Available online at www.ijpab.com

DOI: http://dx.doi.org/10.18782/2320-7051.2764

ISSN: 2320 – 7051

Int. J. Pure App. Biosci. **5 (3):** 373-377 (2017)

Research Article

International Journal of Pure & Applied Bioscience

OPEN ACCESS

Study of Genetic Divergence in Finger Millet (*Eleusine coracana* (L.) Gaertn) Germplasm

Mahanthesha M.[1*], M. Sujatha[2], S. R. Pandravada[3] and Ashok Kumar Meena[4]

[124]Department of Genetics and Plant Breeding, College of Agriculture, Rajendranagar, ANGRAU, Hyderabad

[3]Department of Economic Botany, National Bureau of Plant Genetic Resources, Regional station, Hyderabad

*Corresponding Author E-mail: manth54@gmail.com

Received: 28.03.2017 | Revised: 10.04.2017 | Accepted: 11.04.2017

ABSTRACT

Genetic divergence was studied in finger millet with 11 characters viz., grain yield per plant, main ear width, total no. of basal tillers per plant, total no. of fingers on the main ear, finger width, main ear length, plant height, no. of leaves on the main tiller, total productive tillers per plant, finger length and grain yield per plot, which partitioned the 48 germplasm lines into eight clusters. Maximum number of germplasm lines (24) were included in cluster I followed by twelve germplasmlines in cluster II, five germplasm lines in cluster IV, cluster VI with three genotypes and one each in cluster III, V, VII and VIII. The maximum intra-cluster distance was shown by cluster VI. Maximum divergence was observed between cluster VI and VIII, while minimum was between cluster I and V suggesting, more variability in genetic makeup of germplasm lines included in these clusters.

Among the 11 quantitative traits studied, the most important trait contributing to the divergence was grain yield per plant followed by main ear width, total no. of basal tillers per plant, total no. of fingers on the main ear and finger width. Usefulness of parents has been identified based on genetic divergence for improving finger millet. Higher yielding clusters were VI, II and IV.

Key words: *Finger Millet, Cluster, Diversity, Divergence.*

INTRODUCTION

Finger millet (*Eleusine coracana* (L.) Gaert) is cultivated under varied ecological conditions for both grain and fodder purposes in Africa and South Asia. It ranks fourth in importance among millets in the world.

In India, it is very popularly known as 'ragi' and is grown in an area of two million hectares with a production of 2.6 million tonnes. Finger millet provides staple food for a large section of farming community and economically weaker sections in many parts of India. Important finger millet growing states are Karnataka, Tamil Nadu, Andhra Pradesh, Maharashtra, Orissa, Jharkhand, Chattishgarh and Uttarakhand.

Cite this article: Mahanthesha, M., Sujatha, M., Pandravada, S.R. and Meena, A.K., Study of Genetic Divergence in Finger Millet (*Eleusine coracana* (L.) Gaertn) Germplasm, *Int. J. Pure App. Biosci.* **5(3):** 373-377 (2017). doi: http://dx.doi.org/10.18782/2320-7051.2764

The higher fibre content of finger millet helps in many ways as it prevents constipation, high cholesterol formation and intestinal cancer. Hence, people suffering from diabetics are advised to eat finger millet and other small millets instead of rice[1].

This crop has accumulated considerable diversity over the years for vegetative, reproductive and physiological traits. 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. 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 D^2 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 germplasms available in India.

MATERIAL AND METHODS

The experimental materials consisting 48 genetically diverse genotypes of finger millet were evaluated in National Bureau of Plant Genetic Resources (NBPGR), regional station, Hyderabad, Andhra Pradesh. A randomized block design (RBD) with three replications during *Kharif* 2013. Recommended package of practices were followed to raise good and healthy crop stand.

Randomaly three competitive plants were selected from each replication and observations were recorded for eleven quantitative traits *viz.*, Plant height (cm), total no. of basal tillers per plant, no. of leaves on the main tiller, productive tillers per plant, main ear length (cm), main ear width (cm), finger length (cm), finger width (cm), total no. of finger on the main ear, grain yield per plant (g) and grain yield per plot (g). The mean values were subjected to statistical analysis. Wilk's criterion was used to test the significance of difference in mean values for all the studied traits. Genetic divergence was calculated following Mahalanobis's D^2 statistics[2] and clustering of germplasms was done on the basis of D^2 values according to Tocher's method as described by Rao[3]. Statistical analysis was done using WINDOSTAT^{TM} program.

