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Studies on Genetic Diversity in Fox-Tail Millet (*Setaria italica* Beauv.)*

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Fifty genotypes of fox-tail millet (*Seteria italica* Beav.), the genetic diversity by Mahalanobis'D analysis and to identify the various contributing factors for the genetic divergence. A wide genetic diversity was revealed by the D_2 analysis wherein the fifty genotypes fall into as many as fifteen clusters. The geographic distribution was not related to genetic diversity. Genotypes chosen from the same eco-geographic region were found scattered in different clusters. This points to the availability of wide genetic variability in types from the same eco-geographic region. Based on the average inter-cluster distances (D), the clusters XV, XIV and XII were found to be highly divergent from the others. The type ISe 380 (Cluster IV) was superior for grain weight, panicle length, number of branches, plant height and straw yield. The type ISe 207 (Cluster VIII) Ranked first in grain yield while ISe 10 (Cluster XIV) was earlier with regard to number of days to half bloom. Utilizing these types which are highly divergent is likely to result in wide spectrum of variability through hybridization. The rank total analysis disclosed that number of branches, grain yield, panicle length and grains per branch contributed maximum to genetic divergence.

In earlier days different geographical source were also regarded as a primary criterion for genetic diversity. But, recently it is observed that genetic materials from the same eco-geographic origin also possess diverse genetic make up and it is also not uncommon that the genetic materials of different eco-geographic origin possess similar genetic architecture. The divers genetic collections in Fox tail millet were not utilized fully in this aspect and so far less work has been reported. Hence as a primary to genetic improvement a study was undertaken, to quantitatively estimate the genetic diversity by Mahalanobis' D^2 analysis method in this crop and the results are presented hereunder

MATERIAL AND METHODS

Fifty genotypes of fox-tail millet with diverse geographical origin, were chosen from the germplasm bank maintained at the Millet Breeding Station, Tamil Nadu Agricultural University, Coimbatore, for the study. The experiment was laid out in a randomised block design replicated thrice. A spacing of 40 × 15 cm was adopted. The recommended agro-

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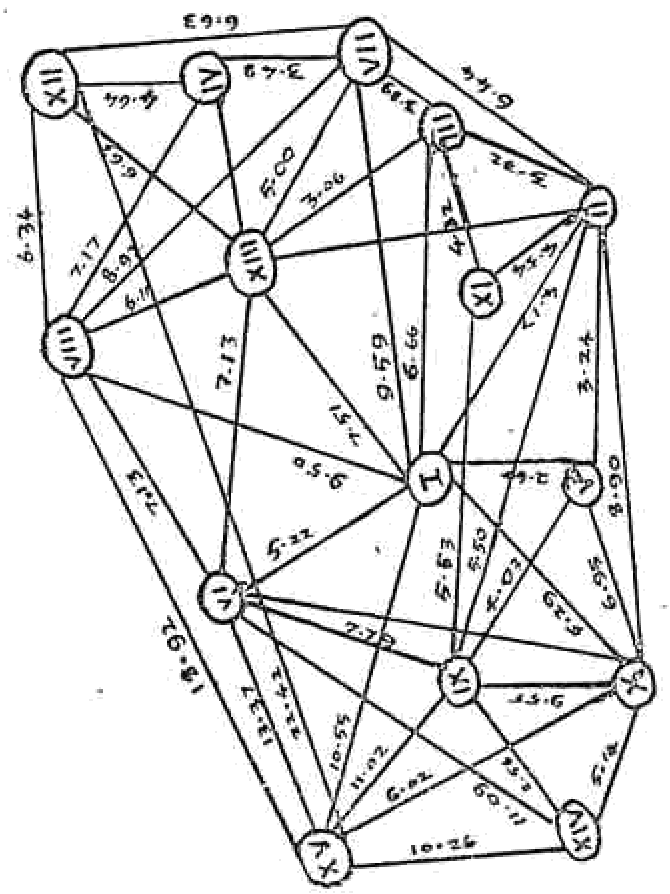

