

STUDIES ON GENETIC DIVERSITY IN GUINEA GRASS *PANICUM MAXIMUM* JACQ THROUGH D² ANALYSIS

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ABSTRACT

Genetic diversity in 51 genotypes of Guinea grass was estimated through D² analysis. The genotypes were grouped into seven clusters. The clustering pattern indicated no relationship between the genetic divergence and geographic distribution. The intra cluster generalised distance was the highest in cluster I (35 genotypes) and lowest in cluster III (2 genotypes). The inter cluster distance was the highest between clusters IV and VII and was the least between clusters II and III. Cluster VI exhibited the maximum mean values for plant height, leaf weight, leaf-stem ratio and crude protein content and least value for crude fibre content. Cluster V recorded the maximum mean values for stem weight and green fodder yield per plant. The best genotypes from different clusters were identified for future crossing programme for improvement of green fodder yield and quality.

KEY WORDS: Guinea grass, Genetic divergence.

Among forage grasses that are popular throughout the world Guinea grass occupies the prime position. It comes up very well both under irrigated as well as rainfed situations; both for cut and stall fed and as a pasture grass for grazing by animals. It is also suitable for silage. It grows very well under tropical and sub tropical conditions. It is a highly tillering perennial grass with thin stems, high dry matter content, fairly nutritious and high palatability. Though it is cultivated in every continent, only a few varieties like Hamil, Makuenii, Riversdale, Green panic, Tobiatum, Centinario, etc., have been recognised. Ecotypes with different chromosome numbers like 2n:18, 32, 48 have been identified and this has resulted in great variability in the germplasm. A large germplasm collection has been assembled at the Department of Forage Crops, TNAU and knowledge of the genetic diversity existing in the population will help to generate a rich base for commencing proper selection.

MATERIALS AND METHODS

Fifty one genotypes of guinea grass assembled and maintained at the Department of Forage Crops, Tamil Nadu Agricultural University were selected and planted during kharif '96'. The genotypes were planted using root slips in single rows of 4.5 m length adopting a spacing of 50 x 30 cm in a randomised block design with three replications. Uniform cultural practices were followed. The first cut was taken on the 80th day and subsequent two cuts at 45 day intervals.

Biometric observation on 10 different characters including green fodder yield, crude protein, crude fibre and dry matter content were recorded at each harvest. The data generated was utilized to calculate the genetic diversity through the Mahalanobis D² statistic (Mahalanobis, 1936). Using the general distance between two populations, the group constellation or clustering pattern was determined by Tocher's method as given by Rao (1952). Intra and inter cluster distances were also calculated.

RESULTS AND DISCUSSION

The D² values were computed for all possible pairs of genotypes. By the application of clustering technique, the 51 genotypes were grouped into seven clusters (Table 1). The first cluster was the biggest one and included genotypes from Punjab, Jhansi, Coimbatore and USA. Cluster V was the next largest with six genotypes from Punjab and Jhansi. Clusters III and IV had two genotypes each and Clusters VI and VII were represented by a single genotype each. The clustering pattern revealed that the tendency of genotypes from diverse geographic regions to group together in one cluster might be due to similarity of the nature of selection pressure operating under the respective domestic conditions (Timothy 1963; Arunachalam and Jawahar Rani, 1967). The existence of wide genetic diversity among the genotypes chosen from the same geographic region was also obvious as evident from such genotypes grouping in different clusters. The

Table 1. Composition of D² clusters in guinea grass genotypes

Cluster No	Total Number of accessions	Genotypes	Origin/source
I	35	CP 59897, CP 59900, CP 59901, CP 59902 CP 59903, CP 59905, CP 59907, CP 59910 CP 59912, CP 59915, CP 59944, CP 59949 CP 59926, CP 59936, CP 59955, CP 59956 CP 59965, CP 59967, CP 59974, GG 4, GG 5, Tobiatum, Centenario, LSPM Blue, LSPM-3 PGG 518, PGG 552, PGG 310, PGG 598, PGG 600 PGG 297, NEH-PM: 3, Dhan PM-281, Hamil, SLG-PM-3	Ludhiana, Coimbatore, USA, Jhansi
II	4	PGG 510, PGG 9, PGG 489, CP 59969	Jhansi Ludhiana
III	2	CP 59963, CP 59906	Ludhiana
IV	2	PGG 101, PGG 14	Jhansi
V	6	CP 59961, CP 59962, CP 59964, PGG 511, Makueni, Green pants	Ludhiana Jhansi, USA
VI	1	Co-1	Coimbatore
VII	1	PGG 519	Jhansi

clustering pattern thus indicated no relationship between the genetic divergence and geographic distribution.