RESULTS AND DISCUSSION

The quantitative assessment of genetic divergence was made by adopting Mahalanobis D^2 statistic for yield and its contributing characters. Genetic divergence was estimated between 48 finger millet germplasm lines and the results obtained from the study are presented below. Wilk's 'V' (statistic) criterionwas used to test the significant differences between the groupsbased on the pooled effects of all the characters. The significance of 'V' (statistic) value was tested by % at 5 degrees of freedom. The 'V' statistic value was highlysignificant indicating that the genotypes differed significantly when all the characters were considered simultaneously. The significance of 48 genotypes in the analysis of variance of dispersion clearly indicated the significant pooled effect of all the characters studied between different genotypes. Hence, further analysis was made to estimate D^2 analysis.

The correlated unstandardized means of 11 quantitative characters studied were transformed to standardized uncorrelated set of variables by using pivotal condensation method. The statistical distance (Mahalanobis's D^2 value) between a pair of genotypes was obtained as sum of squares of differences between pairs of corresponding uncorrelated values of any two genotypes. These values were considered at a time and these were used for final grouping of genotypes.

Fourty eight genotypes were grouped into eight clusters based on D^2 values using Tocher's method[3] such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters.The distribution of genotypes into various clusters is shown in Table 1. Out of eight clusters, cluster I was the largest comprising of 24 genotypes followed by clusters II with 12 genotypes, cluster IV with five genotypes, cluster VI with three genotypes and clusters III, V, VII, and VIII with one genotype each indicating high degree of heterogeneity among the genotypes.

Table 1: Cluster classification of finger millet germplasm (Tocher's method)

Cluster	Number of genotypes	Germplasms
I	**24**	13434, 13484, 13486, 13487, 13489-1, 13492, 13502, 13523, 13555, 13567, 13652, 13661, 13665, 13672, 13673, 13674, 13676, 13677, 13678, 13689, 13690, 13691, GPU-45, PR-202
II	**12**	13426, 13517, 13539, 13542, 13565, 13568, 13569, 13571, 13710, GPU-67, VL-149, VR-708
III	**1**	13651
IV	**5**	13631, 13632, 13709, 13712, 13713
V	**1**	13660
VI	**3**	13528, 13570, 13675
VII	**1**	13433
VIII	**1**	13650

The number of times that each of the 15 characters appeared in first rank and its respective per cent contribution towards genetic divergence. The results showed that the contribution of grain yield per plant was highest towards genetic divergence (61.88%) by taking 698 times ranking first, followed by main ear width (14.54%) by 164 times, total no. of basal tillers per plant (10.28%) by 116 times, total fingers on the main ear (3.63%) by 41 times, finger width (3.10%) by 35 times, main ear length (1.95%) by 22 times, plant height (1.42%) by 16 times, no. of leaves on the main tiller (1.24%) by 14 times, productive tillers per plant (0.89%) by 10 times, finger length (0.71%) by 8 times and grain yield per plot (0.35%) by 4 times, respectively to the genetic divergence in decreasing order.

Among the 11 quantitative characters studied, the most important character contributing to the divergence was grain yield per plant followed by main ear width, total no. of basal tillers per plant, total no. of fingers on the main ear and finger width.

Intra-cluster D^2 values ranged from zero (cluster III, V, VII and VIII) to 24.20 (cluster VI). Maximum intra-cluster distance was observed in cluster VI (24.20), followed by cluster IV (19.80), cluster II (15.60) and cluster I (14.82). The intra-cluster distance varied from a maximum 24.20 for cluster VI to minimum 14.82 for cluster I having 4 genotypes though it was zero for solitary clusters (III, V, VII, and VIII) (Table 2). This reveals that genotypes occupying the same cluster have low level of diversity and selection of parents with in the cluster may not be considered promising as has been reported by Kumar *et al*.[4].

From the inter-cluster D^2 values of the eight clusters, it can be seen that the highest divergence occurred between cluster VI and VIII (270.27), followed by cluster II and VIII (149.08), cluster I and VIII (65.93), cluster VII and VIII (52.41), cluster IV and VIII (40.96), cluster V and VIII (39.56) and cluster III and VIII (35.76).

