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GENETIC ANALYSIS OF IMPORTANT MORPHOLOGICAL TRAITS FOR FORAGE YIELD IN NAPIER GRASS (*PENNISETUM PURPUREUM* SCHUM.), USING CLUSTER ANALYSIS

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ABSTRACT
Twenty eight genotypes were evaluated in randomized block design for forage yield and its components. Significant differences were observed for all characters studied. High heritability estimates were observed for all the characters studied, accompanied by high genetic advance as percentage of mean was reported for characters *viz.*, number of tillers, dry matter yield and green forage yield, indicating presence of additive gene action thereby, suggesting traits for *per se* selection and there scope for Napier improvement.

INTRODUCTION

Napier grass (*Pennisetum purpureum* Schum.) is an important forage crop of tropical and sub tropical region distributed in Asia, Africa, Southern Europe and America. This is an important forage crop of dry and semiarid areas of India. It is now widely recognized as a valuable fodder grass. Now in all states of India this crop is grown as a main fodder for dairy animals. Napier is nutritious and contains 5-7 % protein, with both calcium and phosphorous in proper balance and in adequate quantities. It is also palatable to livestock, it makes good gains in live weight and hence, napier grass is recommended for fatting animals for market. It is said to be variable and comprises several forms, differing in size, colour and structure of the inflorescence and its parts.

Information on genetic variability of these characters with yield is most essential for formulating effective selection schemes in any crop improvement programme. A very limited work of this kind has been done on Napier grass. There is a great scope for its improvement and to increase the forage yield by developing high productive, fertilizer responsive varieties with improvement in nutritive value. Good amount of variability has been reported in Napier grass by Poli *et al.* (1994), Sukanya (1995), Suthamati and Dorairaj (1997) and Khan and Sukumar (2001) for various characters such as number of tillers, plant height, no. of leaves, leaf length, leaf width, protein content etc. However their utilization in breeding programme resulted in identification and release of good number of varieties in Napier grass.

A systematic evaluation and characterization of germplasm lines not only help in identification of superior and genetically divergent germplasm lines but also provide information on the utility of the genetic resources. Success of any breeding programme depends upon the amount of genetic variability available in the crop species besides the efficiency of selection techniques adopted by the plant breeder. Quantification of degree of divergence in a given material is of immense value in identification of divergent genotypes for further use in hybridization to create new variability. Mahalanobis D^2 statistics has been proved to be a powerful tool for quantifying genetic diversity in a given population. The D^2 classifies the genotypes into homogenous groups/ clusters with little diversity within cluster and usually high between clusters. Sukanya (1995) and Suthamati and Dorairaj (1997) shown representative genotypes from diverse clusters can be remarked for utilization in hybridization programme depending upon breeding objectives.

The objective of this study was to evaluate 28 Napier cultivars for forage yield and their components as well as other important agronomic traits. The results might be capable in the selection criteria in further studies in order to increase the selection efficiency.

MATERIALS AND METHODS

The experimental material used for study consisted of 28

genotypes of Napier grass. The experiment was conducted at Grass Breeding Scheme, MPKV, Rahuri, during Oct 2012 to May 2013 in a Randomized Block Design. Each genotype was planted in two rows of 7.20 m length with spacing 90 x 60 cm. After planting a irrigation was given and subsequent irrigations were given at an interval of 10-12 days. As a basal dose 50 kg of 'N' per ha, 40 kg 'P' per ha and 40 kg 'K' per ha were applied, for top dressing 25 kg of 'N' per ha after each cut was applied. Other cultural practices like weeding were done manually on regular basis. Observations on various characters except green forage yield and dry matter yield were recorded on ten randomly selected plants in each experimental plot at the time of second cut and averages were worked out. Observations on green forage yield and dry matter yield were recorded for a period of Oct 2012 to May 2013 (3 cuts in total) and expressed in kg / plant. First cut was taken 60 days after planting and subsequent cuts were taken at an interval of 45 days. In total observations for 3 cuts were recorded. Nitrogen percentage determined by Microkjeldahl's method (Thimmaiah, 1999). Percent nitrogen was multiplied by conversion factor 6.25 to obtain % crude protein content. Oxalic acid content was estimated by the method given by Abaza *et al.* (1968).

The average data on individual characters were subjected to the method of analysis of variance commonly applicable to the Randomised Block Design (Panse and Sukhatme, 1967). The phenotypic and genotypic coefficient of variation were computed, as the ratio of corresponding standard deviation to the mean of the character, expressed as percentage, as per the formulae given by Burton (1952). Heritability in broad sense for each character was estimated as suggested by Hanson *et al.* (1956). The genotypic correlations among forage yield and yield contributing characters were calculated as per the method suggested by Johnson *et al.* To establish a cause and effect relationship, the genotypic and phenotypic correlation coefficients was partitioned into direct and indirect effects by path analysis as suggested by Dewey and Lu (1959). The genetic divergence among genotypes was computed by means of Mahalanobis (1936) D^2 technique. The genotypes were grouped into clusters by following Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance (Table I) revealed significant genotypic differences for all the characters studied. The mean values and range for each characters studied are presented in Table II along with genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance as percentage of mean.

