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Divergence Analysis for Important Yield Contributing Characters in Foxtail Millet (*Setaria italica* (L.) P. Beauv.)

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Abstract

Genetic diversity was assessed in 57 genotypes of foxtail millet *Setaria italica* (L.) P. Beauv. By using D^2 analysis. The genotypes were grouped into eight clusters. The maximum number of genotypes were included in cluster III (11 genotypes), which was followed by cluster I, IV, V, VI, VII, II and cluster VIII. Cluster with small statistical distance considered less diverse than those with large distances. The intra cluster value was maximum in cluster VI and minimum in cluster VIII. Cluster VII showed the highest mean values for Flag leaf length, flag leaf width, ear length, biological yield and grain yield/plant. The characters responsible for genetic divergence were plant height, biological yield, grain yield, flag leaf length, flag leaf width and ear length.
Key words : Genetic divergence, Cluster analysis, Foxtail millet, Yield.

Foxtail millet *Setaria italica* (L.) P. Beauv is one of the world's oldest cultivated crops. Its domestication and cultivation is estimated to have occurred over 4000 years ago 1. It is the most important small millet in India and grown extensively in diverse agro climatic regions for grain and fodder. It provides approximately 6 million tonnes of food to millions of people, mainly in southern Europe and subtropical Asia. Known for its drought tolerance, it is an indispensable crop of vast rainfed areas in semi-arid regions in India 2. The grain is a good source of protein and contains high amount of beta carotene, which is the precursor of vitamin-A. There is wide genetic diversity available in foxtail millet, and characterizing these resources is a prerequisite for the genetic improvement of its cultivars. Germplasm may be considered as one of the important natural resources. The primary goals of germplasm enhancement are high yielding, good quality, resistance to biotic stress and wider adaptation. Genetic improvement is the only component to stabilize the crop and crop improvement. Evaluation of genetic diversity is important to know the source of genes of a particular trait within the available germplasm 3. Knowledge of genetic di-

Table 1. Different clusters, genotypes, Intra and inter cluster distance in foxtail millet.

Clusters	No.of genotypes	Name of genotypes
I	10	SIA-3015, VFMC-319, GBISC-97, GBGS-1339, GBGS-779, GBGS-1832, GBGS-1663, GB KRISHNAMODEVARAYA, GBGS 1175, GBGS-537
II	4	RFM-13, RFM-11, GBGS-2236, GBGS-1097
III	11	SR-17, KSE-11, CO-6, SR-51, TANU-170, TANU-201, TANU-207, GBGS-848, GB NARSIMBARAYA, GBSIA-92, GB SRILAKASHMI
IV	10	CO-5, CO-7, TANU-190, GBSIA-2870, GBGS-2143, GB PRASAD, GB KRISHNAMODEVARAYA, GBGS-2252, GBGS-702, GBSIA-2720
V	8	SIA-3017, SIA-2867, SIA-2876, TNAU-193, PS-4, TANU-192, TANU-04, GBGS-1494
VI	7	SIA-2881, SIA-2871, TNAU-200, TNAU-196, TNAU-186, GBGS-97, GBGS-1566
VII	6	SIA-2882, SIA-326, SIA-3020, TANU-173, TANU-198, TANU-199
VIII	1	VFMC-308

Table 2. Average intra-and inter-cluster D^2 values in 57 genotypes of foxtail millet. * Figures in bold font indicate intra-cluster D^2 values.

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**1.589***							
II	2.911	**1.732**						
III	2.938	5.338	**1.649**					
IV	1.945	3.297	3.016	**1.385**				
V	2.697	4.490	2.148	2.296	**1.290**			
VI	4.136	6.210	2.009	3.340	2.253	**1.663**		
VII	4.441	6.938	2.592	4.150	3.456	2.545	**2.269**	
VIII	11.147	12.911	9.195	10.077	9.935	8.330	7.387	**0.001**

versity among population usually helps a breeder in choosing desirable parents for breeding program as selection of parents on the basis of divergence analysis. Therefore, to initiate hybridization, the genotypes are to be classified into clusters based on the genetic diversity and the extent of genetic divergence between them needs to be estimated. The D^2 statistics is one of the powerful tools to assess the relative contribution of different component traits to the total diversity, to quantify the degree of divergence between populations and to choose genetically diverse parents for obtaining desirable recombinants. Therefore, the present investigation was undertaken to estimate the extent of genetic diversity between 57 genotypes of foxtail millet.

Methods

The experimental material consisted of 57 diverse foxtail millet accessions collected from different reliable sources. The material was grown in simple randomized block design with two replication at the research form attached to the Department of Genetics and Plant Breeding at Ch. Charan Singh University campus, Meerut. All the recommended agronomic and cultural practices were followed for raising a good crop. Data were recorded on five randomly selected plants per replication of each genotype for ten-agronomic characters viz., days to 50% flowering, days to maturity, plant height (cm), flag leaf length (cm), flag leaf width (cm), spike length (cm), grain yield/plant, biological yield/plant (g), harvest index. These data were used to statistical analysis 4,5. Statistical analysis was done by using the following computer software SPAR-1 developed by scientists at Indian Agricultural Statistics Research Institute, New Delhi.

