Assessment of Genetic diversity among Finger millet (*Eleusine coracana* L. Gaertn.) genotypes during *kharif* season in Western Maharashtra (India)

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Abstract- The experimental material comprised 50 diverse genotypes of finger millet (*Eleusine coracana* L. Gaertn.). The present investigation was carried out to study the genetic divergence among 50 finger millet genotypes for thirteen quantitative characters using Mahalanobis D^2 statistics during *kharif*, 2018 at Botany Farm, College of Agriculture, Pune Maharashtra (India). D^2 statistics indicated that the genotypes studied were genetically diverse. The 50 genotypes of finger millet were grouped into five non-overlapping clusters. Maximum genotypes (40) were included in cluster I followed by cluster II (4) and III (4) . Cluster IV and V were monogenotypic included one genotype only. D^2 analysis revealed that, there was a wide diversity between the genotypes with D^2 values ranging from 123.65 to 556.48. The highest D^2 value was observed between the cluster II and V having genotypes KOPN-1181, KOPN-1182, KOPN-1178, KOPN-1168, KOPN-1174. This suggests that these genotypes have large source of variation and are useful for future breeding programme.

Index Terms- Finger millet, genetic diversity, cluster analysis, divergence.

I. INTRODUCTION

Finger millet (*Eleusine coracana* (L.) Gaertn.) is an allotetraploid (2n = 4X = 36, AABB) belonging to the family poaceae and the genus *Eleusine.* It is an annual herbaceous cereal crop widely grown and consumed by poor people in Africa and Asia. ***Eleusine coracana***, or **finger millet**, is an annual herbaceous plant widely grown as a cereal crop in the arid and semiarid areas in Africa and Asia. It is commonly called nachani in Maharashtra and **kodo in Nepal**. In Maharashtra, a type of flat bread is prepared using finger millet (ragi) flour.. Normally due to high calcium and iron content nachni is considered as nutritional crop. The achievement in plant breeding programme largely depends upon the genetic variability available in breeding population and the efficiency of selection technique. The importance of genetic diversity in plant breeding is obvious from results obtained in different crops. The recognition and measurement of such diversity, its nature and magnitude are beneficial, perhaps crucial to any breeding programme. This is particularly important in a crop like finger millet where hybridization is difficult, there being limited scope for making large number of crosses by random mating and hence, the information regarding the nature of genetic diversity of the parents to be used in the hybridization is of paramount importance in finger millet breeding programme.

Mahalanobis D^2 statistics is a powerful tool to know the clustering pattern to establish the relationship between genetic and geographic divergence and to determine the role of different quantitative characters towards the maximum divergence. 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

II. MATERIAL AND METHODS

The experimental material consisted 50 finger millet genotypes collected from AICRP on Small millet, Z.A.R.S. Kolhapur, Maharashtra, India. The material was grown in simple randomized block design with three replications at Botany research farm, College of Agriculture Pune during *kharif* season. Total 490 mm rainfall was received within 40 rainy days during the season. The distribution of rainfall per meteorological weeks from 20th to34th week was 402 mm within 30 rainy days. Particularly irregular, untimely, ill-distributed and inadequate rainfall with unfavorable climatic conditions with extreme variations in values of different weather parameters influences the growth of crop during season. All the recommended agronomic and cultural practices were followed for raising a healthy crop. Data were recorded on five randomly selected plants per replication of each genotype for thirteen characters *viz.*, days of 50 per cent flowering, days to maturity, plant height (cm), number of fertile tillers per plant, length of finger, number of fingers per ear, ear weight per plant, fodder yield per plant (g), grain yield per plant (g), harvest index, protein content and iron content. 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 fifty genotypes. Based on genetic distance, all the genotypes were grouped into different clusters (Rao, 1952).

III. RESULTS AND DISCUSSION

Genetic divergence as a measure of choosing potent parent for crossing: the success of any crossing programme depends on selection of parents having high expression for the economically important characters. Therefore diversity is the basic need of crop improvement programme. Among the different approaches of selecting parents, selection based on diversity has its own merit. Therefore, in the present study diversity among different genotypes was studied, which yielded valuable information that could be useful in suggesting potent parents for crossing, Hays and Johnson (1939) and East (1936) obtained greater heterosis from crosses between diverse parents than those between close related ones. Timothy (1963) found that genetic divergence is one of the criteria for selecting the parents for hybridization, which may produce transgressive seggregants in the later generations.

In the present investigation 50 genotypes were grouped into V clusters. Cluster I comprised the highest number of fourty genotypes, followed by cluster II and III with four genotypes, whereas remaining all other clusters *viz.*, IV and V were solitary(Table No. 1). Kadam (2007), Dineshkumar *et al*, (2010) and Negi *et al*,(2017) were also reported the similar results

The calculated D^2 values varied from 180.36 to 556.48 (Table 2.). The lowest value was observed in between cluster I and IV (180.36) while, the highest value was observed between the cluster II and V (556.48) having genotypes KOPN-1181, KOPN-1182, KOPN-1168 and KOPN-1174.

