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RESEARCH

GENETIC ASSESSMENT OF FINGER MILLET (*ELEUSINE CORACANA* L.) GERMPLASM CULTIVATION FOR CROSSABILITY PARAMETERS AND GRAIN YIELD

Bhavna Sinha[1]*, Kishor Kumar[1], Khushboo Gupta[1], R.R. Kanwar[2], Prafull Kumar[2], N.K. Nag[3] and D.P. Singh[4]

Department of Genetics and Plant Breeding, S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur, Bastar 494001 (C.G.)
Department of Agronomy, S. G. College of Agriculture and Research Station Kumhrawand, Jagdalpur, Bastar 494001 (C.G.)
Department of Agricultural Statistics and Social Science, S. G. College of Agriculture and Research Station Kumhrawand, Jagdalpur, Bastar 494001 (C.G.)
Email:bhavnasinha642@gmail.com

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Abstract: The trail was conducted in Finger millet (*Eleusine coracana* L.) undertaken at the Research cum Instructional Farm of S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur, Bastar (C.G.) during *Kharif* 2023. The genetic divergence was estimated in finger millet developed by multivariate analysis using mahalanobis (1936). 100genotypes of finger millet grouped into six clusters based on D^2 analysis. The Cluster I and Cluster III was largest with 24 lines followed by Cluster II with 20 lines, Cluster IV with 17 lines and Cluster V with 10 lines but Cluster VI was lowest 9 lines.D^2 values were computed intra- and inter-cluster D^2 and D values using divergence analysis. The maximum intra-cluster distance was found in cluster IV indicating in within cluster. The highest inter- cluster distance was recorded between Cluster V and cluster IV followed by Cluster VI and II indicates a significant genetic distance between current generations. Cluster VI and II came next each the higher genetic divergence of these clusters and the higher level of heterotic expression and a range that then from mixing genotypes from these clusters in the resulting segregating populations.In current experiment of D^2 analysis suggested that there by exhibiting higher genetic diversity and thus genotypes of these cluster may be used for inter varietal hybridization proggramme for getting higher yielding recombinants in finger millet.

Keywords: Finger millet, *Eleusine coracana*, Genetic diversity, Cluster analysis

INTRODUCTION

Finger millet *Eleusine coracana* (L). (2n=4x=36,AABB) and exhibits morphological similarity to two weedy species, *E. coracanassp.africana* (2n = 36) and *E. indica* (2n = 18) is anannual herbaceous millet crop widely grown and consumed in Africa and Asia.It is self- pollinated and allotetraploid cereal crop and one of the most important nutraceutical millet crops belonging to the family Poaceae and sub family Cloridoideae. It is also known as bird's foot millet, coracana, African millet, ragi, and kurukkan. Ancient Indian Sanskrit literature, finger millet, one of the oldest plants in India, is known as "nrtta-kondaka," which translates to "Dance Dance." It is also known as "rajika" or "markataka" (Achaya, 2009).Millet is 6th cereal cropin terms of world agriculture production. Africa and Asia produce about 98% of the world's millets (Adebowale *et al*., 2012).The United Nations (UN) declared 2023 to be the "International Year of Millets" effort to increase millet production and enhance the general awareness of the crop. Its main benefit is that, while light loams and well-drained soils are preferred, it can be produced economically on poor sandy soil in low rainfall places (Balasubramanian *et al*.,2014).Finger millet is nutritionally comparable to rice and wheat and ranks 4th among millets in the world. It was first native & domesticate in Ethiopian highlands and Western Uganda (Mirza, 2019). Ragi is the third most popular millet in India, grown on 1.02 million hectares of land and yields in 1.39 million tonnes annually. Major millet-growing districtsin Chhattisgarh include Kawardha, Koriya, Jashpur, Sukma, Narayanpur, Bijapur, Baster, and Dantewada. Its average yield is 1394 kgha-1, with a total cultivated area of 0.4% and production of 0.1%.nutrient content found that finger millet contains comparatively higher amounts of calcium, potassium, and phosphorus in its fodder than maize and sorghum. It has higher levels of magnesium (137 mg 100 g^{-1}), potassium (408 mg

*Corresponding Author

100 g^{-1}), phosphorous (283 mg 100 g-1), copper (0.47 mg 100 g^{-1}), zinc (2.3 mg 100 g^{-1}), and iron (4.6 mg 100 g^{-1})(Deosthale *et al.*, 1970).Characterization and evaluation are essential requirements for both identifying the source of beneficial genes and making efficient use of germplasm. Before beginning any systematic breeding effort, it is important to have a thorough understanding of the type and extent of genetic diversity present in the gene pool.

