Electronic Journal of Plant Breeding, 4(3): 1242-1245 (Sep 2013)
ISSN 0975-928X

Research Note

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

S. R. Shinde[1], S. V. Desai[2], and R. M. Pawar[3]
[1,2] Mahatma Phule Krishi Vidyapeeth, Rahuri.
[3]Department of Agricultural Botany, BV's College of Agriculture, Kadegaon,Tal - Kadegaon, Dist - Sangli.
PIN – 415 304.
Email: ranveer_1972@rediffmail.com

(Received: 03 Jun 2013; Accepted: 04 Sep 2013)

Abstract
The genetic distance for 41 genotypes of finger millet collected from different geographical areas was estimated using D^2 statistics. These genotypes were grouped into seven clusters. Cluster II, I, V, VI, and III comprised 17, 10, 7, 3 and 2 genotypes, respectively. The clusters IV and VII were mono-genotypic indicating wide divergence from other clusters. Most of the strains were from same origin and found to be one or more components of seven clusters indicating the presence of wide genetic variability among the material belonging to same geographical origin. The highest inter-cluster distance was observed between clusters II and VII followed by IV and VII suggesting the use of genotypes from these clusters to serve as potential parents for hybridization. The characters iron content (70.12%) contributed maximum towards divergence followed by plant height (11.72%) , days to physiological maturity (7.07%) and days to 50% flowering (5.49%).

Key words
Eleusine coracana, .Genetic diversity, Cluster analysis, D^2 analysis

After sorghum and pearl millet, finger millet is an important cereal crop amongst millets in the country. It is cultivated mostly as rainfed crop in India for its valued food grains and is adaptable to wide range of geographical areas and agro-ecological diversity in African and Asian countries. In India, over 50 per cent of the crop area (0.9 million ha) is in Karnataka with higher productivity (1.9 t/ha) than national average. A logical way to start any breeding programme for crop improvement is to survey the variation present in the germplasm. Assessment of genetic diversity in germplasm collection can facilitate classification and identification of diverse genotypes. Precise information on the nature and degree of genetic divergence helps the plant breeder in choosing the diverse parents for specific utilization in hybridization. In breeding programme, progenies derived from diverse parents selected on the basis of genetic divergence analysis are expected to show a broad spectrum of genetic variability, providing a greater scope for isolating transgressive segregants in advanced generations (Singh and Mishra, 1996) and promising heterotic effect may be observed in early generation. Therefore, the present study was undertaken to identify suitable finger millet parents having diverse characters through genetic divergence analysis.

A set of 41 genotypes of finger millet obtained from AICRP, Igatpuri were evaluated in a randomized block design experiment with three replications at Post Graduate Research Farm, College of Agriculture, Kolhapur during *Kharif*-2011. Each genotype was represented by a single row plot of 3 m length with inter and intra-row spacing of 22.5 cm and 10 cm, respectively. Recommended agronomic practices were followed to raise a good crop. Data were recorded on five randomly selected competitive plants at different growth stages of the crop for the characters listed in Table 3. Average data of these five plants were utilized for the statistical analysis. The genetic divergence was computed using Mahalanobis (1936) D^2 statistics among all of 41 genotypes for the characters *viz*., days to 50% flowering, days to physiological maturity, productive tillers / pant, plant height (cm), finger length (cm), number of fingers / main ear head, main ear head spread (cm), 1000 grain weight (g), harvest index (%), iron content (mg/100g), protein content (%) and grain yield / plant (g). Based on the genetic distance, all the genotypes were grouped into different clusters (Rao, 1952).

The analysis of variance revealed the significant differences among the genotypes for all the 12 characters under study. Based on relative magnitude of D^2 values, 41 genotypes were grouped into seven clusters (Table 1). The distribution pattern of the genotypes into clusters indicated that cluster II was the largest, containing 17 genotypes followed by cluster I with 10 genotypes, cluster V with seven genotypes, cluster VI with three genotypes and cluster III with two genotypes. Two clusters IV and VII were solitary containing one genotype each.

