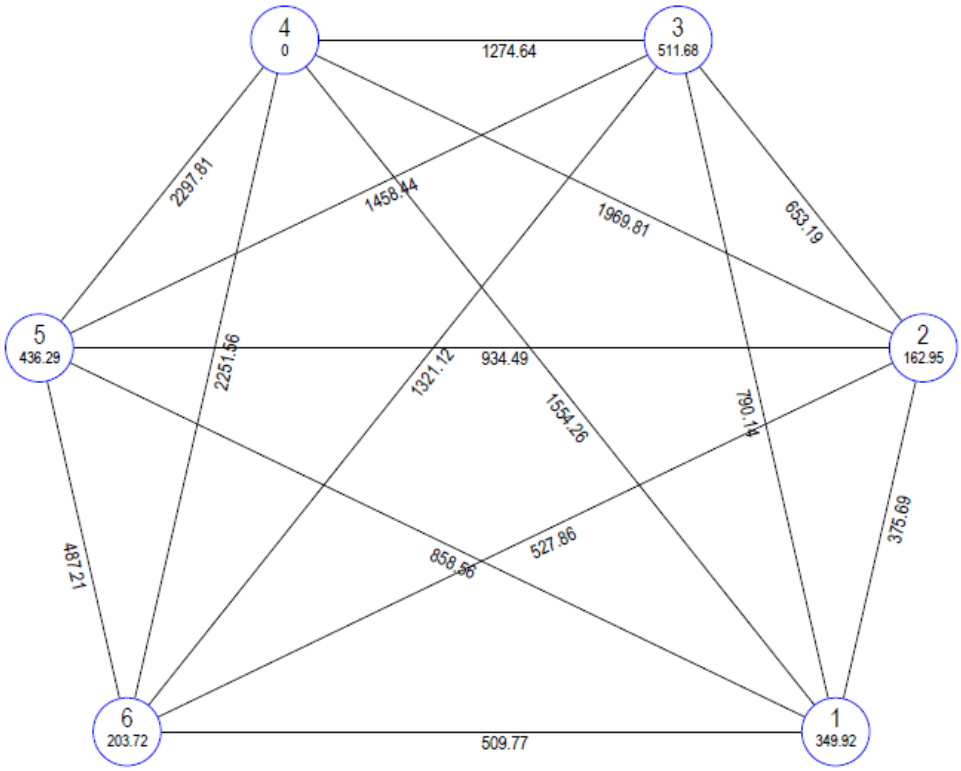

Table.1 Clustering pattern of 35 genotypes of finger millet on the basis of genetic divergence

Clusters	Number of genotypes	Genotypes
I	8	IC-308917, EC-522485, IC-257855, IC-308849, IC-308868, IC-308853, IC-354217, IC-354383
II	7	IC-520490, EC-522488, IC-3522490, IC-308899, IC-354422, IC-257862, IC-308928
III	4	IC-354384, IC-354410, PRM-2, EC-522482
IV	1	IC-308771
V	7	EC-130783, IC-3543177, EC-522495, VL-149, IC-354381, PRM-1, IC-354407
VI	8	IC-308905, EC-3522489, EC-533489, IC-308878, IC-308916, IC-308884, IC-308883, IC-308853

Table.2 Intra and inter cluster distance $\sqrt{D^2}$ values among 35 genotypes of finger millet

	I	II	III	IV	V	VI
I	**349.92**	375.69	790.14	1554.25	858.56	509.76
II		**162.95**	653.19	1969.80	934.49	527.85
III			**511.68**	1274.63	1458.44	1321.12
IV				**0.00**	2297.81	2251.55
V					**436.29**	487.21
VI						**203.72**

Table.3 Intra cluster group means for various components of 35 finger millet genotypes

