Assessment of genetic diversity in germplasm of Guinea grass (Panicum maximum Jacq.)

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ABSTRACT

In the present study, sixty genotypes of Guinea grass were evaluated for assessing genetic diversity for ten different quantitative characters for exploitation in a breeding programme aimed at improving yield potential of Guinea grass by using Mahalanobis D2 statistics. The genotypes were grouped into ten clusters suggesting the presence of genetic diversity. The cluster I had maximum of 30 genotypes followed by II and III having 15 and 7 genotypes, respectively. These clusters having maximum number of genotypes, reflecting narrow genetic diversity. The inter cluster distances were greater than intra cluster distances, revealing that the selected genotypes were highly divergent. The maximum intra cluster distance was recorded for cluster III (5.63) while clusters IV, V, VI, VII and VIII and X (0.00) were solitary and showed no intra-cluster distance values. The genetically more divergent genotypes present in cluster III and IX as indicated by inter cluster distance value (21.63). Cluster VIII and Cluster V had least number of single genotype and emerged with contained highest cluster mean value for number of tillers/plant, number of leaves/plant, good leaf weight, leaf: stem ratio, green fodder yield/plant and crude protein content. Hence, GGLC 12 genotype in cluster VIII and GGLC 19 in cluster V can be successfully utilized in breeding programme for development of Guinea grass varieties with improved fodder yield and quality.

Key words: D2 analysis, Genetic diversity, Germplasm, Guinea grass, Quantitative traits.

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 biomass 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 exists in the population which also helps in their conservation and germplasm management (Tiwari and Chandra, 2010). The presence of genetic diversity and genetic relationships among genotypes is a prerequisite and paramount important for successful breeding programme. Inclusion of diverse genotypes in breeding programme serves the purpose of producing desirable genotypes. Multivariate analysis by means of Mahalanobis D2 statistic is a powerful tool in quantifying the degree of divergence at genotypic level. Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse genotypes for purposeful breeding. Therefore, the present study was undertaken with the aim of examining the magnitude of genetic diversity, so as to select the potential genotypes for breeding programme to attain the anticipated improvement in fodder yield and quality of Guinea grass.

MATERIALS AND METHODS

The experimental material consisted of 60 genotypes 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 meters length, adopting a spacing of 60 x 50 cm in a completely randomized block design with two replications during 2013. All packages of practice were followed to raise a healthy crop. The biometrical observations on different characters were recorded on single plant basis at the time of harvesting as per descriptors for Panicum miliaceum L. (UPOV, 2007) and characterization of perennial Panicum species (Wouw et al., 2008). In each genotype per replication three randomly selected plants were observed for 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

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crude protein, crude fiber and crude fat content (AOAC, 1995). Average of these three plants was used for statistical analysis. Mahalanobis D² statistic (1936) was employed to assess the genetic diversity and clustering of genotypes was done according to Tocher’s method as described by Rao (1952). The data were analyzed using INDOSTAT version 9.1 developed by INDOSTAT Services Ltd. Hyderabad, India.

RESULTS AND DISCUSSION

Genetic diversity is the basic requirement for successful breeding programme. Collection and evaluation of genotypes of any crop is a pre-requisite for breeding programme, which provides a greater scope for exploiting genetic diversity. The multivariate analysis (D²) is a powerful tool to measure the genetic divergence within a set of genotypes (Murthy and Arunachalam, 1966). The present study was planned to examine the trend of genetic divergence in 60 genotypes 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). Based on Mahalanobis’ D² analysis, the 60 genotypes were grouped into 10 clusters (Table 2 and Fig 1) indicating the greater genetic diversity in the material. The similar results were also reported earlier by More et al. (2006) in fodder maize. Cluster I was the largest and consists of 30 genotypes followed by cluster II have possessed 15 genotypes, cluster III with 7 genotypes, cluster IX had 2 genotypes and cluster IV, V, VI, VII, VIII and X had included only single genotype in each. It means the overall genetic similarity was found in the genotypes were presented within the cluster and the pattern of distribution of genotypes in different clusters exhibited that geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different cluster and vice-versa, as supported by earlier finding of Langade et al. (2013). Similarly sixty genotypes were dispersed in 10 clusters. The possible reason for grouping of genotypes of different places into one cluster could be free exchange of germplasm among the breeder of different region or unidirectional selection practiced by breeder in tailoring the promising cultivar for selection of different region (Verma and Mehta, 1976).