FIG. I. STATISTICAL DISTANCE AMONG FIFTEEN CLUSTERS OF FOX-TAIL MILLET (not to scale)

TABLE I Analysis of Variance for Nine characters in fox Tail Millet

Source		Plant height	Days to half bloom	Productive tillers	Panicle length	No. of branches	Grains per branch	Grain weight	Straw yield	Grain yield
Genotypes	49	1222.171**	79.428**	9.262**	26.122**	901.510**	643.340**	6209.921**	902.743**	10.335**
Error	98	35.942	4.517	1.160	1.493	114.347	59.863	3287.549	86.807	10.412

** Significant at 1 per cent level.

TABLE II Composition of D_2 Clusters

Cluster	No. of types	Designation	Source
I	2	ISe 182	Tamil Nadu
		ISe 259	Karnataka
II	6	ISe 5	Andhra Pradesh
		ISe 198A	Tamil Nadu
		ISe 236	Karnataka
		ISe 172	Madhaya Pradesh
		ISe 31	West Bengal
		ISe 109	Himachal Pradesh
III	3	ISe 23	West Bengal
		ISE 271	Karnataka
		S.I. 76/4	Tamil Nadu
IV	2	ISe 454	U.S.A.
		ISe 380	Tiripura
V	5	360	Uttar Pradesh
		192	Tamil Nadu
		220A	Meha
		315B	Uttar Pradesh
		270	Karnataka
VI	12	99B	Gujarat
		344	Uttar Pradesh
		249A	Karnataka
		383	Manipur
		93	Bihar
		269	Karnataka
		Co. 4	Tamil Nadu
		268	Karnataka
		144	Madhya Pradesh
		155	Madhya Pradesh
		186B	Tamil Nadu
		63	Bihar
VII	3	ISe 142A	Madhya Pradesh
		SI 80/2	Tamil Nadu
		ISe 140	Kerala
VIII	2	203	Tamil Nadu
		207	Tamil Nadu
IX	4	CO 3	Tamil Nadu
		228A	Karnataka
		142B	Madhaya Pradesh
		165	Madhaya Pradesh

X	3	237	Karnataka
		9	Andhra Pradesh
		284	Karnataka
XI	2	233A	Karnataka
		220B	Maharastra
XII	2	201	Tamil Nadu
		176	Tamil Nadu
XIII	2	330	Uttar Pradesh
		205	Tamil Nadu
XIV	1	10	Andhra Pradesh
XV	1	8	Andhra Pradesh

nomical practices were followed. Five plants were selected at random in each genotype in each replication. The date were subjected to multivaiate analysis (Rao, 1952). The original mean values (X's) were transformed to normalized variables (X's) and the correlated normalized variables were converted into uncorrelated variables (Y's) as follows:

$$Y_1 = X_1$$
$$Y_2 = X_2 - a_{2\,1}\ Y_1$$
$$Y_3 = X_3 - a_{3\ 2}\ Y_2 - a_{2\ 1}\ Y_1$$
$$. = \ldots\ldots\ldots$$
$$Y_P - X_P - a_{P-1}\ Y_{P-1} \ldots a_{P\,1}\ Y_1$$

where,

X_1 = normalized variables

$$a_{ij} = \frac{b_{ij}}{V(Y)j} \quad j\ i-1$$

$$b_{ij} = \lambda\, ij - \sum_{t=i-1} a_{jt}\ b_{it}$$

$$V(Y_i) = \lambda\ ii - \sum_{j=1}^{i-1} a_{ij}\ b_{ij}$$

$\lambda\, ij$ = Co-variance of i and j

All possible $\left|\frac{n(n-1)}{2}\right|$ D^2 values were calculated by taking the sum of the differences between pairs of corresponding Y values considering two genotypes at a time. All the above said computations were made in TDC 312 electronic computer installed at the Computer Centre, PSG College of Technology, Coimbatore.