MATERIALS AND METHODS

The current experiment study on genetic divergence in finger millet was carried out in *Kharif* 2023 at theInstructional cum Research farm of S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur, Bastar (C.G.), which is located in college campus. Positioned at 19°4'0" N and 82°2'0" E in Bastar plateau, at an elevation of 552 metres above mean sea level. The 100 accessions of finger millet was laid out as an Augmented Randomized Block design (ARBD) with 5 blocks with 4 check varieties-namely IR 01, CG Ragi 02, GPU 28 and GPU 67 in agriculture field. Seeds were sown in each block in theprepared field condition. Standard cultural practices and management techniques were followed to grow the crop. At harvest stage, quanlitative and quantitative characters were selected for determining the genetic diversity in finger millet.At the harvest stage,plant pigmentation at leaf juncture, seed colour, ear shape, DF-days to 50% flowering, DM-days to maturity, PH-plant heigth (cm), FLL-flag leaf length (cm), FLW-flag leaf width (cm), FL-finger length (cm), NOF-number of finger, NOPT-number of productive tillers, TW-test weight (g), HI-harvest index (%), FY-fodder yield, BY-biological yield and GY-grain yield. Estimation of genetic divergence was done by multivariate analysis using mahalanobis' (1936). D^2 statistic calculated as described by Rao (1952). The contributions of each trait to the divergence, intra and inter-cluster distances and cluster means were estimated In the current investigation.

RESULTS AND DISCUSSION

Genetic diversity give knowledge on genetic basic information on genotypes' genetic features, which is used to create breeding approaches to crop improvement. These studied are also useful in understanding the nature and extent of diversity that can be attributed to a variety of factors, such as crop sensitivity to the environment and genetic divergence. The Mahalanobis D^2 statistics approach help in quantifying the divergence between two populations that can be used as an index for selecting parents of different origins while clustering genotypes using Rao's Tocher approach. Mahalanobis' (1936) concept of D^2 statistics utilised plant breeders can effectively to classify genotypes into distinct groups based on genetic divergence. the basic concept behind cluster formation is calculating intra- and inter-cluster distances. The index is used to select parents with a diversity of backgrounds. Genetic divergence was measured for 50 different finger millet germplasms. These genotypes were categorized, by following Mahalanobis' D^2 as described by Rao (1952). The main concept underlying clusters classification involves determining intra- cluster and inter- cluster distance. The index is employed for choosing parents from a variety of backgrounds. Genetic divergence was evaluated a cross 100 distinct finger millet germplasm. These genotypes were divided using Mahalanobis D^2 as stated by Rao (1952).

Grouping of genotypes into cluster

The finger millet examined in this experiment is grouped into 6 clusters namely Cluster I, Cluster II, Cluster III, Cluster IV, Cluster V and Cluster VI. The clusters along with genotypes included in them are presented in (Table 1). The cluster I and cluster III was largest with 24 lines followed by cluster II with 20 lines, cluster IV with 17 lines and cluster V with 10 lines but cluster VI was lowest 9 lines. These results indicate a significant level of genetic diversity within the studied samples, making them a valuable source of genes with economically important traits. These genetic resources could be used in a hybridization program to separate desired offspring for the development of finger millet varieties,with high yield potential Mahalle (2020).An indicator for the relative genetic closeness of lines is clustering. The genotypes of the same cluster are considered to be highly closely related by origin, ancestry and genetic makeup compared to genotypes of different cluster. In transgressive breeding and crop improvement clustering is crucial in getting various parents in combination and it is advised that parents be selected from distinct clusters. The fundamental objective of cluster formation is to measure the intra- and inter-cluster distances, which be used as an indicator to selecting parents with various origins. The cluster elements D^2 values are used to calculate the means of the intra- and inter-cluster values. It will be more accurate to cross-genotype clusters with large inter-cluster distances in order desired outcomes. It can be used for various breeding objectives as well as a robust screening technique. Earlier it was utilized as practical criterion by Devaliya, *et al.*, (2017) carried out an experiment with 68 distinct finger millet genotypes. Using information from 13 quantitative traits, the degree of genetic divergence for yield and yield contributing factors was evaluated. The genotypes studied in this study were genetically varied, as indicated by the D^2 statistic. Based on genetic distances, eight clusters containing the eight genotypes under research were identified. Six clusters are solitary, with Cluster I having the most genotypes (60), followed by Cluster

VII (2 genotypes) and Cluster III (2 genotypes). The largest distance between clusters was found in clusters III and VIII.Based on D^2 values, (Kumari and Singh 2015) defined six groups of finger millet genotypes and concluded that there was no formal association between geographic diversity and genetic diversity. Earlier it was also used as viable criteria for effective selection and other breeding purposes (Suryanarayana*et al*., 2014 Kumari and Singh 2015). The cluster formation in kodomillet was reported by Nirubana*et al*., (2017),Mahanthesha*et al*., (2017)and Thakur *et al*., (2018).

