Research Article

Genetic Diversity in Guinea Grass (*Panicum maximum* Jacq.) for Fodder Yield and Quality using Morphological Markers

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Abstract

Divergence analysis of 60 genotypes for ten biometrical traits was carried out using Mahalanobis D2 statistic. The genotypes were grouped into ten clusters. The cluster I was the largest with 30 genotypes followed by cluster II with 15 genotypes, cluster III with seven genotypes, cluster IX with two genotypes and clusters IV, V, VI, VII, VIII and X had accommodated only single genotype each. The inter cluster distances were greater than intra cluster distances, revealing that considerable amount of genetic diversity existed among the accessions. Based on cluster mean, cluster VIII had highest mean values for leaf weight, leaf stem ratio and green fodder yield per plant, cluster V had highest mean values for number of tillers per plant, number of leaves per plant and crude protei content. The accessions GGLC 12 and GGLC 19 may serve as potential genotypes for development of Guinea grass varieties with improved fodder yield and quality.

INTRODUCTION

Among the grasses, Guinea grass (*Panicum maximum* Jacq.) is an important forage grass of tropical and semi tropical regions, largely apomictic and predominantly exist in tetraploid form. It is also endowed with virtues like profuse tillering, high leafiness, thin stems, short duration, *etc.,* all of which contributed towards high biomasss production and better palatability. It is extensively cultivated under irrigated condition on fairly rich soils and is popular with dairy farmers. At present in India there is a deficit of 64 per cent of green fodder, and hence there is a need of over production of quality fodder especially the range grasses which could rejuvenate the fast degrading grasslands. In order to improve the productivity, adaptability and quality of Guinea grass, it is important to understand the genetic diversity that exist in the population which also helps in their conservation and germplasm management [1]. Genetic diversity is an important factor and also a pre-requisite in any breeding programme. Inclusion of diverse genotypes in breeding programme serves the purpose of producing desirable genotypes. Multivariate analysis by means of Mahalanobis D^2 statistic is a powerful tool in quantifying the degree of divergence at genotypic level. Therefore, the present study was undertaken to estimate the amount of genetic diversity among 60 germplasm accessions of Guinea grass (*Panicum maximum* Jacq.) and to identify genetic diverse genotypes for breeding programme aimed at yield and quality improvement in this crop.

MATERIAL AND METHODS

The experimental material consisted of 60 germplasm accessions of Guinea grass (*Panicum maximum* Jacq.) obtained from various countries and maintained at Department of Forage Crops, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. The accessions were planted using rooted slips on one side of ridge of 4 metres length, adopting a spacing of 60 x 50 cm in a Randomized Block Design with two replications. All the agronomic practices were followed to maintain the crop stand. The biometrical observations on fodder yield were recorded on single plant basis at the time of harvesting as per descriptors for *Panicum miliaceum* L. [2] and characterization of perennial *Panicum* species [3].

For recording single plant observations, three plants from each entry/replication were randomly selected. Average of these three plants in respect of plant height, number of tillers and leaves per plant, leaf weight, leaf stem ratio, green fodder yield per plant and dry matter content and the same plants were subjected for the estimation of quality parameters such as crude protein, crude fibre and crude fat content was used for statistical analysis. Mahalanobis D^2 statistic [4] was employed to assess the

genetic diversity and clustering of genotypes was done according to Tocher's method as described by Rao [5].

RESULTS AND DISCUSSION

Genetic diversity is the basic requirement for successful breeding program. Collection and evaluation of germplasm lines and genotypes of any crop is a pre-requisite for any breeding programme, which provides a greater scope for exploiting genetic diversity. The multivariate analysis (D^2) is a powerful tool to measure the genetic divergence within a set of genotypes [6]. The present study was planned to examine the trend of genetic divergence in 60 germplasm accessions of Guinea grass. The analysis of variance revealed highly significant differences among accessions for all the characters under investigation thereby indicating the presence of a considerable magnitude of genetic variability among the experimental material (Table 1).

All the accessions were grouped into ten clusters thereby indicating large amount of genetic diversity exist among the accessions are presented in (Table 2) and the same depicted in (Figure 1). Among the ten clusters, the cluster I was the largest having 30 accessions indicating overall genetic similarity among them, followed by this, the cluster II have possessed 15 genotypes and cluster III consisted seven genotypes, cluster IX had two genotypes and clusters IV, V, VI, VII, VIII and X had included only single genotype each. The clustering pattern showed that the genetic diversity and geographic origin need not necessarily be related since genotypes belonging to different centres of origin were found to be present in the same cluster. The similar results were also reported earlier by More et al. [7] in fodder maize.

The intra and inter cluster D^2 values among the clusters are presented in (Table 3). The intra cluster distances were lower than that of inter cluster distances. Thus, the genotypes included within a cluster had less diversity among themselves. Cluster III recoded the highest intra cluster distance of 5.82 followed by cluster IX with a distance of 5.65, cluster II with a distance of 5.39 and cluster I with a distance of 5.20. There was six solitary clusters (clusters IV, V, VI, VII, VIII and X) possessing no intra cluster value.