Wide range of variability was observed for characters *viz.,* green forage yield followed by dry matter yield and number of tillers. Genotypic coefficient of variation was highest for green forage yield (72.17) and that of lowest for oxalic acid content (4.76). Phenotypic coefficient of variation was highest for green forage yield (72.98) and that of lowest for oxalic acid content

Table I: Analysis of variance for green foage yield and yield contributing characters in Napier grass (*Pennisetum purpureum* Schum.)

Sr.	Characters	Replication	Treatment	Error
Degrees of Freedom		1	27	27
1	Plant height (cm)	1100.323	3135.788**	93.540
2	Number of tillers	15.846	82.487**	3.402
3	Number of leaves	1.591	4.024**	0.829
4	Number of internodes	6.541	7.685**	0.587
5	Leaf length (cm)	12.164	227.623**	15.450
6	Leaf width (cm)	0.069	0.458**	0.027
7	Leaf: Stem ratio	0.005	0.031**	0.003
8	Dry matter yield (kg/plant)	0.612	1.604**	0.063
9	Crude protein content (%)	0.993	1.436**	0.291
10	Oxalic acid content (%)	0.303	0.100*	0.046
11	Green forage yield (kg/plant)	6.026	29.556**	0.656

* Significant at 5% level of significance; ** Significant at 1% level of significance.

Table II: Parameters of Genetic variability for yield and yield contributing characters in Napier grass

Sr.	Characters	(σ^2g)	(σ^2p)	(σ^2e)	GCV	PCV	h^2 (bs)	GA	GA as % of mean
1	Plant height (cm)	1521.12	1567.89	46.77	22.26	22.60	97.00	79.13	45.16
2	Number of tillers	39.54	41.24	1.70	45.60	46.57	95.90	12.68	91.99
3	Number of leaves	1.597	2.012	0.41	10.10	11.34	79.40	2.32	18.55
4	Number of internodes	3.549	3.84	0.29	23.31	24.26	92.40	3.72	46.16
5	Leaf length (cm)	106.09	113.81	7.73	13.37	13.85	93.20	20.48	26.60
6	Leaf width (cm)	0.22	0.23	0.01	18.56	19.15	94.00	0.92	37.07
7	Leaf: Stem ratio	0.01	0.02	0.00	17.05	17.97	90.10	0.23	33.34
8	Dry matter yield (kg/plant)	0.770	0.80	0.03	69.47	70.89	96.00	1.77	140.24
9	Crude protein content (%)	0.573	0.72	0.17	11.20	12.55	79.70	1.39	20.61
10	Oxalic acid content (%)	0.027	0.05	0.02	4.76	6.52	53.30	0.24	7.15
11	Green forage yield (kg/plant)	14.450	14.78	0.33	72.17	72.98	97.80	7.74	147.01

GCV = Genotypic coefficient of variation; h^2 (b.s.) = Broad sense σ^2g = Genotypic variance; σ^2e = Environmental variance; PCV = Phenotypic coefficient of variation; G.A. = Genetic advance; σ^2p = Phenotypic variance

Table III: Distribution of 28 genotypes in different clusters in Napier grass

Cluster	No. of genotypes	Name of genotypes	Origin
I	21	GBN-2001-9, GBN-2001-10, FD-448, FD-451, FD-444, GBN-2001-2, GBN-2001-4, GBN-2001-3, GBN-2001-5, GBN-2001-6, FD-1890-1, GBN-2001-7, FD-436, GBN-2001-1, FD-473, FD-432, FD-1890-2, GBN-2001-8, CN-092, FD-472, FD-453	All GBN series from MPKV, Rahuri All FD series from TNAU, Coimbatore
II	1	FD-468	TNAU, Coimbatore
III	1	CN-014	TNAU, Coimbatore
IV	1	CN-011	TNAU, Coimbatore
V	1	FD-461	TNAU, Coimbatore
VI	3	FD-483, FD-482, FD-477	TNAU, Coimbatore

Table IV: Cluster means for nine different traits in Napier grass

Cluster	Plant height (cm)	No. of tillers	No. of leaves	No. of internodes	Leaf length (cm)	Leaf width (cm)	Leaf:Stem ratio	Dry matter yield (kg/plant)	Green forage yield(kg/plant)
I	161.44	10.97	12.18	7.51	74.59	2.37	0.73	0.92	3.75
II	237.50	17.92	14.10	10.28	77.92	1.98	0.52	1.46	5.56
III	220.40	16.70	15.33	10.90	83.53	3.58	0.61	1.98	8.14
IV	235.86	20.00	12.98	10.28	89.90	2.71	0.63	2.14	7.17
V	166.88	22.52	13.10	9.40	63.22	2.06	0.82	1.25	4.65
VI	218.26	26.22	12.98	9.19	91.67	3.31	0.59	3.07	14.42