Intra and inter cluster distances

Cluster formation and intra- and inter-cluster divergence measurements are used to select genetically diverse parents from different clusters. The statistical distance (D) is thought to serve as a genetic diversity measure. D^2 values were computed intra- and inter-cluster D^2 and D values using divergence analysis. The maximum intra- cluster distance was found in cluster IV (2.768), followed by cluster I (2.757), cluster II (2.677), cluster III (2.581), cluster VI (2.513) and intra- cluster distance was recorded for the cluster V (2.374). Table 4.7 display the intra- cluster distance among different clusters. This suggests the genotypes within each of these clusters have distinct genetic makeup. Minimum intra-cluster shows the genotypes measure of genetic closeness. Cluster V and cluster IV had the highest inter- cluster distance, which were (4.662). Higher inter- cluster distance indicates a significant genetic distance between current generations. Cluster VI and II came next (4.393) each the higher genetic divergence of these clusters and the higher level of heterotic expression and a range that then from mixing genotypes from these clusters in the resulting segregating populations. Parallel results work by Wolie and Belete (2013) reported that genetic variability and divergence in a few collections of Ethiopian finger millet germplasm using Mahalanobis D^2 statistics. Finger millet germplasmswere separated into eight clusters for the purpose of multivariate analysis in the genetic divergence analysis. While cluster VII and cluster VIII had thegreatest inter-cluster distance (D^2=1280), cluster VIII had the highest intra-cluster D^2 value (D^2=7.568). The study also showed that, although germplasms collected from different geographic areas were grouped together in a single cluster, germplasms collected from the same geographic area were divided into distinct cluster groups.Meanwhile, cluster IV and II had the lowest D^2 value (5.44), indicating that there is less genetic variation in the genotypes of these two clusters. The extent to which these loci recombine in the F_2, F_3, and next generations will affect the success of breeding programmes and the value of breeding material produced. The number of contrasting alleles at the desired loci will increase with increasing parental distance. Mahanthesha(2017) observed highest average inter-cluster D^2 in their studies, indicates greater genetic divergence among every cluster and crossing of genotypes from these two clusters produces individuals exhibiting higher heterosis.Itwas noticed that lines with high cluster mean values for a particular character might be used in a breeding program for trait enhancement. Sao *et al*., (2016)studied intra and inter cluster divergence in kodomillet and found variability for most of the traits.

Cluster means for different Quantitative characters

The cluster means for all 13 characters shows table 2 and 3. Appreciable differences between clusters were observed for the characters studied which days to 50% flowering, days to maturity, plant heigth (cm), flag leaf length (cm), flag leaf width (cm), finger length (cm), number of fingers, number of productive tillers, test weight (g), harvest index (%), fodder yield, biological yield and grain yield. Clusters I genotype include 24 genotypes none of the character in Cluster I had the high mean value viz. number of productive tillers (1.67) had the high mean value. Cluster II genotype include 20 had the highest mean value for none of the traits. Cluster III include 24 genotypes had the highest mean value for none of the traits. Cluster IV include 17 genotypes recorded the maximum number of highest clusters mean values for traits viz. days to 50% flowering (77.78), days to maturity (112.60), finger length (7.32), number of finger (5.62), harvest index (28.32), fodder yield (54.63), biological yield (76.52) and grain yield (21.68). cluster V include 10 genotypes recorded the maximum number of highestcluster mean values for traits viz. test weight (4.32). whereas clusters VI include 9 genotypes observed maximum number of highest cluster mean values for traits viz. plant height (102.81), flag leaf length (32.16) and flag leaf width (1.16). parallel result work by Shinde*et al*., (2013) demonstrated that there was a genetic relationship between 41 genotypes of finger millet that were identified using D^2 statistics from different geographic areas. 41 genotypes were divided into seven groupings. Clusters II, I, V, VI, and III had 17, 10, 7, 3, and 2 genotypes, respectively. Significant divergence from other clusters has been shown by the mono-genotypic nature of clusters IV and VIII.Since most of the strains had the same origin and were found to be components of seven clusters, it was clear that there was a significant amount of genetic variation among the material that shared the same geographic origin. The characters with the highest divergence were related with the iron content (70.12), plant height (11.72%), days to physiological

maturity (7.07%), and days to 50% flowering (5.49%).

