

D² ANALYSIS FOR FODDER YIELD IN NAPIER GRASS (*PENNISETUM PURPUREUM* (K.) SCHUM)

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ABSTRACT

Forty diverse genotypes of napier grass (*Pennisetum purpureum* (K.) Schum) evaluated for genetic diversity were grouped into seven distinct clusters. The pattern of D² clusters demonstrated that the geographical distribution need not be related to genetic diversity.

Key words: Napier grass, genetic divergence.

Napier grass, a heavy yielder of green fodder, offers much scope for improvement through breeding. Selection of genetically diverse genotypes is important for exploitation of heterosis and development of desirable recombinants. An assessment of the nature and magnitude of diversity between genotypes will help to choose better parents for hybridization [1]. The present investigation has been undertaken to study genetic divergence with respect to fodder yield and its components in napier grass (*Pennisetum purpureum* (K.) Schum) to select better genotypes for use in breeding programmes.

MATERIALS AND METHODS

Forty genotypes of diverse sources chosen from the germplasm maintained at the Department of Forage Crops, Tamil Nadu Agricultural University, Coimbatore were raised in randomized block design with two replications. The genotypes were planted using rooted slips on one side of ridges of 3 m length at 50 x 50 cm spacing. Observations were recorded on five random plants for green fodder yield and its contributing characters when the crop was 6.5 months old, reaching the fourth harvest after planting. Representative plant samples from each replication were taken after the harvest for estimating quality characters like dry matter content, ash content, crude protein content, crude fat content, crude fibre and oxalic acid content. The mean values were transformed into uncorrelated linear functions for Mahalanobis' generalized distance (D²) analysis and the genotypes were grouped into clusters by the Tochers' method [2].

RESULTS AND DISCUSSION

Analysis of variance indicated highly significant differences among the genotypes for all the sixteen characters studied. Based on Mahalanobis' D^2 values, the forty genotypes were grouped into seven clusters (Table 1). Among them, cluster I was the largest with 16 genotypes followed by clusters III (10 genotypes) and II (8 genotypes). Clusters IV and V had two entries each, and VI and VII only one genotype each.

Table 1. Composition of clusters based on D^2 values in napier grass

Cluster No.	No. of genotypes	Genotypes	Origin
I	16	FD 453, 462, 466, 461, 451, 452, 463, 458 FD 444, 445, 447 FD 434, 440, 427, 430 FD 426	Kenya USA Puerto Rico Hawaii
II	8	FD 456, 460, 467, 455, 465 FD 470, 471 FD 441	Kenya Australia Puerto Rico
III	10	FD 431, 442, 435, 439, 437, 432, 436 FD 446, 448 FD 450	Puerto Rico USA Kenya
IV	2	FD 429 FD 459	Puerto Rico Kenya
V	2	FD 428 FD 457	Puerto Rico Kenya
VI	1	FD 464	Kenya
VII	1	FD 454	Kenya

Many genotypes of different geographical origin, viz. eight from Kenya, four from Puerto Rico, three from USA and one from Hawaii were grouped in the same cluster (cluster I). In contrast, genotypes originating from the same place were scattered in different clusters. Geographic diversity, though important, is not the only factor in determining genetic divergence.

Considering the intra- and intercluster distances (Table 2), the highest intercluster distance ($D=199.4$) was noted between clusters II and IV. Cluster II was highly divergent from clusters IV, VII, V and VI, and cluster I from clusters IV, VII and V. Similarly, clusters III and IV were highly divergent as also clusters IV and VI.

Table 2. Intracluster (in bold) and intercluster average *D*² and *D* values (within parentheses) in napier grass

Clusters	I	II	III	IV	V	VI	VII
I	704.5 (26.5)	2127.6 (46.1)	3290.0 (57.4)	26086.1 (161.5)	10271.7 (101.4)	4623.4 (68.0)	11335.4 (106.5)
II		689.3 (26.3)	8125.8 (90.1)	39755.5 (199.4)	19173.9 (138.5)	10716.4 (103.5)	20506.0 (143.2)
III			906.2 (30.1)	13261.8 (115.2)	3302.2 (57.5)	1265.8 (35.6)	4040.4 (63.6)
IV				439.1 (21.0)	4374.1 (66.1)	11044.9 (105.1)	4883.5 (69.9)
V					899.87 (30.0)	2610.9 (51.1)	1672.6 (40.9)
VI						—	3361.9 (58.0)
VII							—

Table 3. Character means in different clusters of napier grass

Character	I	II	III	IV	V	VI	VII
Plant height (cm)	66.8	65.9	79.5	59.4	68.6	79.7	84.1
Tillers/plant	16.9	16.0	20.1	25.5	23.2	26.2	22.3
Leaves/plant	140.4	129.2	168.7	228.3	225.7	265.2	205.9
Leaf length (cm)	67.7	63.8	70.9	66.7	78.1	81.8	50.2
Leaf breadth (cm)	2.0	2.1	2.4	2.6	2.4	1.7	1.2
Stem diameter (cm)	1.1	1.0	1.1	0.8	1.1	0.9	0.7
Leaf weight (g)	190.9	118.2	281.8	494.0	388.8	298.5	352.5
Stem weight (g)	91.1	62.8	128.4	189.3	144.8	137.5	208.0
Leaf stem ratio	2.2	2.0	2.2	2.6	2.7	2.2	1.7
Green fodder yield/plant (g)	281.6	181.0	409.9	683.3	533.6	436.0	560.5
Dry matter content (%)	23.4	23.1	22.0	20.8	20.8	20.9	19.7
Ash content (%)	10.1	9.4	9.8	10.2	8.7	12.1	8.4
Crude protein content (%)	9.2	10.3	9.7	9.2	11.0	14.6	9.1
Crude fat content (%)	3.0	2.8	2.9	3.4	2.2	4.9	3.0
Crude fibre content (%)	27.6	27.6	26.6	26.1	26.8	28.6	25.2
Oxalic acid content (%)	2.7	2.8	2.9	2.5	2.8	2.5	2.8

The cluster means of the various characters are presented in Table 3. Cluster IV recorded the highest mean for leaf breadth, leaf weight, green fodder yield per plant, and lowest oxalic acid content. Cluster V recorded maximum stem diameter and leaf stem ratio. Cluster VI had the highest number of tillers and leaves per plant, leaf length, ash content, crude protein and crude fat content. Cluster VII consisted of tallest plants with heaviest stems of lowest crude fibre content. Thus, by involving the genotypes of outstanding mean performance from these four clusters as potential parents in interspecific crosses, hybrids with high green fodder yield and quality can be developed.

REFERENCES

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