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Assessment of Genetic Divergence in Foxtail Millet Genotypes

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ABSTRACT

The experimental material comprised of 134 foxtail millet genotypes representing collections from different parts of India. All the genotypes were characterized for seven traits at the Agricultural Research Station, Vizianagaram during *kharif,* 2019 and were grouped into 16 clusters based on D^2 statastic. Cluster I WAS the largest group with maximum number of genotypes (66) followed by Cluster & II, VII, IV, XVI & XIV with 21, 19, 11, 4 and 3 genotypes respectively. The remaining clusters were solitary. Inter cluster distance was the highest between the clusters XIV and XVI followed by clusters IX and XVI, VII and XVI and VI and XVI. Among the seven quantitative traits studied, the most important trait contributing to the divergence was days to 50% flowering followed by plant height, number of productive tillers and panicle length. Based on mean values and inter cluster distances, the genotypes, FT 3593, SHEIKHOM-53, RFM 67, ESD 90 and L- 273 can be opted for crossing programme for obtaining desirable segregants.

Keywords: *Cluster, D^2 statistic, Foxtail millet, Genetic diversity*.

Foxtail millet (*Setaria italica* (L.) P. Beauv) also known as Italian millet is an important crop next to finger millet among seven small millets. It is also known by different names such as giant setaria, german millet, chinese millet and hungarian millet. It belongs to the family Poaceae and it is the only diploid small millet with 2n=18, while others are mostly tetraploid. In drought prone areas of the world, it is serving as oldest cereal resource to farmers ensuring constant yields because of its ability to grow in poor soils of drier regions where no other cereals can thrive well (Howarth *et al*., 2002). It is fairly drought tolerant but cannot tolerate water logging.

Foxtail millet ranks second in the world's total production of millets. In India it is cultivated in an area of 5 lakh hectares with the production of 2.9 million tons and productivity of 600 kg per hectare (Anonymous,2016). At present, foxtail millet is cultivated in Andhra Pradesh, Karnataka, Maharashtra, Tamil Nadu, Rajasthan, Madhya Pradesh, Uttar Pradesh and North Eastern states of India. Foxtail millet grains are rich in protein, fibre, β carotene, minerals *viz*., potassium, magnesium, calcium, iron, , zinc, antioxidants and vitamins (Rai, 2002). The protein in foxtail millet is relatively high with essential aminoacids like leucine and methionine.

In this context Mahalanobis D^2 statistics is an effective tool in quantifying the degree of divergence at genetic level and also provides quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936). It is used to measure the genetic divergence and to classify the genetic stock into distinct groups. Intercrossing between more divergent parents is expected to generate a broad spectrum of variability and selection to be adopted in the segregating generations. Considering this, the present study was taken up in foxtail millet to understand the diversity available in the genetic stocks.

MATERIAL AND METHODS

The experimental material comprised of 134 foxtail millet genotypes collected from different parts of the country received under CRP on Ago-biodiversity trial. All these genotypes were evaluated at the Agricultural Research Station, Vizianagaram during *Kharif*, 2019 in a randomized block design (RBD) with three replications and with a spacing of 30cm between rows and 10cm between plants. Each genotype was sown in 2 rows of 2m length. Fertilizers, DAP (87 kg/ha), MOP (42 kg/ha) and urea (22 kg/ha) were applied basally at the time of land preparation and remaining 22 kg/ha urea was applied three weeks after sowing. Standard operational practices were followed to maintain a healthy crop. Observations were recorded for plant

height (cm), No. of productive tillers/plant and panicle length (cm). Days to 50% flowering and days to maturity were recorded by visualizing the entire plot. Fodder yield and grain yield were recorded on per plot basis and then converted into per hectare. Mahalanobis D^2 statistic was used to assess the diversity among genotypes and they were grouped into different clusters using the Tocher's method as described by Rao (1952).