The highest inter cluster distance was found between clusters III and IX (21.63) followed by clusters III and VIII (18.35), clusters III and V (17.67), clusters III and IX (16.84) and clusters II and III (15.77). The genotypes belonging to these clusters separated by high statistical distance would have greater genetic divergence and may be used in breeding programme for improvement of fodder yield and quality. The least inter cluster distance was found between clusters VI and VII (5.57). These findings are in conformity with the findings of More et al. [7] in fodder maize and Ganesan et al. [8] in maize germplasm. The mean values of ten characters for ten clusters are presented in (Table 4). Cluster VIII exhibited highest mean values for leaf weight, leaf stem ratio and green fodder yield per plant followed by cluster V for number of tillers per plant, number of leaves per plant and crude protein content, cluster IV for plant height and crude fat content, cluster I for dry matter content, cluster III for crude fibre content and cluster IX for leaf stem ratio. Thus by involving genotypes from these clusters (except cluster III which showed high crude fibre content and that may affect the digestibility) in breeding programme, high green fodder yield and quality could be achieved. To improve fodder yield and quality, the accession from cluster VIII (GGLC 12) and cluster V (GGLC 19) would be right choice. From the present investigation, it was concluded that Guinea grass displayed a wide range of diversity and there were few accessions with unique characters. The accessions GGLC 12 and GGLC 19 were distinctly separated from the other Guinea

Table 1: ANOVA showing values of mean squares for different characters in Guinea grass.

S. No.	Source of variation	Plant height (cm)	Number of tillers per plant	Number of leaves per plant	Leaf weight (g)	Leaf stem ratio	Green fodder yield per plant (g)	Dry matter content (%)	Crude protein (%)	Crude fibre (%)	Crude fat (%)
1.	Treatment	527.18*	20.45**	2152.79**	792.64**	0.0078**	5001.93**	19.44*	2.85**	8.52**	0.07**
2.	Error	332.26	10.32	369.01	170.12	0.0020	1097.98	11.68	0.44	0.21	0.03

** Significant at 1% level
 * Significant at 5% level

Table 2: Clustering pattern in 60 Guinea grass germplasm accessions.

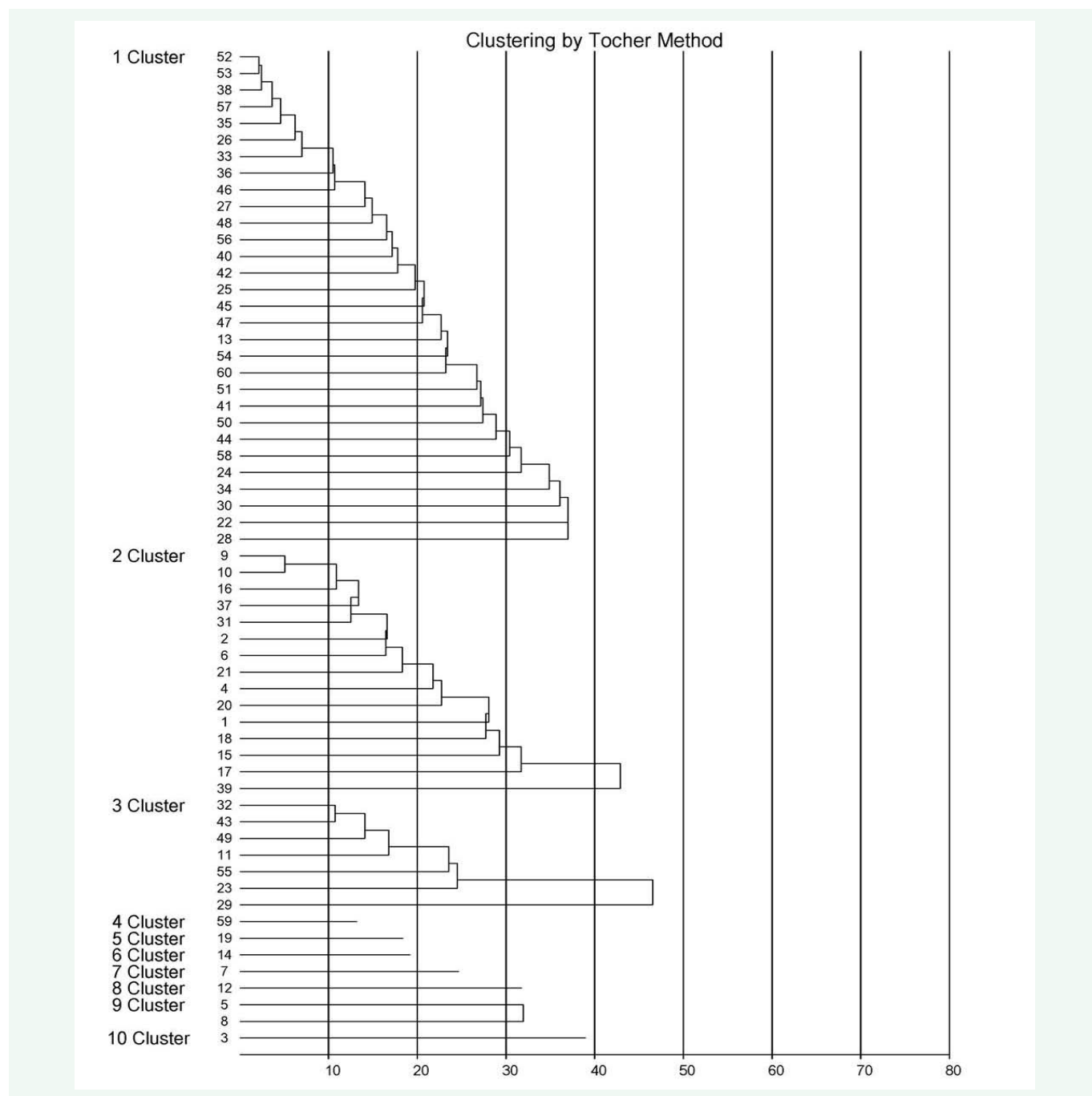| Cluster No.	Number of accessions	Accessions
I	30	FD 2192, FD 2193, FD 682, FD 2214, GG09-5, GG09-3, FD 663, FD 675, FD 791, FD 606, FD 2719, FD 2209, FD 692, FD 703, FD 137, FD 786, FD 1659, GGLC 13, FD 2199, GG09-7, FD 2189, FD 699, FD 2186, FD 783, FD 2219, FD 135, FD 667, FD 657, GGLC 22 and FD 637.
II	15	GGLC 9, GGLC 10, GGLC 16, FD 678, FD 661, GGLC 2, GGLC 6, GGLC 21, GGLC 4, GGLC 20, GGLC 1, GGLC 18, GGLC 15, GGLC 17 and FD 679.
III	7	FD 662, FD 744, FD 2184, GGLC 11, FD 2206, GGLC 23 and FD 653.
IV	1	GG09-6
V	1	GGLC 19
VI	1	GGLC 14
VII	1	GGLC 7
VIII	1	GGLC 12
IX	2	GGLC 5 and GGLC 8
X	1	GGLC 3

