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Genetic divergence studies in foxtail millet (*Setaria italica* (L.) P. Beauv)

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Abstract
The experiment was conducted at the field of Agril. Botany Dr. PDKV, Akola (MH) during *Kharif*-2018 and *Kharif*-2019and assessed 52diverse genotypes of Foxtail millet (*Setaria italica* (L.) P. Beauv) for genetic diversity. The data on 12 quantitative traits were recorded to assess the magnitude of genetic divergence for yield and yield contributing traits. In the present investigation, D2 statistic indicated that the genotypes studied were genetically diverse. Based on genetic distances the 52genotypes under study were grouped into five clusters. Cluster I contains highest 36 genotypes, Cluster III and II were the next large clusters which involve 7 and 6 genotypes respectively belonging to diverse origin. Remaining clusters IV and V contained two and one genotype respectively. The maximum inter-cluster distance was observed between cluster V and III. In overall, D^2 analysis suggested genotypes belonging to the distinct cluster (V and III) could be used in hybridization programme for enhance the productivity of foxtail millet.

Keywords: genetic divergence, foxtail millet, inta-cluster, inter-cluster

Introduction
Foxtail millet (*Setaria italic* (L.) P. Beauv) is also known as Italian millet, German millet, Chinese millet and Hungarian millet. In India common names are Navanein Kannad, Korraluin Telgu, Tenaiin Tamil, Kanginiin Gujrathi and Hindi, Kang and ralain Marathi. It is one of the oldest crops cultivated for food grain, hay and pasture. According to Vavilov (1926) [17], the principal centre of diversity for foxtail millet is East Asia, including China and Japan. The most recent archaeological evidence demonstrated that the foxtail millet is the most ancient crop as its domestication in China dates back to 8,700 years ago (Lu *et al.*, 2009) [7]. It is an important grain crop in temperate, subtropical, tropical Asia and in parts of southern Europe. China, India and Japan are the major foxtail millet growing countries in the world. In India, the cultivation of foxtail millet is confined to Andhra Pradesh, Karnataka and Tamil Nadu and some parts of Maharashtra.

With the rapid development of maize and other crops, foxtail millet has gradually become a minor crop in the last 80 years but it is still widely cultivated in Asia, Europe, North America, Australia and North Africa as grain food or forage (Austin, 2006) [3]. It is not correct to consider foxtail millet as a low yielding crop, the actual problem being that growing conditions in many areas are poor and grown as rainfed beside lack of improved cultivars. The yield level of 1,500-2,250 Kg ha^{-1}has been reported from China (Jiaju, 1986) [5]. At present, in India the crop is cultivated on a very limited area of around 5.90 lakh hectares in sporadic patches in the states of Andhra Pradesh, Karnataka, Tamil Nadu, Maharashtra, Rajasthan, Madhya Pradesh, Uttar Pradesh and North Eastern states with annual production of 3.86 lakh tonnes and productivity of 655 Kg ha^{-1} (Anonymous, 2015-16) [2].

Materials and Methods
The experimental material consisted of 52 elite foxtail millet genotypes collected from all over India. These genotypes grown in randomized block design with three replications at field of Agril. Botany Dr. PDKV, Akola (MH) during *Kharif*-2018 and *Kharif*-2019. Twelve yield contributing characters were taken to assess the magnitude of genetic divergence for 52 genotypes of foxtail millet. Each entry was grown in 3meter row with spacing of 30 cm between the rows and 10 cm within the plants. Five randomly selected plants from each genotypes in each replications were used to record observations on plant height, total numbers of tillers per plant, number of productive tillers per plant, panicles length, panicle girth, grain yield per plant, straw yield per plant, thousand grain weight except 50 per cent flowering and

days to maturity. Days to 50 per cent flowering and days to maturity was noted on plot basis. The mean of five plants was subjected to statistical analysis, data were statistical analyzed to estimate genetic divergence was estimated by multivariate analysis using Mahalanobis (1936) [8] D^2 statistic as described by Rao (1952) [12]. On the basis of D^2 values genotypes were grouped into different clusters according to Tocher's method given by Rao (1952) [12].

Results and Discussion

Genetic diversity studies provide basic information regarding the genetic parameters of the genotypes based on which breeding methods are constituted for further crop improvement. These studies are also helpful to know about the nature and extent of diversity that can be attributed to different causes, sensitivity of crop to environment and genetic divergence.

D^2 statistics, a concept developed by Mahalanobis (1936) [8] is important tool to plant breeder to classify the genotypes into different groups based on genetic divergence between them.