Determination of the group constellations or clusters

For determining the group constellations, a relatively simple criterion suggested by Tocher (Rao, 1952) was followed. The criterion of grouping was that, any two population belonging to the same cluster should, atleast on the average, show a smaller D^2 than those belonging to different clusters. To start with, two closely associated types were selected and a third type which had the smallest average D^2 from the first two was added. Similarly, the fourth one was chosen to have the smallest average D^2 from the first three and so on, as outlined below:

Population added to a cluster	D^2	Number of terms (n)	$\frac{\text{Increase in } D^2}{\text{Increase in n } D^2}$	Average $D^2 = \frac{D^2}{n}$	Cluster

Ranking of component D^2 values

Ranking of individual D^2 values contributed by each character was worked out for nine characters by using the principle that the highest contribution of a particular character is indicated by its lowest rank total and *vice versa* (Murty *et al.*, 1965b).

RESULTS AND DISCUSSION

Analysis of variance showed significant differences among the types for all the characters studied (Table I). The plot means of the fifty genotypes were transformed into standardised uncorrelated mean values and the D^2 values were computed for all the possible $\left(\frac{n\ (n-1)}{2} = 1255\right)$ pairs of varieties. The generalised D^2 values ranged from 1.40 to 530.60. By the application of clustering technique, the fifty types were grouped into fifteen different clusters. The constituents of the clusters with their source are presented in Table II. Among the fifteen, cluster VI was the largest consisting of twelve types followed by Cluster II which had six types. Cluster V and cluster IX had five and four types respectively. Clusters III, VII and X had three types each. The clusters I. IV, VIII, XI, XII and XIII included two types each and the clusters XIV and XV consisted of only one type each.

The clusters VIII and XII comprised types from same geographic region (Tamil Nadu) indicating identical genetic architecture among them. Such a parallalism was also reported by Ram and Panwar (1970) in rice. Each one of the other 13 clusters had types from different geographic regions. This leads to the inference that factors other than geographic diversity may be responsible for such grouping. Many earlier studies on D^2

statistic in crops like rice (Vairavan et al., 1973) wheat (Yadav et al., 1974) maize (Moll et al. 1962) and sorghum (Mehndiratta et al., 1971) revealed the lack of relationship between geographical diversity and genetic diversity. This may perhaps be due to the free exchange of breeding materials from one place to other (Verma and Mehta, 1976) and varieties evolved under similar selection pressure will cluster together irrespective of their geographic origin (Singh and Bains, 1968).

The thirteen types of Tamil Nadu were found to be one or more components of ten of the fifteen clusters. This indicates the presence of wide genetic variability among the materials though they belong to same eco-geographic region. Clausen and Heisey (1958) and Singh et al. (1971) felt that even the temperature and rainfall pattern respectively could influence crop characters of the same races. Another reason which may be attributed to such varieties is the differential adaptation of various types belonging to the same eco-geographic region. Murthy and Arunachalam (1966) explained that such a wide adaptability could be possible due to reasons such as heterogenity, genetic architecture of the populations, past history of the selection, developmental factors and degree of general combining ability.

For pedigree breeding, inter-crossing these groups of parents from the same geographic region which are divergent among themselves are more desirable than choosing parents from other region (Gupta and Singh, 1970).

The intra and inter-cluster D^2 and D values among the fifteen clusters are presented in Table III. The statistical distances among the clusters based on D values are also represented diagrammatically (Fig). The intra-cluster generalised distances ranged from 1.10 to 4.97. The lowest intra-cluster distance was recorded by the cluster I and maximum by XIII. The highest Inter-cluster divergence was recorded between the clusters XII and XV (22.42) while the clusters I and V were the closest (2.66)

Based on the inter-cluster distances (D), the clusters XV, XIV and XII were found to be highly divergent from others. The types involved in these clusters on one hand and the types of other clusters on the other may serve as potential parents in heterosis breeding. Adequate relationship between the extent of heterosis and genetic divergence was reported in tomato by Rajanna et al. (1977). It is also claimed that there exists a positive relationship between the specific combining ability and the degree of genetic diversity (Murthy and Anand, 1966).