Results and Discussion

The analysis of variance (ANOVA) exhibited significant differences among genotypes for all the ten characters studied. Based on D^2 values, 57 foxtail millet genotypes were grouped into eight different clusters by using clustering technique. The genotype dis-

Table 3. Cluster mean values for nine characters in foxtail millet and their contribution.

	Cluster mean values							
Characters	I	II	III	IV	V	VI	VII	VIII
Days to 50% flowering	56.15	51.12	56.55	58.05	52.12	58.14	72.67	**106.00**
Days to maturity	92.65	82.88	95.59	92.75	88.88	92.21	119.00	**139.00**
Plant height (cm)	104.22	91.30	112.59	112.59	119.16	126.57	128.90	**141.90**
Flag leaf length (cm)	32.25	31.70	39.16	36.57	33.01	39.64	37.15	**52.95**
Flag leaf width (cm)	1.73	1.80	1.97	1.80	2.00	2.09	2.00	**2.47**
Ear length (cm)	17.48	12.82	20.82	19.13	20.06	24.68	22.75	**28.35**
Biological yield (g)	10.20	7.69	14.86	12.52	15.93	16.86	16.24	**28.40**
Grain yield (g)	3.34	1.75	5.65	3.01	4.79	5.39	6.04	**6.80**
Harvest index (%)	33.27	22.47	**37.88**	24.12	30.13	32.04	37.26	23.95

Table 4. Genetically divergent clusters and their desirable characters.

Cluster no.	Desirable traits
VII	Flag leaf length, Flag leaf width, Ear length, Biological yield and Grain yield.
II	Days to 50% flowering, Day to maturity and Plant height.
III	Harvest index.

Table 5. Genetically divergent genotypes identified from different clusters and their desirable characteristics.

Genotype	Cluster no.	Desirable traits
VFMC-308	VIII	Flag leaf length, flag leaf width, ear length, biological yield and grain yield.
RFM-3	II	Days to 50% flowering, days to maturity and plant height.
CO-6	III	Harvest index.

tributions are presented in Table 1. The number of genotype in each cluster varied. The maximum number of genotypes were included in cluster III (11 genotypes), which was followed by cluster I, IV, V, VI, VII, II and cluster VIII. The pattern of distribution of genotypes in eight clusters confirmed the existence of diversity among the genotypes indicated by analysis of variance.

The intra and inter cluster values among the eight cluster are presented in Table 2. The intra cluster distance ranged from 0.001 (cluster VIII) to 2.269 (cluster VII). Maximum intra cluster distance in cluster VII indicated that genotypes in this cluster were relatively more diverse than the genotypes within other clusters. The inter cluster distance varied from 12.911 between clusters VIII and II to 1.945 between clusters IV and I. Therefore, hybridization between lines selected from different clusters.i.e. male parent from one cluster and female parent from the other and vice-versa is likely to produce most heterotic hybrids. The relative divergence of each cluster from other cluster (i.e. inter cluster distance) has been of high order and divergence particularly between the members of cluster VIII with the members of all other cluster (Table 2), hence, crossing between the genotypes of such clusters too may be rewarding.

The genetic differences between the clusters were reflected in the cluster means. A comparison of cluster means for the various characters is presented in Table 3. The desirable genotypes within the divergent clusters can be identified on the basis of the mean performance of individual genotypes within the clusters. The following points need to be considered while selecting desirable genotype : Choice of clusters that were separated by maximum inters cluster distance; selection of particular genotypes that showed good performance in the selected clusters. Table 3 shows that divergent cluster VIII had highest mean value for a no. of characters including flag leaf length,flag leaf width, ear length, biological yield and grain yield but it is late maturing and tall. Likewise, cluster II had lowest mean value for days to 50% flowering, days to maturity and plant height and cluster III had highest mean value for harvest index.

The genetic diversity may not be straightway related to geographical diversity and the similar trend was observed in foxtail millet 6. Murugan and Nirmalakumari (7) stated that type of clustering pattern could be utilized for cross combination to generate the highest possible variability for various important characters.

The mean values of the different cluster indicating the utility of divergence analysis in identifying useful parents for hybridization. In selection of the parent for hybridization, genetic divergence of both genotypes should be taken into account. Contribution of characters towards divergence are presented in Table 4 and based on the genetic diversity and superiority with respect to any of the traits the identified genotypes are presented in Table 5. The cluster VI showing maximum divergence for flag leaf length, flag leaf width, ear length, biological yield and grain yield/plant. The result indicated that these five traits contributed maximum towards diversity of genotypes. It may be concluded that the greater divergence in the genotypes due to these characters in the respective clusters would offer a good scope for the improvement of foxtail millet through rational selection.

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