In the present study magnitude of D^2 Values 52 genotypes were grouped into five clusters (Table 1). Cluster I had the maximum of 36 genotypes each. Cluster III and II were the next large clusters which involve 7 and 6 genotypes respectively belonging to diverse origin. Remaining clusters IV and V contained two and one genotype respectively.

Intra and inter cluster D^2 values were worked out using D^2 values from divergence analysis (Table 2).The mean D^2 values of cluster elements were used as measure of intra and inter-cluster distance. The maximum inter-cluster distance was found between cluster III and cluster V (D^2 =1677.12) followed by cluster II and cluster III (D^2 =1296.00), cluster IV and cluster V (D^2 =880.31). The cluster I showed the maximum inter-cluster distance with cluster IV (D^2 =341.14) followed by cluster V (D^2 =336.72) and cluster III (D^2 =285.61).The maximum inter-cluster distance of cluster II was observed with cluster III (D^2 =1296.00) followed by cluster IV (D^2 =583.22) and cluster IV (D^2 =265.36).The cluster III was most distant from cluster V (D^2 =1677.12) and cluster IV (D^2 =686.44).The cluster IV showed the maximum inter cluster distance with cluster V (D^2 =880.31). High value of inter-cluster distance points out towards high amount of diversity between the clusters involved.

Hence, from the above discussion we can conclude that the genotypes from the cluster III and V were more divergent than any other cluster. Hence, the genotypes belonging to the distinct cluster (III and V) could be used in hybridization programme for obtaining a wide spectrum of variation among the segregrants.

The Intra cluster D^2 values ranged from zero to 105.47. Maximum intra cluster distance was observed in cluster III (D^2 =105.47) followed by cluster I (D^2 =76.04), cluster IV (D^2 =62.25) and cluster II (D^2 =43.16). The cluster in which only one genotype was grouped, the intra cluster distance was zero. The cluster means for all the characters are presented in table 3. The cluster mean for days to 50% flowering was lowest in cluster I (57.43) while it was highest in cluster IV (64.92). For days to maturity the cluster mean was lowest in cluster I (88.61) followed by cluster III (89.24) while it was highest in cluster IV (96.00). Cluster mean for total No. of tillers was highest in cluster V (6.18) and lowest in cluster IV (3.37). For No. of productive tillers cluster mean was highest in cluster V (5.32) and lowest in cluster IV (2.27). The cluster mean for plant height was highest in cluster IV (166.83) and the lowest in cluster II (119.33).Panicle length was highest in cluster III (19.37) and lowest in cluster V (15.37). Panicle girth has recorded highest mean in cluster IV (7.50) and lowest in cluster II (4.58). Cluster mean for grain yield per plant was highest in cluster IV (18.02) and lowest in cluster II (12.25). For straw yield per plant cluster mean was highest in cluster IV (31.53) and lowest in cluster II (21.71). 1000 grain weight was highest in cluster IV (2.79) and lowest in cluster II (2.40). For grain Fe content the cluster mean was highest in cluster III (48.41) and lowest in cluster V (21.03).Cluster mean for grain Zn content was highest in cluster III (46.22) and lowest in cluster II (21.44). It is observed that number of cluster contained at least one genotype with all the desirable traits, which ruled out the possibility of selecting one genotype directly for immediate use. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

The Genotype group into cluster IV had highest yields for grain yield/plant associated high panicle girth, straw yield/plant, 1000 grain weight, plant height. Genotype group in cluster V had high total number of tillers and productive tillers. Genotype group in cluster III had high panicle length, grain Fe content and Grain Zn content. Genotype group in cluster I had low days to 50% flowering, and days to maturity. Intercrossing the genotypes of these clusters may result in enlarged variability ands election for these traits could result in higher yield combined with high tillers. These results were reported by Murugan & Nirmalakumari (2006) [10], Sheriff (1992) [15], Maloo and Bhatta chargee (1999) [9], Satish (2003) [13], Shanmuganathan *et al.* (2006) [14], Bedis *et al.* (2007) [4], Nirmala kumari and Vetriventhan (2010) [11], Kumuda *et al.* (2011) [6], Yogeesh *et al.* (2015) [18] and Amarnath *et al.* (2019) [1].