Table 2: Intra (diagonal) and inter-clusters D^2 value and extent of diversity among the clusters

Clusters	I	II	III	IV	V	VI	VII	VIII
I	3.85 **(14.82)**	6.44 **(41.47)**	4.98 **(24.80)**	6.13 **(37.57)**	5.10 **(26.01)**	10.96 **(120.12)**	5.92 **(35.04)**	8.12 **(65.93)**
II		3.95 **(15.60)**	9.45 **(89.30)**	8.23 **(67.73)**	9.17 **(84.08)**	6.60 **(43.56)**	9.42 **(88.73)**	12.21 **(149.08)**
III			0.00 **(0.00)**	6.95 **(48.30)**	4.16 **(17.30)**	14.07 **(197.96)**	6.00 **(36.00)**	5.98 **(35.76)**
IV				4.45 **(19.80)**	6.49 **(42.12)**	12.04 **(144.96)**	6.80 **(46.24)**	6.40 **(40.96)**
V					0.00 **(0.00)**	13.69 **(187.41)**	5.74 **(32.94)**	6.29 **(39.56)**
VI						4.92 **(24.20)**	14.32 **(205.06)**	16.44 **(270.27)**
VII							0.00 **(0.00)**	7.24 **(52.41)**
VIII								0.00 **(0.00)**

The inter-cluster D^2 values ranged widely with minimum value of 14.82 between clusters I and V and maximum value of 270.27 between clusters VI and VIII indicating high diversity among the genotypes of these clusters. The maximum amount of heterosis is expected from the crosses with parents belonging to the most divergent clusters has been reported by Kumar *et al.*[4], Anantharaju and Meenakshiganesan[5] and Kadam[6]. Hence, it is desirable to select the genotypes from the cluster showinghigh inter-cluster distance in breeding programme for obtaining the desirable segregants. The inter-cluster distances were higher than the intra-cluster distances indicating the presence of wider genetic diversity between the clusters rather than within the clusters.

The cluster means for each of eleven characters are presented in Table 3. From the data it can be seen that considerable differences existed for all the characters under study. The data indicated that the cluster mean for plant height was highest in cluster VII (90 cm) and the lowest in cluster V (28.33 cm). No. of basal tillers per plant was highest in cluster VIII (16) and lowest in cluster VII (6.67). No. of leaves on the main tiller was highest in cluster VII (10.67) and lowest in cluster IV (7.67). A productive tiller per plant was highest in cluster VIII (17.67) and lowest in cluster VII (6.33). Cluster VII recorded the highest main ear length (13.33 cm) and the lowest was recorded in the cluster III (6.33 cm). Main ear width was highest in cluster IV (15.00 cm) and lowest in cluster III (5.33 cm). Finger length was recorded highest in cluster VII (10.67 cm) and lowest in cluster III (5.00 cm). Cluster VI recorded highest finger width (1.00 cm) and the lowest was recorded in the cluster III (0.81 cm). Total fingers on the main ear were highest in cluster VII (10.00) and lowest in cluster VIII (6.33). Grain yield per plant was highest in cluster VI (86.22) and lowest in cluster VIII (8.33). Grain yield per plot was highest in cluster VI (2653.33) and lowest in cluster VIII (250). The result indicates that selection of genotypes having high values for particular trait could be made and used in the hybridization programme for improvement of that character.

Genotype groups into cluster VIII were low yielder for grain yield per plant associated with very low grain yield per plot. Genotype groups in cluster III were low grain yielder, short main ear length, main ear width, finger length and finger width. These results have been reported by Kumar *et al.*[4] and Reddy *et al.*[7].

Table3: Mean values of clusters for 11 characters in 48 finger millet germplasm (Tocher's method)

Cluster	Plant height (cm)	No. of basal tillers/ plant	No. of leaves on the main tiller	Productive tillers/Plant	Main ear length (cm)	Main ear width (cm)	Finger length (cm)	Finger width (cm)	Total fingers on the main ear	Grain yield/ plant (g)	Grain yield/plot (g)
I	66.19	10.33	8.08	9.72	7.39	6.88	6.01	0.95	8.93	28.29	857.64
II	76.97	9.58	8.50	9.31	7.96	7.54	6.14	0.97	9.25	55.89	1700.28
III	64.67	13.33	8.67	13.33	**6.33**	**5.33**	**5.00**	**0.81**	8.67	12.00	360.00
IV	69.60	13.13	**7.67**	13.00	10.07	**15.00**	9.60	0.95	8.33	31.73	971.33
V	**28.33**	11.00	8.00	7.67	7.67	7.00	6.00	0.82	7.33	12.00	360.00
VI	73.67	13.00	9.00	13.00	8.00	7.11	6.56	**1.00**	8.00	**86.22**	**2653.33**
VII	**90.00**	**6.67**	**10.67**	**6.33**	**13.33**	10.33	**10.67**	0.94	**10.00**	9.33	320.00
VIII	54.67	**16.00**	9.00	**17.67**	11.00	14.00	8.67	0.92	**6.33**	**8.33**	**250.00**

CONCLUSION

It is observed that no cluster contained at least one genotype with all the desirable traits, which ruled out the possibility of selecting directly one genotype for immediate use. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

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