Table V: Intra cluster and inter cluster D^2 values of 6 clusters in Napier grass

Cluster	I	II	III	IV	V	VI
I	10.121	13.476	14.480	14.348	13.569	31.214
II		0	12.710	8.546	14.917	30.861
III			0	13.731	19.517	27.031
IV				0	13.313	29.830
V					0	34.327
VI						12.867

(6.52). In general magnitude of PCV is observed to be higher than the GCV. High estimates of GCV and PCV were observed for green forage yield (GCV=72.17, PCV=72.98) followed by dry matter yield (GCV=69.47, PCV=70.89) and number of tillers (GCV=45.60, PCV=46.57). Similar findings were reported by Suthamathi and Dorairaj (1997), Khan and Sukumar (2001) and Singh *et al* (2013).

Maximum heritability was observed for the character green forage yield (97.80 %) and that of minimum for the character oxalic acid content (53.30 %). High heritability (>30 %) was observed for all the characters studied, indicating additive gene action. Plant height also showed the high heritability (97.00) followed by dry matter yield (96.00), number of tillers (95.90), leaf width (94.00), leaf length (93.20), number of internodes (92.40), leaf: stem ratio (90.10), crude protein content (79.70), number of leaves (79.40) and oxalic acid content (53.30). These results were similar as Suthamathi and Dorairaj (1997) and Singh *et al* (2013).

High estimates of genetic advance as percentage of mean were observed for all the characters except oxalic acid content (7.15), number of leaves(18.55) and crude protein content(20.61). Green forage yield showed maximum GA as % mean (147.01) followed by dry matter yield (140.24) and number of tillers (91.99). Similar results reported by Suthamathi and Dorairaj (1997), Khan and Sukumar (2001) and Singh *et al* (2013).

For selection of parents for hybridization programme, information on clusters, intra and inter cluster distance and cluster means are of paramount importance. In the present study, 28 genotypes were grouped into 6 clusters (Table 3) by using Tocher's method described by Rao (1952). The maximum per cent contribution towards genetic divergence (Fig. I) was shown by Green forage yield (29.89) followed by Plant height (23.02). The intra D^2 values between all possible selections of 28 genotypes ranged between 0.00 and 12.86. The maximum intra cluster distance was observed in cluster-VI (D=12.86) followed by cluster- I. Suggesting that genotypes included in these clusters might have different genetical constitution (Table 3). Monogenotypic clusters *viz*. clusters-II, III, IV and V indicated that genotype of these clusters differs significantly from other genotypes genetically and appeared to be evolved from different gene pool. The inter cluster D^2 values varied from 8.54 and 34.32. Maximum inter cluster distance was observed between the clusters- V and VI (D= 34.32) followed by clusters- I and VI (31.21), indicating wide divergence among the clusters, suggesting that genetic base of the genotypes in one cluster differs entirely from those included in the other cluster. Maximum amount of heterosis can be expected in cross combination involving the genotypes of most divergent cluster. Minimum cluster distance was observed between cluster- II and IV (D= 8.54), suggesting that the genotypes in this cluster may be used as parents in hybridization programme to obtain desirable recombinants. The criteria used for selection of varieties as parents for hybridization using D^2 analysis is the inter cluster distance. Suthamathi and Dorairaj (1997) and Sukanya (1995) also reported similar results.

On the basis of inter cluster distance, cluster means and *per se* performance observed in present study, the tentative hybridization programme is suggested with genotypes viz. GBN- 2001-8, FD- 461, FD- 468, FD- 483, CN- 092 and CN-011, in order to obtain better recombinants in the segregating

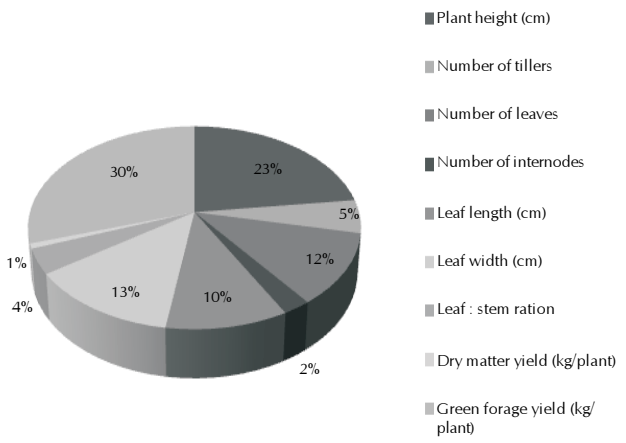

Figure I: Per cent contribution towards genetic divergence

generations.

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