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GENETIC DIVERGENCE IN FOXTAIL MILLET (*SETARIA ITALICA* B.)

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ABSTRACT

225 genotypes of foxtail millet were subjected to multivariate analyses through Mahalanobis' D^2 statistic and canonical analysis. Both analyses suggested the existence of considerable divergence among the material. D^2 statistic resulted in 33 clusters. Genetic divergence has not been found to be related with geographical diversity.

Key words: Foxtail millet, genetic divergence, D^2 statistic, canonical analysis.

The generalized distance concept of Mahalanobis' [1] is based on multivariate analysis of quantitative traits. 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.

MATERIALS AND METHODS

225 genotypes of different geographic origin were grown in simple lattice of 15 x 15 with 2 replications at the Main Research Station, Hebbal, Bangalore. Each entry was grown in 2 rows of 1.5 m length at the spacing of 22 x 10 cm. The mean data recorded on ten random plants per entry in each plot were subjected to analysis of variance as well as multivariate analysis of D^2 statistic according to Mahalanobis' [1]. The genotypes were grouped on the basis of minimum generalized distance using Tocher's method as described by Rao [2]. Canonical analysis was also done following [2].

RESULTS AND DISCUSSIONS

The analysis of variance showed highly significant differences among the genotypes for 14 out of 16 characters studied. Wilk's criterion has shown highly significant differences (χ^2=8864 for 3584 d.f.) among the genotypes for the aggregate effect of all the characters.

The differences suggest the existence of considerable divergence among the genotypes. Following Tocher's method of clustering, all the genotypes were grouped into 33 clusters (Table 1).

The intracluster D^2 values ranged from 25.5 (cluster 4) to 57.0 (cluster 18). There were 15 solitary clusters possessing single entries with no intracluster distance. The intercluster D^2 values varied from 53.8 (between clusters 12 and 18) to 981.7 (between clusters 29 and 32).

Canonical analysis was employed to obtain the spatial positions of all the 225 genotypes on a graph. Arbitrarily these were grouped into eight clusters. The genetic distance was superimposed on these groups.

The knowledge of the characters influencing divergence is an important aspect for a breeder. In the present study, Mahalanobis' D^2 statistic indicated that days to maturity, panicle weight, grain weight, seed density, leaf angle and peduncle length contributed for the maximum divergence which were also confirmed by the canonical analysis.

The present findings reveal that genetic divergence has no relationship with the geographic distance as observed by the random pattern of distribution of genotypes into various clusters from different eco-geographic regions. Relationship between genetic diversity and geographic diversity has been observed in some crops [3–7]. The absence of relationship between genetic diversity and geographic diversity suggests that forces

Table 1. Composition of clusters based on D^2 statistic in foxtail millet

Cluster	No. of genotypes	Source	No. of genotypes from different sources
1	2	3	4
1	87	India	69
		USA	14
		Kenya	2
		Africa	1
		Turkey	1
2	26	India	21
		Ethiopia	1
		USA	3
		China	1
3	19	India	15
		USA	1
		Ethiopia	1
		Africa	1
		China	1
4	8	India	7
		USA	1
5	11	India	9
		USA	2
6	14	India	13
		USA	1
7	12	India	10
		USA	2
8	8	India	8
9	5	India	5
10	3	India	2
		USA	1
11	3	India	3
12	2	India	1
		USA	1
13	2	India	1
		Africa	1
14	2	India	2
15	2	India	2
16	2	India	1
		China	1
17	2	India	2

(Contd.)

other than geographic origin, such as, exchange of breeding material, genetic drift, variation, natural and artificial selection are responsible for diversity, as reported earlier [8–15].

It is suggested that selection of parents for hybridization should be based on genetic diversity and not on geographic diversity. The importance of this aspect has also been emphasized by earlier workers [3, 16, 17].

The present study concluded that considerable amount of genetic diversity is present among the entries for yield and yield attributes. Six solitary clusters were superior, viz. clusters 24, 26, 27, 30, 31 and 32. Intercrossing between genotypes of these diverse clusters would generate a broad spectrum of variability for effective selection in the segregating generations for the development of high yielding cultivars.

Table 1 (Contd.)

1	2	3	4
18	2	India	2
19	1	USA	1
20	1	India	1
21	1	India	1
22	1	India	1
23	1	Kenya	1
24	1	Turkey	1
25	1	USA	1
26	1	Turkey	1
27	1	India	1
28	1	India	1
29	1	USA	1
30	1	India	1
31	1	India	1
32	1	USA	1
33	1	India	1

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