RESULT AND DISCUSSION

The analysis of variance revealed significant variation among 134 genotypes for all the characters included under the study indicating that the genotypes under study were genetically divergent to each other. To assess the true genetic divergence among all genotypes Mahalanobis D^2 statistic was utilized for yield and its contributing characters. All 134 genotypes were grouped into 16 clusters (Table-1). Among different clusters, cluster I contained maximum number of genotypes (66) followed by cluster II consisting of 21 genotypes, cluster VII with 19 genotypes, cluster IV with 11 genotypes, cluster XVI with four genotypes, cluster XIV with three genotypes and all the remaining clusters were having solitary genotype. It is in accordance with Anuradha *et al*.(2017) in finger millet where the grouping pattern indicated that genotypes having more similarity since they were grouped in same cluster and it also indicated that 10 genotypes were very diverse from other and formed solitary clusters. Similar results were also found by earlier works by Murugan and Nirmalakumari (2006) and Selvarani and Gomathinayagam (2000).

Intra and inter cluster distances were worked out using D^2 values from divergence analysis (Table 2). The inter-cluster distance values ranged widely with minimum value of 0.18 between clusters VIII and IX and maximum value of 2.07 between clusters XIV and XVI indicating high diversity between the genotypes of these clusters. The maximum amount of heterosis is expected from the crosses with parents belonging to these clusters. Higher inter cluster distance was also observed between clusters IX and XVI (2.06) and clusters VII and XVI (1.90). This suggested that there is wide genetic diversity between these clusters. The cluster I with maximum number of genotypes recorded less inter cluster distances with remaining other clusters indicating low level of divergence. The intra-cluster distance ranged from 0.00 to 0.32. The maximum intra cluster distance was observed in cluster XVI (0.31) and cluster IV (0.29). The intra cluster distance was also very low for cluster I along with inter cluster distance indicating its less usage for breeding. 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.

Cluster means indicate average performance of all genotypes present in a particular cluster. The cluster mean values for seven characters are presented in (Table 3). Cluster mean for number of productive tillers is the highest in cluster XIV (7.49) followed by cluster XII (7.12). Cluster mean for days to 50 per cent flowering was the lowest in both clusters VI and IX (42.80). The genotypes in these clusters can be utilized for breeding earliness in foxtail millet. Cluster mean for plant height was the lowest in cluster VII (93.54) followed by cluster VI (97.42) and genotypes of these clusters can be utilized for breeding non-lodging types and highest in cluster VIII (138.91). Cluster mean for panicle length is highest in cluster XV (19.84) followed by Cluster VIII (17.92). Similar results were reported by Gangrude *et al*. (2016). Cluster mean for days to maturity was the lowest in cluster VI (74.80 days) followed by cluster VII (76.59 days). The highest grain yield was recorded by cluster X (3254.30) followed by cluster XII (3102.20). The highest fodder yield was recorded by cluster XV (8712.30) followed by cluster XVI (7688.78).

The mean performance of the clusters of seven characters showed that the cluster IX consisting of single genotype (GS-2030GIGUGS-11) recorded more number of productive tillers per plant (6.48) and also characterized with the lowest plant height (97.42 cm). They can be used for breeding non-lodging genotypes. Whereas the cluster VI having solitary genotype (FT 3593) was the earliest with 75 days to maturity. The cluster XV (L- 273) recorded higher panicle length (19.84) and was also characterized with higher grain yield (7864.20kg/ha) and fodder yield (8712.30). The solitary cluster XIV recorded more number of productive tillers per plant (7.49) and having lower plant height (100.87cm) and had shorter duration. The genotypes included in all these clusters can be used as diverse sources in future breeding programmes.

Based on number of times that each of the seven characters appeared in first rank the per cent contribution towards genetic divergence was

calculated (Table 4). The results showed that the contribution of days to 50% flowering was the highest towards genetic divergence (31.28%) by taking 2787 times ranking first followed by plant height (20.53%) by 1829 times, number of productive tillers per plant (16.19%) by 1443 times, grain yield per plant (10.81%) by 963 times, panicle length (10.19) by 908 times, fodder yield per plant (5.97) by 532 times and days to maturity (5.04) by 449 times. Among the seven quantitative characters studied, the most important character contributing to the divergence was days to 50% flowering followed by plant height, number of productive tillers and panicle length.