The intra-cluster D² value ranged from 0.00 to 31.70 while, inter cluster D² value ranged from 31.92 to 467.86 indicated that the selected genotypes were highly divergent (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 recorded highest intra cluster D² value of 31.70 with a distance of 5.63 followed by cluster IX (D²=31.02) with a distance of 5.57, cluster II (D²=29.05) with a distance of 5.39 and cluster I (D²=27.03) with a distance of 5.20 while
Table 2: Clustering pattern of 60 Guinea grass genotypes into 10 clusters on the basis of $D^2$ analysis.

| 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 |

Fig 1: Dendrogram showing genetic diversity in a set of 60 Guinea grass genotypes.
Table 3: Estimates of intra-cluster (bold diagonal) and inter cluster $D^2$ and distance (D) value for ten clusters in Guinea grass.

| Clusters | I | II | III | IV | V | VI | VII | VIII | IX | X |
|----------|---|----|-----|----|---|----|-----|------|----|---|
|          | 27.04 | 29.05 | 31.70 | 31.70 | 31.00 | 31.00 | 21.00 | 25.75 | 31.00 | 0.00 |
|          | (5.20) | (5.39) | (5.63) | (5.63) | (0.00) | (0.00) | (0.00) | (5.57) | (5.57) | (0.00) |
| Value in parentheses are distance values (D).

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

| Cluster | Plant height | Number of tillers per plant | Number of leaves per plant | Leaf weight | Leaf: stem ratio | Dry matter content | Crude protein | Crude fiber | Crude fat | Green fodder yield per plant |
|---------|--------------|------------------------------|---------------------------|-------------|-----------------|-------------------|---------------|-------------|----------|----------------------------|
| 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                      |

Values in parentheses are distance values (D).

Clusters IV, V, VI, VII, VIII and X possessing no intra cluster distance value as they were solitary cluster indicating comparatively homogenous nature of the genotype within the cluster. The highest inter cluster $D^2$ value was found between cluster III and IX ($D^2=467.86$) with a distance of 21.63 followed by cluster III and VIII ($D^2=336.72$) with a distance of 18.35, cluster III and V ($D^2=312.23$) with a distance of 17.67, cluster III and IX ($D^2=283.59$) with a distance 16.84 and clusters II and III ($D^2=248.69$) with a distance of 15.77 indicated that genotypes belonging to these clusters have greater genetic divergence and genotypes in these clusters could be used in breeding programme for improvement of fodder yield and quality. The least inter-cluster $D^2$ value was found between cluster VI and VII ($D^2=31.92$) with a distance of 5.63 indicated close relationship among the genotypes included in these clusters. These are in accordance with the findings of More et al. (2006) in fodder maize Ganesan et al. (2010) in maize germplasm. Cluster means of each trait toward divergence are presented in Table 4. It is evident that different cluster exhibit distinct mean values for almost all the characters studies. A wide range of variation was observed among different clusters for all the cluster means. Cluster VIII had highest cluster mean for number of tillers per plant (21.00 Nos), leaf weight (204.78 g), leaf: stem ratio (0.54g) and green fodder yield per plant (587.13 g) and, second highest cluster mean for number of leaves per plant (234.16 g). Cluster V had high mean value for number of tillers per plant (21.00 Nos), number of leaves per plant (246.50 g) and crude protein content (11.20 %) and, second highest cluster mean for leaf weight (167.99 g), leaf: stem ratio (0.47g) and green fodder yield per plant (534.19 g). Thus, to improve fodder yield and quality, the genotypes belonging to these clusters would be the right choice. Cluster IV had highest mean value for plant height and crude fat content, cluster I for dry matter content, cluster III for crude fiber content and cluster IX for...
leaf: stem ratio. Thus by involving genotypes from these clusters (except cluster III which had highest mean for crude fiber content and that may affect the digestibility) in breeding programme, high green fodder yield and quality could be achieved. In this study, cluster V and VIII had the highest mean values for number of tillers per plant, number of leaves per plant, leaf weight, leaf: stem ratio, green fodder yield per plant and crude protein content. Therefore, genotype from the cluster VIII (GGLC 12) and cluster V (GGLC 19) could be effective in breeding programme for development of Guinea grass varieties with improved fodder yield and quality.

**CONCLUSION**

Thus, it is evident from the present finding that substantial genetic divergence was envisaged in the genetic material. The genotypes of same geographical region clustered with the genotypes of other geographical region due to selection pressure and genetic drift. This indicates that there is no parallelism between genetic diversity and geographical region. The genotypes fall into same cluster having lowest degree of divergence while, the genotypes belonging to different clusters having maximum divergence and can be successfully utilize in breeding programmes to develop variety with desirable characteristics.

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