Table 1: The distribution of 52 genotypes of Foxtail millet into five different clusters on the basis of Mahalanobis D^2 Statistics

Clusters	Total no. of genotypes	Genotypes included in the clusters		
I	36	(40) IC-120237	(51) PS4	(20) IC-97296
		(45) IC-120236	(1) IC-28471	(32) IC-120201
		(33) IC-120204	(30) IC-120195	(13) IC-97188
		(24) IC-120166	(50) IC-333258	(27) IC-120182
		(21) IC-120148	(49) IC-326779	(9) IC-97167
		(25) IC-120167	(43) IC-120247	(12) IC-97185
		(48) IC-326751	(26) IC-120177	(3) IC-97107
		(37) IC-120221	(34) IC-120208	(18) IC-97196
		(38) IC-120226	(4) IC-97109	(2) IC-97105
		(10) IC-97172	(6) IC-97144	(5) IC-97111
		(41) IC-120243	(44) IC-120255	(14) IC-97189
		(46) IC120406	(15) IC-97191	(11) IC-97177
II	6	(17) IC-97195	(47) IC-120408	(42) IC-120244

		(52) Lepakshi	(7) IC-97116	(8) IC-97130
III	7	(28) IC-120183 (29) IC-120192 (19) IC-97293	(35) IC-120213 (16) IC-97194 (39) IC-120235	(23) IC-120150
IV	2	(22) IC-120149	(31) IC-120200	
V	1	(36) IC-120234		

Table 2: Average Intra and Inter-cluster (D2) values for 52 genotypes of Foxtail millet

Clusters	I	II	III	IV	V
I	8.72 (76.04)	16.43 (269.94)	16.90 (285.61)	18.47 (341.14)	18.35 (336.72)
II		6.57 (43.16)	36.00 (1296.00)	24.15 (583.22)	16.29 (265.36)
III			10.27 (105.47)	26.2 (686.44)	40.96 (1677.12)
IV				7.89 (62.25)	29.67 (880.31)
V					0.00 (0.00)

Table 3: Cluster means for 12 characters in 52 genotypes of Foxtail millet.

Sr. No.	Character	Clusters				
		I	II	III	IV	V
1	Days to 50% flowering	57.43	59.39	58.12	64.92	60.67
2	Days to maturity	88.61	90.61	89.24	96.00	91.83
3	Total No. of tillers	4.06	4.33	4.09	3.37	6.18
4	No. of productive tillers	3.01	3.31	3.10	2.27	5.32
5	Plant height (cm)	142.63	144.22	150.19	166.83	119.33
6	Panicle length (cm)	16.97	16.44	19.37	19.05	15.37
7	Panicle girth (cm)	4.65	4.58	4.95	7.50	5.15
8	Grain yield / plant (gm)	12.68	12.25	12.95	18.02	12.51
9	Straw yield / plant (gm)	22.49	21.71	23.04	31.53	21.94
10	1000 grain weight (gm)	2.52	2.40	2.44	2.79	2.64
11	Grain Fe Content (mg/kg)	32.62	29.37	48.41	32.58	21.03
12	Grain Zn Content (mg/kg)	38.19	21.44	46.22	35.17	33.77