The cluster means for the various characters are presented in Table IV. The cluster IV had the highest mean values for plant height, panicle length, number of branches, grain weight and straw yield. While the cluster VIII possessed the highest mean values for

TABLE III Intra and inter Cluster Average D^2 and D (Within Parenthesis) Values

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	1.40 (1.18)	17.35 (4.17)	44.41 (6.66)	106.39 (10.31)	7.08 (2.66)	27.30 (5.22)	91.88 (9.59)	90.30 (9.50)	13.16 (3.63)	27.97 (5.29)	38.20 (6.18)	144-94 (12.04)	56.41 (7.51)	46.06 (6.79)	113.43 (10.65)
II		3.74 (1.93)	11.05 (3.32)	47.86 (6.92)	10.49 (3.24)	25.17 (5.02)	41.52 (6.44)	46.35 (6.81)	30.22 (5.50)	79.15 (8.90)	21.51 (4.64)	73.52 (8.57)	18.99 (4.36)	83.51 (9.14)	209.93 (14.49)
III			2.26 (1.50)	19.80 (4.45)	26.80 (5.18)	48.64 (6.96)	15.11 (3.89)	42.85 (6.55)	56 02 (7.48)	126.99 (11.27)	18.65 (4.32)	40.63 (6.37)	9.35 (3.06)	113.55 (10.66)	294.86 (17.17)
IV				2.14 (1.46)	72.96 (8.54)	99.22 (9.96)	12.12 (3.48)	51.43 (7.17)	115 99 (10.77)	220.71 (14.86)	43.41 (6.59)	21.75 (4.66)	25.86 (5.09)	188.81 (13.74)	425.07 (20.62)
V					4.72 (2.17)	31.08 (5.57)	60.11 (7.75)	74.36 (8.62)	16.28 (4.03)	48.34 (6.56)	9.50 (4.42)	116.69 (10.80)	36.90 (6.07)	52.51 (7.25)	157.12 (12.53)
VI						19.81 (4.45)	103.87 (10.19)	50.86 (7.13)	60.61 (7.79)	83.09 (9.12)	70.43 (8.39)	116.82 (10.81)	50.95 (7.14)	123.05 (11.09)	178.66 (13.37)
VII							5.76 (2.40)	79.61 (8.92)	89.44 (9.46)	86.07 (13.64)	25.04 (5.00)	43.93 (6.63)	25.07 (5.00)	141.34 (11.89)	391.24 (19.78)
VIII								4.44 (2.11)	136.26 (11.67)	206.28 14.36)	93 61 (9.68)	40.17 (6.34)	37.31 (6.11)	239.21 (15.47)	391.24 (18.92)
IX									10.21 (3.20)	26.90 (5.19)	30.60 (5.53)	175.05 (13.23)	72.96 (8.54)	20.79 (4.56)	121.37 (11.02)
X										9.16 (3.03)	91.29 (9.55)	286.43 (16.92)	144.74 (12.03)	26.45 (5.14)	46.51 (6.82)
XI											9.28 (3.05)	96.11 (9.80)	31.09 (5.58)	59.85 (7.74)	244.42 (15.63)
XII												11.12 (3.33)	44.00 (6.63)	274.74 (16.58)	502.43 (22.42)
XIII													24.68 (4.97)	136.75 (11.69)	314.32 (17.73)
XIV														0.00 —	109.47 (10.46)
XV															0.00