S. No.	Characters	Cluster Means					
		I	II	III	IV	V	VI
1	**Days of 50% flowering**	102.04	96.04	102.16	135.66	97.81	96.62
2	**Days to maturity**	157.91	154.09	155.58	165.00	155.81	155.16
3	**Plant height (cm)**	86.61	92.26	74.93	84.06	80.77	92.68
4	**Flag leaf area (cm^2)**	23.04	22.63	25.63	22.78	23.80	21.25
5	**Peduncle length (cm)**	9.15	8.23	6.06	4.57	8.12	8.92
6	**No. of leaves on main culm**	9.64	9.70	11.11	12.83	10.24	9.66
7	**No. of productive tillers per plant**	2.97	2.06	2.18	2.63	2.85	3.05
8	**No. of fingers per ear**	7.33	7.52	7.28	6.60	7.84	7.49
9	**Finger length (cm)**	8.66	9.87	5.41	4.96	5.43	10.37
10	**Ear length (cm)**	10.12	10.61	6.37	6.68	6.12	11.25
11	**Biological yield per plant (g)**	32.64	30.21	21.92	36.33	50.83	47.58
12	**Harvest index (%)**	16.21	17.96	14.68	15.16	13.56	13.67
13	**1000 seed weight (g)**	2.70	2.73	2.32	2.13	2.67	2.57
14	**Grain yield per plant (g)**	5.21	5.42	3.31	5.51	6.77	6.46

Table.4 Contribution of different plant growth and grain yield characters to total divergence in 35 finger millet genotypes

S. No.	Characters	Number of times appearing first in ranking	Per cent contribution
1	**Days of 50% flowering**	48	8.07
2	**Days to maturity**	17	2.86
3	**Plant height (cm)**	2	0.34
4	**Flag leaf area (cm^2)**	47	7.90
5	**Peduncle length (cm)**	40	6.72
6	**No. of leaves on main culm**	5	0.84
7	**No. of productive tillers per plant**	48	8.07
8	**No. of fingers per ear**	2	0.34
9	**Finger length (cm)**	3	0.50
10	**Ear length (cm)**	45	7.56
11	**Biological yield per plant (g)**	321	52.44
12	**Harvest index (%)**	1	0.16
13	**1000 seed weight (g)**	25	4.20
14	**Grain yield per plant (g)**	0	00

Cluster group means for 14 characters are presented Table 3. Cluster I, having 8 genotypes showed highest cluster mean for peduncle length. Cluster II having 7 genotypes, exhibited highest cluster mean for harvest index and 1000 seed weight.

The 4 genotypes of cluster III resulting highest cluster mean for flag leaf area. The monogenotypic cluster IV resulting highest cluster mean for days to 50 per cent flowering, days to maturity and number of leaves on main culm.

Cluster V, which was represented by 7 entries, possessed highest cluster mean for number of fingers per ear, biological yield per plant and grain yield per plant. Cluster VI having 8 genotypes, exhibited highest cluster means for plant height, number of productive tillers per plant, finger length and ear length. On the basis of above results it is evident that cluster VI had maximum cluster means for most of desirable characters *viz.*, plant height, number of productive tillers per plant, finger length and ear length. 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 Bedis *et al.,* 2007 and 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 biological yield per plant contributed maximum (52.44 %) towards genetic divergence followed by days to 50 per cent flowering (8.07 %), number of productive tillers per plant (8.07 %), flag leaf area (7.90 %), ear length (7.56 %), peduncle length (6.72 %) and 1000 seed weight (4.20) while remaining 5 characters played negligently role less (<1%) in contributing genetic diversity.

The low contribution was however measured on other characters, *viz*., plant height (0.34 %), number of leaves on main culm (0.84 %), number of fingers per ear (0.34 %), finger

length (0.50 %) and grain yield per plant (0.00 %).

These were considered to be the most important characters for the genetic diversity point of view. The observation is in confirmed by Bedis *et al.,* 2007 and Shinde *et al.,* 2013.

Considering the high inter-cluster distances, cluster means and mean performance of genotypes, crossing of entry of clusters IV (IC-308771) with entries of cluster V (EC-130783, IC-3543177, EC-522495, VL-149, IC-354381, PRM-1,IC-354407) and those of cluster VI (IC-308905, EC-3522489, EC-533489, IC-308878, IC-308916, IC-308884, IC-308883, IC-308853) would be fruitful for obtaining transgressive segregants for developing high yielding and better quality finger millet varieties.

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