The intra and inter-cluster D² and D values among the seven clusters are furnished in Table 2 along with the grading of the clusters as highly divergent, moderately divergent and less divergent. The intra cluster generalised distance was the

highest in cluster I (151.45) and the lowest in cluster III (14.02). The inter cluster distance was the highest between clusters IV and VII (268.36) and was the least between clusters II and III (26.59). Cluster I was less divergent from cluster II (45.99), cluster III (56.97) and cluster VII (37.19) while moderately divergent from cluster IV (63.26), cluster VI (74.66) and cluster V (95.16) Cluster II

Table 2. Inter and intra (diagonal) cluster average of D² and D values (within parenthesis) and the extent of diversity among the clusters in guinea grass genotypes

Clusters	I	II	III	IV	V	VI	VII
I	22938.45 (151.45)	2114.92 (45.99)	3246.23 (56.97)	4797.03 (63.26)	9055.64 (95.16)	5573.82 (74.66)	1383.76 (37.19)
II		L	L	M	M	M	L
III		437.37 (20.91)	706.99 (26.59)	5738.96 (75.76)	15680.35 (125.22)	18141.93 (134.69)	1725.45 (41.54)
IV			L	M	H	H	L
V			196.46 (14.02)	7737.15 (87.96)	17169.63 (131.03)	19604.98 (140.01)	2705.13 (52.01)
VI				M	H	H	L
VII				220.40 (14.85)	10669.46 (103.29)	7251.17 (85.15)	72016.92 (268.36)
					H	M	H
					4415.18 (66.45)	2726.79 (52.22)	11290.30 (106.26)
						L	H
							13686.75 (116.99)
							H

H : Highly Divergent (above 100)

M : Moderately Divergent (60-100)

L : Less Divergent (less than 60)

Table 3. Cluster means for 10 characters in Guinea grass genotypes

Characters	General Mean	Clusters						
		I	II	III	IV	V	VI	VII
Plant height (cm)	159.95	150.57	157.17	167.20	139.14	166.63	168.46	152.39
No. of tillers/plant	25.25	23.73	29.38	17.38	46.08	21.16	31.00	38.57
No. of leaves/plant	134.57	126.42	129.40	118.23	269.13	120.07	219.77	206.33
Stem weight (g)	193.09	184.61	116.30	114.85	183.05	317.45	283.53	137.32
Leaf weight (g)	93.78	84.24	56.79	53.47	99.73	172.93	201.99	61.58
Leaf-stem ratio	0.48	0.44	0.48	0.47	0.55	0.56	0.71	0.45
Green fodder yield per plant (g)	285.75	267.17	172.88	168.35	282.18	490.93	485.42	198.87
Dry matter content %	23.54	22.47	26.57	47.23	16.28	19.06	23.98	16.91
Crude protein %	7.48	7.37	6.69	7.08	5.59	9.11	11.20	5.55
Crude fibre %	28.79	29.59	29.94	26.89	23.66	28.75	20.66	25.66

Cluster	Characters	Genotypes
III	Dry matter content	CP 59906
IV	Number of tillers per plant and number of leaves per plant	PGG 101
V	Stem weight and green fodder yield per plant	PGG 511 Makueni Green panic
VI	Plant height, leaf weight, leaf stem ratio, crude protein content and low crude fibre	Co-1

was highly divergent from clusters V and VI. Similarly cluster III was also highly divergent from clusters V and VI; cluster IV from clusters V and VII and clusters V and VI each from cluster VII. Genotypes from these highly divergent clusters may yield the best parents for an effective crossing programme. Once a better hybrid is identified from such a crossing programme, guinea grass offers a better means of vegetative propagation for further multiplication and maintenance.

The mean values of different characters for the genotypes in each cluster were worked out and is given in Table 3. Perceptible difference were observed in cluster mean values for all characters. Cluster VI exhibited the maximum mean values for plant height, leaf weight, leaf-stem ratio and crude protein content while the crude fibre content was the lowest. Cluster V exhibited maximum mean values for stem weight and green fodder yield per plant; cluster IV for number of tillers per plant and number of leaves per plant and cluster III for dry

matter content. Thus by involving genotypes from these clusters in a crossing programme, high green fodder yield and quality can be achieved. The following genotypes of outstanding mean performance from the selected clusters may serve as potential genotypes for any breeding programme.

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