The genotypes collected from the same origin (i.e. IGPFM series from Igatpuri) were grouped into different clusters and the genotypes belonging to different origins were grouped into a same cluster (Cluster VI and I). This grouping pattern of the genotypes suggested no parallelism between genetic divergence and geographical distribution of the genotypes. Murty and Arunachalam (1966) stated that genetic drift and selection in different environments could cause greater genetic diversity than geographical distance. Further, the free

exchange of seed material among different regions consequently causes character constellations because of human interference and material may lose its individuality. Similar findings were reported by Nagarajan and Prasad (1980) in fox-tail millet and Hussaini *et al*. (1977) and Dinesh Kumar *et al*. (2010) in finger millet.

The average intra and inter-cluster distance analysis indicated that the maximum intra-cluster distance was observed for cluster V followed by cluster II, cluster VI, cluster III and cluster I (Table 2). This suggested that the genotypes in cluster V were relatively more diverse among themselves. However, in all cases, the inter-cluster distances were greater than the intra-cluster distances implying presence of greater degree of genetic diversity between the genotypes of two clusters than the genotypes present within the cluster. From the inter-cluster distances for seven clusters (Table 2), it could be seen that the highest divergence was observed between cluster II and VII (D=53.64) followed by cluster IV and VII (D=53.53) and cluster II and VII (D=48.10), indicating the presence of greater diversity between genotypes of these groups. Hence, crossing between genotypes belonging to these clusters might result in high heterosis, which could be exploited in crop improvement. The least inter-cluster distance was noticed between cluster II and IV (D=20.97) indicating the close relationship and similarity for most of the genotypes of these two clusters.

The cluster means for various characters are presented in Table 3. The cluster III had the highest mean value for grain yield/plant, days to physiological maturity, productive tillers/plant and plant height. Similarly, genotypes included in cluster IV recorded the highest mean values for 1000 grain weight, harvest index and protein content and genotypes in cluster V recorded the highest mean values for finger length and main ear-head spread. Cluster VI exhibited early maturing genotypes, whereas cluster II recorded highest mean value for number of fingers / main ear-head and cluster VII exhibited maximum iron content.

The character iron content (70.12%) contributed maximum towards divergence followed by plant height (11.71%), days to physiological maturity (7.07%) and days to 50 per cent flowering (5.49%), while protein content, harvest index and number of fingers/main ear-head contributed very low towards divergence (Table 3).

Hence, on the basis of inter-cluster distances, cluster means, *per se* performance in the present investigation, the five genotypes *viz*., IGPFM-11-30, IGPFM-11-38, IGPFM-11-04, IGPFM-11-05 and PES-400 were found superior and could be selected as potential parents for hybridization programme in the improvement of finger millet.

References

Dinesh Kumar, V., Tyagi, Ramesh, B. and Pal, S. 2010. Genetic diversity in finger millet (*Eleusine coracana* L.). *Crop Improv*., **37** (1): 25-28.

Hussaini, S. H., Goodman, M. M. and Timothy, D. H. 1977. Multivariate analysis and the geographical distribution of the world collection of finger millet. *Crop Sci.,* **17** (2): 257-263.

Mahalanobis, P. C. 1936. On the generalized distance in statistics. *Proceed.Nat. Academy of Sci.,* **11**(1): 49-55.

Murty, B. R. and Arunachalam, V. 1966. The nature of divergence in relation to breeding system in some crop plants. *Indian J. Genet.,* **26**(1): 188-198.

Nagarajan, K. and Prasad, M. V. 1980. Studies on genetic diversity in fox-tail millet (*Setaria italica*). *Madras agric. J.*, **67**(1): 28-38.

Rao, C. R. 1952. *Advanced statistical methods in biometrical research*. John Wiley and Sons, New York, pp.383.

Singh, N. K. and Mishra, S. N. 1996. Genetic divergence in oat germplasm. *Indian J. Genet.,* **56**(3): 272-277.