CONCLUSION

100 accessions of finger millet were categorized into 6 Clusters in Which maximum no. of genotypes were found in cluster I & III with 24 finger millet genotypes followed by cluster II with 20 genotypes, cluster IV with 17 genotypes, cluster V with 10 genotypes cluster VI with 9 genotypes. Maximum intra-cluster distance was found in cluster IV (2.768) and maximum inter cluster distance was observed between cluster IV and Cluster V (4.662), there by exhibiting higher genetic diversity and thus genotypes of these cluster may be used for inter varietal hybridization programme for getting higher yielding recombinants.

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Table 1: Number of genotypes in each cluster based in Mahalanobis' D^2 value in finger millet

Clusters	Number of genotypes	Genotypes
I	24	ICO476882, GEC-215, GEC-10, ICO476520, GEC-325, GEC-27, ICO476711, ICO476636, GEC-137, ICO477659-X,ICO477561,ICO587965, GEC-170,ICO4776,ICO476877, ICO477678,ICO477385,ICO476882, GEC-488,ICO587981,ICO477890,GEC-92, GEC-93, GEC-161
II	20	GEC-314, ICO476216, GEC-517, GEC-21,GEC-147,ICO477159,GEC-331, ICO476541, GEC-238, ICO476539, GEC- 341, GEC-61, GEC-144, GEC-252, ICO477157, GEC-58, ICO477963, ICO477264,ICO477312,GEC-294.
III	24	ICO477304, ICO476838, ICO477510, GEC-112,GEC-222,GEC-420,ICO4777831, ICO477132, ICO475933, ICO477340-X, GEC-145, GEC-47, GEC-348, GEC-251, ICO477156-X, GEC-362, ICO587964, ICO476921, GEC-369, GEC-414, ICO477382,ICO477963,GEC-297, GEC- 398.
IV	17	GEC-421, ICO477503, GEC-476, ICO476711,ICO476921,GEC-222,GEC-53, GEC-452, ICO477659, GEC-86, GEC-297, ICO477496, GEC-100, GEC-176, GEC-127, ICO477156,ICO477045
V	10	ICO588007, GEC-11, ICO476864, GEC-46,ICO4777650,ICO477560,GEC- 176, GEC-174,ICO587982, ICO476786
VI	9	GEC-503, ICO588007, GEC-446, GEC-249,ICO477171,ICO477274,GEC- 370, GEC-181, ICO477496

Table 2: Mean inter and intra-cluster D^2 value values in 6 clusters of fingers millet

Clusters	I	II	III	IV	V	VI
I	**2.757**					
II	3.624	**2.677**				
III	3.353	4.015	**2.581**			
IV	3.171	5.44	3.806	**2.768**		
V	2.905	3.115	3.451	4.662	**2.374**	
VI	3.465	4.393	3.644	3.884	3.478	**2.513**

Table 3: Cluster mean component of 6 clusters of finger millet

Clusters	DF	DM	PH (cm)	FLL (cm)	FLW (cm)	FL (cm)	NOF	NOPT	TW	HI(%)	FY	BY	GY
I Mean	72.79	108.67	94.22	29.38	0.88	8.13	6.54	1.67	4.11	22.00	48.96	63.46	13.94
SE±	5.51	6.13	7.64	3.06	0.07	0.90	0.88	0.48	0.21	2.68	2.24	4.69	2.72
II Mean	68.35	99.75	97.20	30.59	0.86	6.86	5.50	1.40	4.18	23.88	27.84	36.95	8.79
SE±	4.53	7.79	7.93	3.36	0.09	1.79	1.50	0.50	0.11	1.55	2.23	3.75	1.31
III Mean	69.58	105.08	96.21	26.56	0.82	4.77	3.08	1.00	4.20	23.41	48.83	64.27	15.16
SE±	7.10	9.04	7.03	2.60	0.07	1.08	1.10	0.00	0.09	3.33	3.78	7.17	3.73
IV Mean	77.78	112.60	95.31	31.84	0.93	7.32	5.62	1.26	4.19	28.32	54.63	76.52	21.68
SE±	4.10	5.01	8.79	3.83	0.08	1.78	1.62	0.41	0.09	2.14	6.07	9.02	3.46
V Mean	65.90	96.50	101.57	31.02	0.95	6.96	5.50	1.60	4.32	20.05	46.02	57.62	11.53
SE±	3.14	4.58	8.08	3.30	0.08	1.11	1.35	0.52	0.13	1.49	3.46	3.99	1.11
VI Mean	75.78	111.67	102.81	32.16	1.16	5.78	4.56	1.00	4.16	21.03	48.03	60.55	12.91
SE±	5.89	4.95	3.77	2.85	0.21	1.19	1.51	0.00	0.07	2.77	2.37	4.87	2.62