The maximum inter cluster distance was found between cluster II and V (23.59), followed by cluster II and III (21.54) and cluster III and IV (19.15), whereas minimum inter cluster distance was found between cluster I and IV (13.43), followed by cluster I and II (13.96). Considering the intra-cluster distance, cluster III had maximum intra cluster distance (13.70), while intra-cluster distance was not found in the cluster IV and V, due to solitary clusters. The maximum inter cluster distance was found between cluster II and IV. The maximum intra cluster distance was observed in the cluster III suggesting that genotypes included in these cluster might have different genetic makeup. The two monogenic clusters *i.e*. cluster IV and V, showed zero intra-cluster distance. The cluster formation and cluster divergence are used as basis for selection of better parents for hybridization programme. Grouping of genotypes into five clusters suggested the presence of relatively wide amount of genetic diversity in the material under investigation.

The genotypes KOPN-1179 and KOPN-1174 were mono-genotypic, which indicated wide diversity from the remaning as well as from each other. Thus, these genotypes have entirely different genetic makeup from the others. These results were confirmed earlier by Karad and Patil (2013), Suryanarayana *et.al* (2014) and Sahu and Pradhan (2017) in finger millet.

The mean performances for cluster values of thirteen characters are presented in Table 3. Based on mean performances of clusters for thirteen characters, it is revealed that a wide range of variability among the clusters were present for all the characters. A considerable inter cluster variation in respect of cluster was observed among the various clusters for thirteen characters studied. Cluster means for different characters indicated that none of the cluster contained genotype with all the desirable traits.

The cluster means for days to 50 per cent flowering varied from 59.25 (cluster II) to 86.00 (cluster V). The remaining cluster means were, Cluster I (71.28) followed by cluster IV (76.33) and cluster III (78.08). Cluster means for days to maturity varied from 98.50 (cluster II) to 131.67 (cluster V). The remaining cluster means were; Cluster I (108.79), cluster IV (115.33) and cluster III (122.42). The cluster means for number of fertile tillers per plant varied from 1.81 (cluster I) to 2.47 (cluster IV). The remaining cluster means were; Cluster III (1.70), cluster V (1.87) and cluster II (2.00). Cluster means for plant height ranged from 80.70 cm (cluster III) to 92.40 cm (cluster IV). The remaining cluster means were; Clusters V (78.9 cm), cluster II (89.10 cm) and cluster I (90.00 cm). Cluster means for length of finger ranged from 4.93 cm (cluster V) to 7.48 cm (cluster IV). The remaining cluster means were; Cluster III (6.47 cm), cluster I (6.81 cm) and cluster II (7.42 cm). Cluster means for 1000- seed weight ranged from 6.66 g (cluster III) to 11.36 g (cluster IV). Cluster means for ear weight per plant varied from 11.87 g (cluster III) to 16.16 g (cluster IV). The remaining clusters were; cluster I (13.00 g), cluster II (14.35 g) and cluster V (15.36 g). Cluster means for number of fingers per ear ranged from 5.70 (cluster V) to 7.00 (cluster IV). Cluster mean for fodder yield per plant varied from 24.80 g (cluster III) to 34.65 g (cluster IV). The remaining cluster means were; Cluster I (26.82 g), cluster II (28.50 g) and cluster V (29.24 g).Cluster mean for harvest index varied from 28.17 % (cluster III) to 36.37 % (cluster IV). The remaining cluster means were; Cluster I (29.76 %), cluster II (31.68 %) and cluster V (34.65 %). Cluster mean for protein content varied from 3.95 % (cluster V) to 6.30 %(cluster IV). The remaining cluster means were; Cluster II (4.54 %), cluster I (4.88 %) and cluster III (5.50 %). Cluster mean for iron content varied from 48.62 ppm (cluster III) to 64.20 ppm (cluster IV). Cluster means for grain yield per plant ranged from 6.66 g (cluster III) to 11.36 g (cluster IV). The remaining cluster means were; Cluster I (7.98 g), cluster II (9.16 g) and cluster V (10.17 g).

The cluster mean for days to 50 per cent flowering and days to maturity was least for cluster II. The cluster IV showed highest cluster mean for number of fertile tillers per plant, plant height, length of finger, grain yield per plant, 1000-seed weight, ear weight per plant, number of fingers per ear, harvest index , protein content and iron content .The cluster V showed highest cluster mean for days to maturity, days to 50 per cent flowering and 1000-seed weight. The cluster III showed lowest cluster mean for plant height, grain yield per plant, 1000-seed weight, ear weight per plant, fodder yield per plant, harvest index and iron content, cluster V showed highest cluster mean for days to maturity, days to 50 per cent flowering and 1000-seed weight and length of finger, number of fingers per ear and harvest index was lowest for cluster V.