Since each cluster is characterized for specific characters based on the objective of improvement one can select genotypes from different clusters keeping in mind the inter cluster distance, for example to have more number of productive tillers per plant with low plant height, one can select genotypes from cluster XIV. The high inter cluster distance was also observed between clusters XIV and XVI and they can be used in breeding programmes. In order to select genotypes having early maturity, cluster VI is promising for earliness. The higher yield with more panicle length can be obtained from cluster XV which is solitary clusters. In order to get high yielding, more panicle length with more number of tillers and which comes to maturity early, one can opt for crossing FT 3593 from cluster VI, SHEIKHOM-53, RFM 67 and ESD 90 from cluster XIV, L- 273 from cluster XV.

Table 1: Distribution of 134 genotypes of foxtail millet into 16 clusters on the basis of Mahalanobis D^2 statastic

Cluster	No. of genotypes	Genotypes
I	66	GS-1793, GS-1795, ISE-1230, AK-224, SHEIKHOM-55, FT 2284, ISE-1306, FT 3597, RFM 27, RFM 67, RFM 54, SHEIKHOM-47, FT 3217, RFM 73, ISe 170A, FT 3596, AK-209, FT 3603, RFM 35, RFM 60, RKSUKP-364, T- 72-13, ISe 161B, ISE- 392, ISE- 722, ISE- 531-A, GS-2040HUIEEGU, ISe 159B, RFM 37, RFM 56, FT 2279, FT 3400, KN9, L- 48, FT 3192, GS-1437, GS-1463, ISE-1395, FT 3115, SE 1892, AKPRS-461, MS 72335-2, FT 3050, FT 3175, SE 408, FT 3179, FT 4300, GS-1300, SE 5204, VK-SK 00-229-B, PGR-976, BDJ-2099, FT 3144, FT 3075, SE 4994, GS-1651, GS-1499, SE 670E 201, SE 1894, SE 72722, FT 3191, ELS 115, KN-693, ISE-1144, T- 62-20-1, AK-275
II	21	GS-1956, GS-1907, GS-1371, GS-1953, GS-1307, T 1334, SE 1896, NSS-7822, FT 3077, SR 211, SSK-209, FT 4271, VRB-MX-483, KDRS-160, FT 4308, FT 3548, VJ99-423, L-300, SE 670, AK-275, FT 4036
III	1	FT 4305
IV	11	GS-1443, GS-1465, T- 88-14, RPSP-825, KSN40, ISE-1401, RAP-206, DHFT-109-3, SiA 3085, L- 4-94, VRB-MX-488
V	1	ISe 32B
VI	1	FT 3593
VII	19	PDRGRKPUR-47, RFM 31, RFM 93, RFM 87, FT 3773, RFM 24, RFM 30, RFM 37, RFM 87, FT 3605, FT 3607, FT 3608, GS-1381, GS-1918, GS-1792, FT 3090, FT 3110, ISE-1133, GS-2029GLNGEEN, AK-86
VIII	1	FT 4306
IX	1	GS-2030GIGUGS-11
X	1	NDS-334
XI	1	N08-02
XII	1	SE 5206
XIII	1	NDS-382
XIV	3	SHEIKHOM-53, RFM 67, ESD 90
XV	1	L- 273
XVI	4	BS-9184, VK-SK 00-230-B, BS-9174, FT 4285