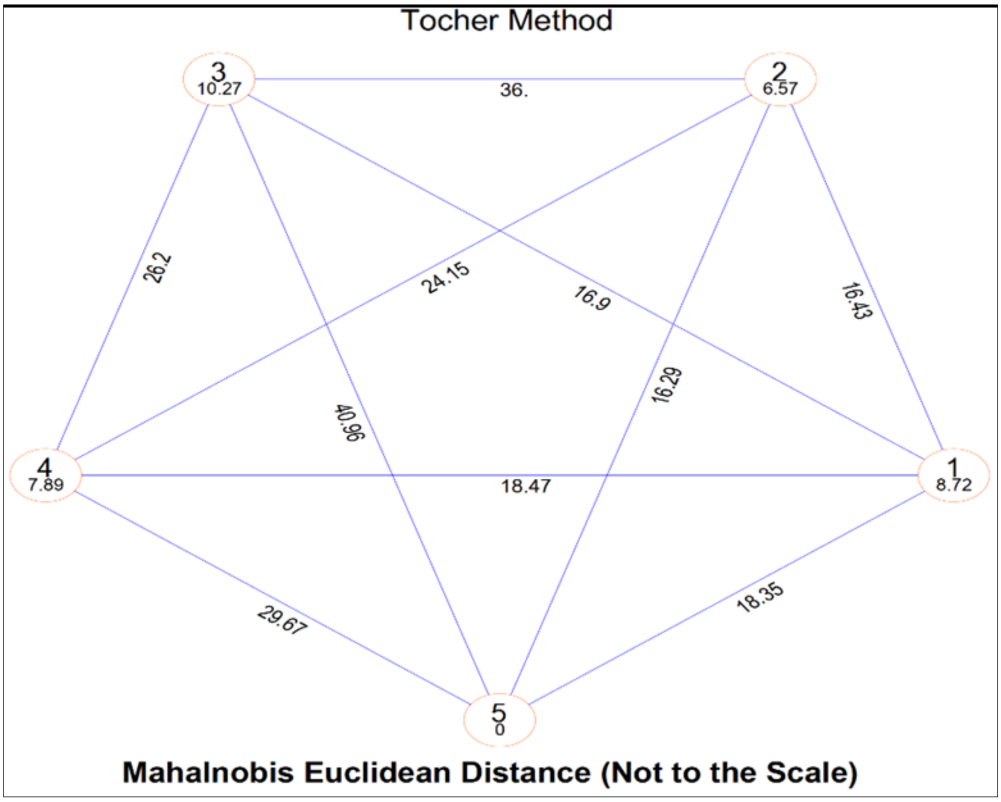

Fig 1: Intra and inter cluster distances among five clusters in foxtail millet at Akola during Kharif(2018-19& 2019-20)

Conclusion

The genotypes from the cluster III and V were more divergent than any other cluster. Hence, the genotypes belonging to the distinct cluster (III and V) could be used in hybridization programme for obtaining a wide spectrum of variation among the segregrants.

References

1. Amaranath K, Durga Parasad AVS, Reddy CVCM. Assessment of genetic diversity in Indian Italian millet

genetic resources [*Setaria italica* (L.) Beauv]. Electron. J Pl. Breed. 2019;10(1):83-91.
2. Anonymous. Directorate of Economics and Statistics, GOI, 2015-16.
3. Austin DF. Foxtail millets (*Setaria:* Poaceae) Abandoned food in two hemispheres, Econ Bot. 2006;60(2):143-158.
4. Bedis MR, Patil HS, Patil VS, Jangle GD. Genetic divergence in finger millet. Natl. J Plant Impr. 2007;9(1):58-59.
5. Jiaju C. Importance and genetic resources of small millets with emphasis on foxtail millet (*Setaria italica*) in China. In: Seetharam, A, Riley K.W and Harinarayana, G (eds). Small millets in Global Agriculture. New Delhi: Oxford and IBH Publishing Company Private Limited, 1986, 93-100.
6. Kumuda CM, Rama CM. Genetic divergence analysis among micromutant lines in finger millet (*Eleusine coracana* G.). J Crop Sci. Biotech. 2011;11(1):63-68.
7. Lu H, Zhang J, Liu KB, Wu N, Li Y, Zhou K, *et al*. Earliest domestication of common millet (*Panicum miliaceum*) in East Asia extended to 10,000 years ago. Proc. Natl. Acad. Sci. USA. 2009;106(18):7367-7372.
8. Mahalanobis CR. On the generalized distance in statistics. Proc. Nat. Inst. Sci., India. 1936;11(1):49-55.
9. Maloo SR, Bhattacharjee I. Genetic divergence in foxtail millet. Recent advances in management of arid ecosystem proceedings of a symposium held in India. March, 1997-1999, 155-158.
10. Murugan R, Nirmalakumari A. Genetic divergence in foxtail millet [*Setaria italica* (L.) Beauv]. Indian J. Genet. 2006;66(4):339-340.
11. Nirmalakumari A, Vetriventhan M. Characterization of foxtail millet germplasm collections for yield contributing traits. Electronic Journal of Plant Breeding. 2010;1:140-147.
12. Rao CR. Advance statistical methods in biometric research. Wiley and Sons, New York, 1952, 390.
13. Satish D. Studies on genetic diversity based on productivity and variability for quality traits in finger millet (*Eleusine coracana* Gaertn.). M.Sc. (Agri.) Thesis, Univ. Agric. Sci., Dharwad 2003.
14. Shanmuganathan M, Gopalan A, Mohanraj K. Genetic variability and multivariate analysis in pearl millet (*Pennisetum glaucum* (L.) R. Br.) germplasm for dual purpose. J Agric. Sci 2006;2(1):73-80.
15. Sheriff RA, Shivashankar G. Genetic divergence in foxtail millet. Indian Journal of Genetics. 1992;52(1):29-32.
16. Sheriff RA. Divergence analysis in finger millet (*Eleusine coracana* Gaertn.). Indian J Genet. 1992;52(1):72-74.
17. Vavilov NI. Studies on the origin of cultivated plants. Inst. Appl. Bot. Plant Breeding, Leningrad, 1926, 248.
18. Yogeesh LN, Shankar KA, Prashant SM, Lokesh GY. Genetic variation and morphological diversity in foxtail millet. International Journal of Science, Environment and Technology. 2015;4(6):1496-1502.