The data collected from present study was used to determine divergence as shown in Table 4. Among 13 characters

studied, iron content (31.27 %) showed maximum contribution to divergence followed by 1000-seed weight (26.86 %), days to maturity (21.31%) and protein content (13.71 %). The character plant height (0.08 %) showed least contribution to divergence, followed by harvest index (0.16 %), fertile tillers per plant (0.24 %), grain yield per plant (0.33 %), number of fingers per ear (0.82 %), days to 50 per cent flowering (2.44 %) and length of finger (2.78 %). The characters ear weight per plant and fodder yield per plant showed no contribution towards divergence. Sahu and Pradhan (2012) reported similar, results for days to maturity. Desai (2012) also reported similar results for days to maturity and iron content.

Based on the results obtained in the present study, it would be desirable to select the parents based on maximum genetic divergence for most of yield contributing components. The study also envisages the relative importance of the characters like pods per plant, days to maturity, number of branches per plant, 1000-seed weight, harvest index, number of days to 50 per cent flowering and number of seed per pod in selecting parents for hybridization programme.

IV. CONCLUSION

The study of present investigation revealed that based on per se performance and intra and inter cluster distance genotypes KOPN-1181, KOPN-1182, KOPN-1178, KOPN-1168, KOPN-1174, KOPN-1179, KOPN-1166, KOPN-1162 and KOPN-1178, were found promising for cultivation in *kharif* season of western Maharashtra and can be used as potential parents in future crop improvement programme. While choosing among the genotypes of a cluster, the *per se* performance of genotypes for different traits such days to maturity, 1000-seed weight, protein content, iron content, length of finger so that desirable segregates would be obtained after hybridization.

Table 1: Distribution of 140 genotypes of finger millet among different clusters on the basis of D^2 analysis

Clusters	Number of genotypes	Name of genotypes
I	40	KOPN-113, KOPN-1138, KOPN-1139, KOPN-1142, KOPN-1141, KOPN-1140, KOPN-1143, KOPN-1144, KOPN-1145, KOPN-1148, KOPN-1147, KOPN-1146, KOPN-1149, KOPN-1150, KOPN-1155, KOPN-1153, KOPN-1154, KOPN-1152, KOPN-1157, KOPN-1158, KOPN-1159, KOPN-1160, KOPN-1186, KOPN-1162, KOPN-1163, KOPN-1164, KOPN-1165 ,KOPN-1166, KOPN-1167, KOPN-1169, KOPN-1171, KOPN-1172, KOPN-1173, KOPN-1176, KOPN-1177, KOPN-1180, KOPN-1183, KOPN-1184, KOPN-1185, KOPN-1161
II	4	KOPN-1181, KOPN-1182, KOPN-1178, KOPN-1168
III	4	KOPN-1151, KOPN-1156, KOPN-1170, KOPN-1175
IV	1	KOPN-1179
V	1	KOPN-1174

Table 2. Average intra-and inter-cluster D (in parenthesis) and D^2 values in 50 genotypes of finger millet.

cluster	I	II	III	IV	V
I	**123.65**	194.88	243.98	180.36	303.45
	(11.12)	(13.96)	(15.62)	(13.43)	(17.42)
II		**146.89**	463.97	254.40	556.48
		(12.12)	(21.54)	(15.95)	(23.59)
III			**187.69**	366.72	291.72
			(13.70)	(19.15)	(17.08)
VI				**0.0**	227.40

					(15.08)
V					**0.0**
					0.0

Table 3. Cluster mean values for 13 characters in 50 genotypes of finger millet

Characters	I	II	III	IV	V
Days to 50% flowering (No)	71.28	59.25	78.08	76.33	86.00
Days to maturity (No)	108.79	98.50	122.42	115.33	131.67
Fertile tillers per plant (No)	1.81	2.00	1.70	2.47	1.87
Plant height(cm)	90.00	89.10	80.70	92.40	78.90
Length of finger (cm)	6.81	7.42	6.47	7.48	4.93
1000 seed weight (g)	7.98	9.16	6.66	11.36	10.17
Ear weight per plant (g)	13.00	14.35	11.87	16.16	15.36
Number of fingers per ear (No)	6.22	5.86	5.75	7.00	5.70
Fodder yield per plant (g)	26.82	28.50	24.80	34.65	29.24
Harvest index (%)	29.76	31.68	28.17	36.37	34.65
Protein content (%)	4.88	4.54	5.50	6.30	3.95
Iron content (ppm)	53.61	59.52	48.62	64.20	58.53
Grain yield per plant (g)	7.98	9.16	6.66	11.36	10.17

Table 4. Per cent contribution of 13 characters for divergence in finger millet.

Sr. No.	Source	Times ranked first	Contribution (%)
1	Days to 50% flowering (No)	30	2.44
2	Days to maturity (No)	261	21.31
3	Fertile tillers per plant (No)	3	0.24
4	Plant height(cm)	1	0.08
5	Length of finger (cm)	34	2.78
6	1000 seed weight (g)	329	26.86
7	Ear weight per plant (g)	0	0.00
8	Number of fingers per ear (No)	10	0.82
9	Fodder yield per plant (g)	0	0.00
10	Harvest index (%)	2	0.16
11	Protein content (%)	168	13.71
12	Iron content (ppm)	383	31.27
13	Grain yield per plant (g)	4	0.33
		Total	100

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