Table 1. Distribution of 41 finger millet genotypes in different clusters on the basis of D^2 statistic

Clusters	Number of genotypes	Name of the genotypes	Source/ origin
I	10	IGPFM-11-01, IGPFM-11-32, IGPFM-11-13, IGPFM-11-06, IGPFM-11-12, IGPFM-11-16, IGPFM-11-11, IGPFM-11-09, IGPFM-11-14.	Igatpuri
		Dapoli-1.	Dapoli
II	17	IGPFM-11-07, IGPFM-11-22, IGPFM-11-23, IGPFM-11-17, IGPFM-11-20, IGPFM-11-35, IGPFM-11-19, IGPFM-11-21, IGPFM-11-15, IGPFM-11-26, IGPFM-11-28, IGPFM-11-10, IGPFM-11-25, IGPFM-11-03, IGPFM-11-29, IGPFM-11-30, IGPFM-11-24.	Igatpuri
III	2	IGPFM-11-04, IGPFM-11-05.	Igatpuri
IV	1	IGPFM-11-18.	Igatpuri
V	7	IGPFM-11-02, IGPFM-11-08, IGPFM-11-34, IGPFM-11-37, IGPFM-11-38, IGPFM-11-31, IGPFM-11-33.	Igatpuri
VI	3	HR-374.	Bangluru
		PES-400.	Pantnagar
		IGPFM-11-27.	Igatpuri
VII	1	IGPFM-11-36.	Igatpuri

Table 2. Average intra and inter-cluster distances (D^2) and D values for 41 genotypes in finger millet

Cluster	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**
I	**258.89**	1157.36	510.76	1077.15	533.15	599.76	775.07
	(16.09)	(34.02)	(22.60)	(32.82)	(23.09)	(24.49)	(27.84)
II		**283.25**	815.10	439.74	1186.80	2313.61	2877.25
		(16.83)	(28.55)	(20.97)	(35.45)	(48.10)	(53.64)
III			**106.71**	671.33	1096.93	974.06	1921.95
			(10.33)	(25.91)	(33.12)	(31.21)	(43.84)
IV				**0.00**	1389.80	1672.81	2865.46
					(37.28)	(40.90)	(53.53)
V					**428.08**	1073.22	569.30
					(20.69)	(32.76)	(23.86)
VI						**217.56**	813.40
						(14.75)	(28.52)
VII							**0.00**

Figures in parenthesis indicate 'D' values.

Table 3. Cluster means for 12 characters in finger millet

Cluster	Days to 50% flowering	Days to physiological maturity	Productive tillers / pant	Plant height (cm)	Finger length (cm)	No. of fingers / main ear head	Main ear head spread (cm)	1000 grain weight (g)	Harvest index (%)	Iron content (mg/ 100g)	Protein content (%)	Grain yield / plant (g)
I	86.17	119.27	1.37	117.34	5.69	5.54	3.99	3.07	33.91	6.1	7.64	7.13
II	90.22	122.08	1.39	115.39	5.78	6.21	3.95	3.16	35.51	4.1	7.01	7.32
III	74.00	102.17	2.07	124.13	5.64	5.94	4.13	2.61	33.40	5.3	7.93	10.42
IV	73.33	105.67	0.87	90.00	4.88	5.12	3.45	3.41	38.34	4.2	8.85	5.11
V	106.43	135.29	1.59	107.13	6.20	5.87	4.39	2.98	36.24	5.9	7.90	8.07
VI	71.89	102.44	1.58	91.81	5.95	5.70	3.94	2.76	34.77	7.2	8.13	5.97
VII	103.67	136.67	0.87	117.80	5.25	5.12	2.88	2.50	36.01	7.5	7.62	4.98
Mean	89.78	121.20	1.44	112.60	5.80	5.89	4.00	3.04	35.17	5.30	7.51	7.34
S.Em.±	0.76	0.60	0.05	0.77	0.10	0.13	0.10	0.05	0.54	0.11	0.31	0.18
%Contribution	5.49	7.07	0.61	11.71	1.59	0.24	0.24	2.20	0.12	70.12	0.00	0.61