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Genetic divergence studies in induced mutants of *Rabi* sorghum (*Sorghum bicolor* (L.) Moench)

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Abstract

The mutant lines analysis based on Mahalanobis's D^2 statistic (D^2 values) fifty-seven genotypes were grouped into thirteen clusters. The cluster III was with the highest number of genotypes (27) followed by cluster I (16), cluster II (04), cluster IV, V, VI, VII, VIII, IX, X, XI, XII, XIII had single genotype. The intra cluster distance (D) range from 4.70 to 20.03. The maximum inter cluster distance ($D = 20.03$) was observed between cluster XIII and cluster II, followed by cluster X and II ($D = 18.08$), cluster X and cluster VIII (17.32), cluster XII and cluster IX ($D = 16.91$). The minimum inter cluster distance ($D = 4.70$) was between VII and V. At inter cluster level, cluster XIII and II had the highest value which was followed by cluster X and II. The D^2 analysis carried out thus helped to identify the diverse accessions from the available mutant lines for the use in crop improvement programmes.

Keywords: sorghum, diversity, D^2

Introduction

Sorghum (*Sorghum* spp.) is one of the common grain which mostly cultivated predominantly in countries like USA, China, India and Africa. Sorghum grain is used as a food to humans and animals. Sorghum is the third most important cereal crop cultivated extensively in India after wheat and rice. Sorghum grown in *rabi* season is characterized by its excellent grain quality, exclusively utilized for human consumption and hence fetches higher market price as compared to *kharif*. Understanding of genetic diversity of a species is fundamental in any crop improvement programme. For such species, in general the parents with more genetic divergence are expected to yield heterotic hybrids in addition to generating a broad spectrum of variability in segregating generations. The D^2 statistic is a useful multivariate statistical tool for effective discrimination among various genotypes on the basis of genetic divergence (Murty and Arunachalam, 1966; Sonawane and Patil, 1991) [4, 8]. Hence, an attempt has been made to study the genetic divergence in available germplasm of sweet grain sorghum for percent threshed grains and fodder yield and its components to provide a basis for selection of parents for hybridization.

Materials and Methods

Experimental material for the proposed work consists of Promising M_4 mutant lines of *rabi* Sorghum variety Parbhani Moti generated by gamma rays and EMS treatments. Total 51 mutant lines and six checks (Parbhani Moti, Parbhani Super Moti, M-35-1, CSV-22R, CSV-29R and PKV kranti), was evaluated at experimental field of Department of Agricultural Botany, VNMKV, Parbhani during *Rabi* season 2019-20 in a randomized block design with two replications. Each entry was planted in 2 rows of 4 m length keeping 45 x 15 spacing. Divergence was estimated by the multivariate analysis using Mahalanobis's (1936) [3] and D^2 statistic as described by Rao (1952) [5]. On the basis of D^2 values obtained, the variables were grouped into different clusters by employing Tocher's method (Rao, 1952) [5]. The percent contribution of each character to the total divergence was calculated by ranking each character on the basis of transformed uncorrelated values. Finally, the percent contribution for each character was calculated by taking total number of ranks of all the characters to hundred.

Results and Discussion

The analysis of variance showed highly significant differences among the accessions for all the characters studied indicating the presence of considerable variability in the experimental material. The percent contribution of different characters to the total diversity is presented in the Table 1.

Fodder yield per plant contributed enormously (39.79%) to the total variation followed by Protein content (12.84%) and Zn content (12.59%).

Clustering pattern on D² values

The clustering pattern obtained on the basis of magnitude of D² values studied, are presented in Table 1.

These fifty-seven genotypes were grouped into thirteen clusters. The cluster III was with the highest number of genotypes (27) followed by cluster I (16), cluster II (04), cluster IV, V, VI, VII, VIII, IX, X, XI, XII, XIII had single genotype. The intra cluster distance (D) range from 4.70 to 20.03. The maximum inter cluster distance (D = 20.03) was observed between cluster XIII and cluster II, followed by cluster X and II (D = 18.08), cluster X and cluster VIII (17.32), cluster XII and cluster IX (D = 16.91). The minimum inter cluster distance (D = 4.70) was between VII and V. The maximum amount of heterosis is expected from the crosses with parents belonging to the most divergent clusters as has been reported by Katiyar and Singh (1990) [2], Arora *et al.*, (1991) [1] and Umakanth *et al.*, (2003) [8]. At inter cluster level, cluster XIII and II had the highest value which was followed by cluster X and II.