Figure 1 Cluster diagram showing the intra and inter cluster distance.

Table 3: Average intra (in bold) and inter cluster D^2 distances.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**5.20**	9.08	9.28	6.73	11.36	7.36	8.37	12.76	11.74	14.50
II		**5.39**	15.77	10.49	7.39	7.42	8.01	9.95	9.41	8.01
III			**5.82**	9.63	17.67	12.22	13.35	18.35	16.84	21.63
IV				**0.00**	13.59	8.26	6.89	14.50	11.84	15.91
V					**0.00**	11.30	11.23	5.63	12.55	7.14
VI						**0.00**	5.57	12.52	9.26	12.60
VII							**0.00**	11.32	9.21	11.88
VIII								**0.00**	14.32	9.75
IX									**5.65**	12.74
X										**0.00**

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Table 4: Cluster mean values for ten biometrical traits in Guinea grass.

Cluster	Plant height (cm)	Number of tillers per plant	Number of leaves per plant	Leaf weight (g)	Leaf stem ratio	Dry matter content (%)	Crude protein (%)	Crude fibre (%)	Crude fat (%)	Green fodder yield per plant (g)
I	185.68	16.88	162.18	101.74	0.30	24.03	9.69	28.28	1.41	436.73
II	172.02	18.63	198.23	104.18	0.33	21.58	10.18	25.48	1.48	422.02
III	185.26	15.90	156.98	101.41	0.32	21.80	8.39	31.21	1.44	418.70
IV	191.50	12.17	116.50	81.60	0.29	19.96	9.51	28.00	2.00	357.13
V	146.16	21.00	246.50	167.99	0.47	22.92	11.20	25.75	1.53	534.19
VI	180.66	20.33	205.83	85.22	0.30	20.59	7.09	26.75	1.51	367.62
VII	174.50	15.00	157.00	103.85	0.35	17.15	7.24	25.75	1.68	396.33
VIII	184.75	21.00	234.16	204.78	0.54	19.29	9.82	25.75	1.43	587.13
IX	159.25	19.58	195.58	114.50	0.54	18.30	9.65	25.25	1.55	329.81
X	145.00	19.50	221.50	118.77	0.34	17.25	10.68	23.00	1.39	477.00

grass genotypes. Hence, the accessions GGLC 12 and GGLC 19 may be effective in future breeding programme for development of Guinea grass varieties with improved fodder yield and quality.

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