DF-days to 50% flowering, DM-days to maturity, PH-plant heigth (cm), FLL-flag leaf length (cm), FLW-flag leaf width (cm), FL-finger length (cm),NOF-numberoffingers,NOPT-numberofproductivetillers,TW-testweight(g),HI-harvestindex(%),FY-fodderyield,BY-biologicalyield GY-grain yield.

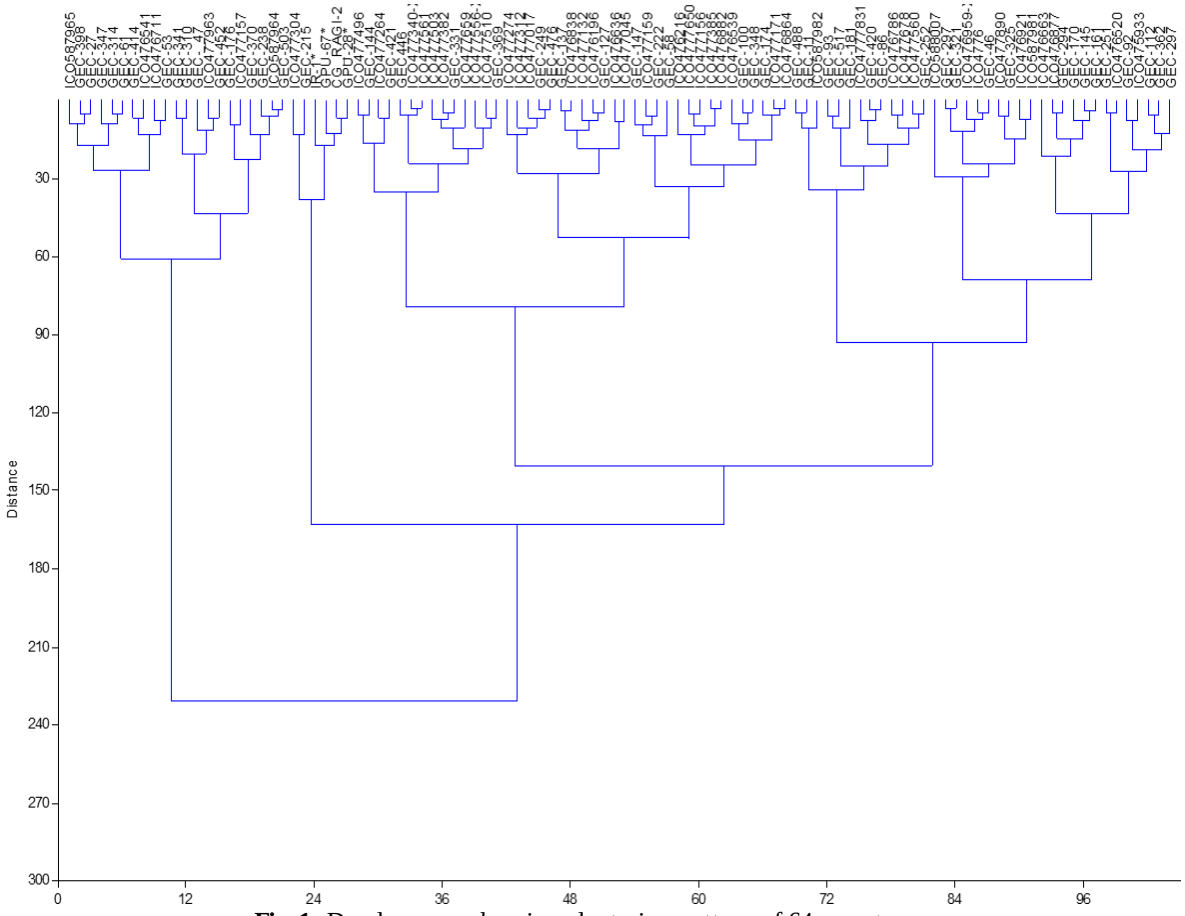

Fig 1: Dendrogram showing clustering pattern of 64 genotypes

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