Cluster means

The cluster mean for the ten characters are presented in Table 4.7. A considerable inter cluster variation was observed among the cluster means for the characters studied *viz.*, days to 50 per cent flowering, plant height, days to physiological maturity, number of primary per panicle, number of grains per

primaries, Panicle length, Panicle width, panicle weight, 100 seed weight, Grain yield per plant, Fodder yield per plant, Fe content, Zn content, protein content.

The cluster mean for days to 50 per cent flowering varied from 67.50 (XII) to 79.63 (II). The highest cluster mean for plant height was 281.00 cm, which was observed in cluster (VIII) and lowest for cluster II (98.75). The cluster means for days to Physiological maturity ranged between 109 (XII) to 125.25 days (II). The cluster mean for the number of primary per panicle ranged from 21.63 (cluster II) to 31.50 (cluster X). The cluster mean for number of grains per primaries ranged between 28.63 (cluster II) to 36.00 (cluster XII). The highest cluster mean for panicle length was 21.0 cm, which was observed in cluster (VI) and lowest for cluster II (14.75). The cluster means for days to Panicle width ranged between 6.50 (IX) to 11.50 (XIII).

The cluster mean for panicle weight was maximum in cluster V (134.50) and it was minimum in cluster II (85.25). The cluster mean for 100 seed weight was maximum in cluster (X) 4.90 and it was minimum in cluster II (3.88). The cluster mean for grain yield per plant was minimum in cluster IV (49.50) and it was maximum in cluster XI (79). The cluster mean for fodder yield per plant ranged between 37 (cluster XII) and 150.50 (cluster IX). The highest cluster mean for Fe content was 40.15, which was observed in cluster (IX) and lowest for cluster VIII (30.65). The cluster means for Zn content ranged between 19.80 (IX) to 28.65 (XI).

The cluster mean for protein content was maximum in cluster VIII (14.26) and minimum in cluster XII (10.49).

Table 1: Percentage Contribution of Different Characters To The Total Diversity

Sr. No.	Characters	No. of times appearing 1 st in ranking	% Contribution
1.	Days to 50% flowering	33	2.07
2.	Plant height (cm)	58	3.63
3.	Days to physiological maturity	21	1.32
4.	Number of primaries per panicle	59	3.70
5.	Number of grains/primaries	36	2.26
6.	Panicle length(cm)	37	2.32
7.	Panicle width(cm)	24	1.50
8.	Panicle weight (gm)	158	9.90
9.	100-seed weight (g)	6	0.38
10.	Grain yield per plant (g)	120	7.52
11.	Fodder yield per plant (g)	635	39.79
12.	Fe content (ppm)	3	0.19
13.	Zn content (ppm)	201	12.59
14.	Protein content (g/100g)	205	12.84
	Total	1496	100%

Table 2: Average Intra and Inter Cluster D² Values In Sorghum.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	41.73	156.25	81.54	67.07	53.29	63.36	57.60	129.96	77.96	87.98	78.67	158.50	133.63
II		29.81	159.26	284.59	217.85	207.64	264.06	255.68	208.80	326.88	156.01	222.60	401.20
III			58.21	94.28	90.44	97.21	98.01	115.34	145.44	133.86	85.00	87.04	175.82
IV				0.00	62.25	58.21	31.34	153.01	94.09	41.34	103.42	139.71	83.17
V					0.00	65.93	22.09	102.01	83.53	39.94	57.30	211.70	58.82
VI						0.00	65.44	216.38	37.69	65.28	80.28	190.99	147.37
VII							0.00	134.09	85.93	32.14	75.86	179.56	63.52
VIII								0.00	299.98	159.51	134.32	144.96	100.60
IX									0.00	89.49	109.20	285.94	206.20
X										0.00	94.67	252.49	52.27
XI											0.00	171.87	119.90
XII												0.00	266.01
XIII													0.00