TABLE IV Cluster Means for Nine Characters in Fox Tail Millet

Cluster	Plant height (cm)	Days to half bloom	Productive tillers	Panicle length (cm)	Number of branches	Grain per branch	Grain weight (mg)	Straw yield (g)	Grain yield (g)
I	136.22	53.70	6.50	16.47	67.84	46.82	372.24	35.62	16.08
II	137.04	52.31	4.97	18.67	73.58	45.43	332.28	28.65	14.66
III	133.74	52.98	4.26	20.54	79.46	59.38	362.67	26.93	15.80
IV	167.54	58.85	3.10	24.82	118.05	68.39	438.20	73.40	15.71
V	145.87	58.76	5.87	19.84	93.86	42.32	369.37	44.95	16.31
VI	121.38	51.80	5.49	16.69	73.27	40.36	307.46	28.47	12.60
VII	141.10	55.01	3.13	22.41	89.84	59.99	402.89	30.87	14.87
VIII	165.15	61.79	4.29	22.16	101.52	52.85	318.27	72.42	19.80
IX	137.95	53.69	6.96	19.38	82.35	42.93	404.48	33.26	16.51
X	119.77	51.94	8.36	16.21	71.56	34.61	382.47	24.00	15.10
XI	149.59	58.68	4.40	20.40	92.04	44.73	407.74	39.95	17.74
XII	158.44	54.74	2.73	21.17	73.50	88.29	363.60	38.70	15.54
XIII	127.57	52.40	3.57	20.21	85.60	47.90	354.90	47.35	19.37
XIV	124.50	49.20	5.97	14.03	62.00	32.07	432.83	23.03	17.08
XV	134.50	56.03	10.93	15.01	86.53	26.30	389.00	33.07	9.35
Range	119 77 to 167.54	49.20 to 61.79	2.73 to 10.93	14.03 to 24.82	62.00 to 118.05	26.30 to 88.29	307.46 to 438.20	23.03 to 73.40	9.35 to 19.80

the characters grain yield and days to half bloom the lowest mean values for days to half bloom, panicle length, number of pranches and straw yield were recorded by the cluster XIV. The types of cluster IV were highly divergent from the types belonging to seven other cluster was also superior for straw yield, grain weight, number of branches, panicle length and plant height. The cluster XIV was highly divergent from nine other clusters and also recorded the lowest number of days to half bloom. Hence, intercrossing the types of these clusters may result in enlarged variability and selection for these traits could result in higher yield combined with earliness. Thus, the following types may be suggested as parents for hybridization based on their means and genetic divergence.

Cluster Number	Characters	Type	
IV	Straw yield, grain weight, panicle length, number of branches and plant height	ISe	380
VIII	Grain yield	ISe	207
XIV	Earliness	ISe	10

As suggested by Murty *et al.* (1965b) the rating technique was adopted to rank the characters in the order of their contribution to total genetic divergence. The rank total for all the characters are furnished in Table V. The number of branches contributed maximum to genetic divergence (rank total 4049) followed by grain yield while days to half bloom contributed least to the genetic divergence with a rank total of 9078. The major contribution of number of branches and grain yield towards genetic divergence was also evident by their cluster means where their range was very wide and grain yield towards genetic divergence was also evident by their cluster means where their range was very wide and this focusses attention on the importance of these characters in differentiation at inter-cluster levels.

TABLE V　Rank totals for nine Characters in Fox-Tail Millet

Character	Rank total
Number of branches	4049
Grain yield	4255
Panicle length	4568
Grain per branch	4874
Straw yield	6093
Grain weight	6557
Plant height	7681
Productive tillers	7921
Days to half bloom	9078

The character days to half bloom contributed the least to genetic divergence. Based on their study in wheat, Somayajulu *et al.* (1970) concluded that selection towards uniformity could cause an eroding effect on genetic diversity. Das and Borthakur (1973) found that genetic variation was reduced in course of selection. The possibility of operation of similar phenomenon towards days to half bloom, productive tillers and plant height cannot be overlooked here also.

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