Table 2: Intra and inter cluster D^2 values among 16 clusters with 134 foxtail millet genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	0.21	0.39	0.28	0.44	0.34	0.37	0.42	0.34	0.35	0.50	0.54	0.68	0.36	0.63	0.64	1.42
II		0.25	0.36	0.49	0.34	0.80	0.84	0.42	0.69	0.39	0.34	0.37	0.32	1.08	0.37	0.88
III			0.00	0.61	0.33	0.48	0.62	0.29	0.54	0.32	0.46	0.72	0.27	0.98	0.70	1.46
IV				0.29	0.47	0.71	0.70	0.54	0.59	0.60	0.59	0.40	0.48	0.66	0.71	1.25
V					0.00	0.92	0.82	0.36	0.39	0.58	0.39	0.58	0.24	0.81	0.70	1.28
VI						0.00	0.23	0.67	0.63	0.63	0.87	1.15	0.68	0.52	1.15	1.86
VII							0.32	0.85	0.68	0.75	0.87	1.23	0.78	0.63	1.10	1.90
VIII								0.00	0.19	0.77	0.80	0.51	0.29	0.69	0.85	1.56
IX									0.00	1.16	1.08	0.94	0.49	0.45	1.13	2.06
X										0.00	0.31	0.48	0.53	1.17	0.70	1.09
XI											0.00	0.58	0.21	1.14	0.44	0.47
XII												0.00	0.53	1.10	0.63	0.90
XIII													0.00	0.72	0.60	0.80
XIV														0.18	1.73	2.07
XV															0.00	0.68
XVI																0.31

Table 3: Mean values of 16 clusters estimated by Tocher's method from 134 foxtail millet genotypes

Cluster	DFF	PH(cm)	NPT	PL(cm)	GY(Kg/ha)	FY(Kg/ha)	DM
I	45.95	115.01	4.42	16.10	2348.54	5158.87	80.00
II	52.09	126.52	4.42	17.75	2787.14	6081.87	85.70
III	45.60	129.01	3.14	14.75	2703.50	5162.20	79.30
IV	49.05	113.53	6.77	15.33	2721.80	6666.31	82.53
V	48.50	127.45	5.44	17.29	2941.30	5751.80	85.70
VI	42.80	97.42	3.44	12.05	1620.70	3560.50	74.80
VII	42.91	93.54	3.81	13.18	1986.68	4422.17	76.59
VIII	47.00	138.91	5.84	17.92	2108.30	4769.30	80.20
IX	42.80	125.15	6.48	17.88	1838.00	4732.00	78.10
X	50.90	113.70	3.28	13.53	3254.30	4735.10	83.20
XI	54.70	116.43	3.59	13.92	2687.20	6406.20	90.20
XII	55.30	130.47	7.12	17.68	3102.20	6303.50	86.90
XIII	51.10	128.99	4.84	14.57	2095.60	5807.70	86.50
XIV	44.20	100.87	7.49	12.32	1430.43	3228.33	79.17
XV	54.80	123.70	3.30	19.84	2846.20	8712.30	87.70
XVI	63.73	121.51	4.12	15.97	2265.03	7688.78	97.70

DFF:Days to 50% Slowening; PH:Plant height; NPT:No. of Productive fillers; PL: Pamide length; GY:Grain Yield;FY:Fodden Yield;DM:Days to modulity

Table 4: Relative contribution of seven characters towards divergence in foxtail millet

S.No	Character	Times Ranked	Contribution %
1	DFF	2787	31.28
2	PH	1829	20.53
3	NPT	1443	16.19
4	PL	908	10.19
5	GY	963	10.81
6	FY	532	5.97
7	DM	449	5.04

DFF: Days to 50% slowening; **PH:**Plant Hight;**NPT:**No.of Productive fillers; **PL:**Pomide Length; **GY:** Grain Yield; **FY:**Fodder Yield;**DM:** Days to Madurity

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. On the basis of inter cluster distances and *per se* performance, crosses can be attempted between FT 3593, SHEIKHOM-53, RFM 67, ESD 90 and L- 273 for getting higher yield, higher fodder yield, early duration and less plant height. These genotypes may serve as potential parents for future hybridization programmes.

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