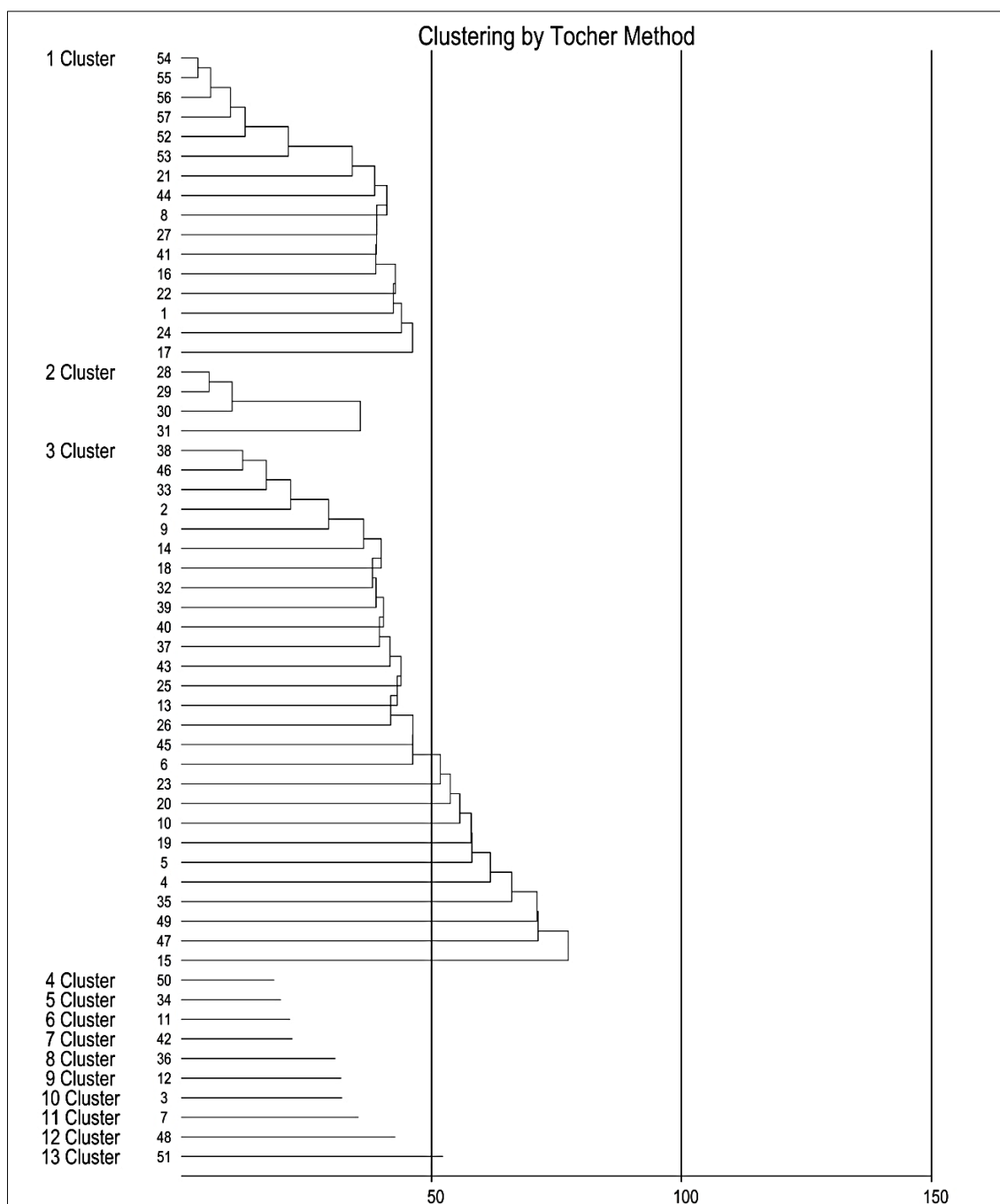


Fig 1: Clustering of Mutant Lines by Tocher's Method

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