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Characterization and comparative analyses of genetic divergence for identification of diverse parents on napier grass germplasm (*Pennisetum purpureum* L. Schumach)

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Abstract
The present study was carried out to characterize 56 Napier grass (*Pennisetum purpureum* L. Schumach) accessions using 17 qualitative traits and to assess the magnitude of genetic diversity among the accessions using 13 biometrical traits in order to select diverse genotypes for using them as parents in future breeding programme. Characterization of the germplasm revealed the presence of discernible variation for majority of the traits with an extremity in the following traits *viz*., presence of prop roots, leaf sheath pigmentation and bristle length ranging from 8.93 % - 67.86 %, 8.93 % - 64.29 % and 3.57 % - 58.93 %, respectively. Genetic diversity among the genotypes was assessed based on Mahalanobis's D^2 statistics and agglomerative hierarchical clustering approach. Based on Tocher's method, the genotypes were classified into 11 clusters. The highest inter cluster distance was observed between cluster X and VI (67.82), VI and IV (57.63) and cluster VIII and VI (52.48). Therefore, the genotypes from the above clusters *viz*., FD 437, FD 470, FD 474, FD 471, FD 461, FD 473, FD 476, FD 462, FD 426 could be used as parents for the development of high yielding Pearl millet Napier hybrids. Clusters V, X and XI exhibited the highest mean values for majority of the yield attributing traits. Therefore, genotypes from the clusters V, X and XI *viz*., FD 459, FD 426, FD 468 could be utilized in future hybridization programme for enhancing the appropriate traits. In agglomerative hierarchical clustering method also, the genotypes were classified into 11clusters. Outcome from Tocher's method and agglomerative hierarchical approach relatively complement with each other and satisfactory to delineate the genetic divergence among the germplasm.

Keywords
Napier grass (*Pennisetum purpureum* L. Scumach), Genetic diversity, Mahalanobis's D^2 analysis, agglomerative hierarchical clustering

INTRODUCTION

As per 19th livestock census of 2012, the total livestock population in India is 512.05 million and Livestock rearing contributes to 4.11 % of National GDP (Ghosh *et al.,*2016). Fodder crops form the primary component of livestock diet. However, at present, the nation experiences a net deficit of 35.6 % of green fodder, 10.95% of dry crop residues, and 44% of concentrate feed ingredients. It has been extrapolated that the demand for green and dry fodder will reach 1012 and 631 million tonnes by the year 2050, respectively (Vision document-2050). This gap between the fodder requirement and availability can be solved either by expanding the area under fodder cultivation or by enhancing the green fodder production per unit area. Under current scenario of population explosion, most

of the arable land has already been allocated for food and cash crops and it would be very difficult to expand the area under fodder crops. This situation warrants the forage breeders to develop high biomass yielding forage crop varieties which could be able to yield more green fodder per unit area.

Napier grass (*Pennisetum purpureum* L. Scumach) is one among the forage crops which could provide year round quality green forage. It is also known as elephant grass, merker grass and Uganda grass. It is ideally suited to cut and carry method of feeding the livestock. It is a monocot and C4 grass species belonging to the family Poaceae. It is an allopolyploid (A'A'BB) with chromosome number 2n=2x=28. It is one of the fastest growing perennial grasses, grown in tropical and subtropical areas for forage purposes. It produces highest biomass yield per unit area. It is adaptable to wide range of soil conditions, can withstand repeated cuttings and rapidly regenerates. It cannot withstand frost and water logging but can cope up with intermittent drought.

Existence of genetic diversity in crop species is considered as a gift from nature. The mainstay of any breeding programme depends on the presence of genetic diversity among the existing breeding material. Efficient assessment and meticulous utilization of genetic diversity forms the cornerstone in every crop improvement programme. Scientific understanding about the presence and extent of genetic diversity generally helps the breeder to select superior genotypes. Analysis of genetic diversity enables the plant breeder to avoid redundancy of genotypes, thereby helping to reduce the number of genotypes and deters the wastage of valuable efforts and scarce resources. Since, the studies on genetic diversity in Napier grass are very limited, the present study was carried out.

MATERIALS AND METHODS

The experimental material comprises of 56 Napier grass accessions which are being maintained as field gene bank at New Area Farm, Department of Forage Crops, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, India (**Table 1**). Each accession was grown in a row of four meter length adopting a spacing of 50 x 50 cm in a Randomized Block Design with two replications. All the recommended standard agronomic practices were carried out to ensure proper crop stand. A total of 17 qualitative traits like, early plant vigour, plant growth habit, leaf sheath pigmentation, leaf sheath pubescence, leaf blade pubescence, leaf angle, leaf colour, presence of prop roots, branching, panicle colour, bristle colour, node pigmentation, internode pigmentation, position of branches, indentation of leaf margin, bristle length and node pubescence was contemplated. Biometrical observations were recorded on five potential competitive plants selected from each genotype in each replication. Thirteen quantitative traits like plant height (cm), number of tillers per plant, number of nodes on main tiller, number of leaves per tiller, leaf length (cm), leaf breadth (cm), stem girth (cm), intermodal length (cm), leaf weight (g), stem weight (g), leaf to stem ratio, green forage yield per plant (g) and dry matter content (%) were recorded. Analysis of Variance for each character was carried out as per the method given by (Fisher, 1954). Genetic diversity among the genotypes was assessed by employing multivariate analysis using Mahalanobis's D^2 statistics (Mahalanobis, 1936) as suggested by (Rao, 1952) and the genotypes were grouped according to Tocher's method. In addition to that, agglomerative hierarchical clustering approach based on Euclidean distance with complete linkage method was attempted for clustering (Mojena, 1977).

RESULTS AND DISCUSSION

The list of 17 qualitative traits observed with details of score, phenotype and per cent frequency of occurrence are presented in **Table 2.** Among the accessions, good early plant vigour was spotted for most of the genotypes (62.50 %), very good early plant vigour was witnessed for 21.43 % of the genotypes and 17.86 % of the genotypes were observed with poor early plant vigour. Considering the trait plant growth habit, majority of the genotypes (80.36 %) were of semi erect type and 19.64 % of the genotypes were of erect type. Substantial amount of variation was detected for leaf sheath pigmentation, in which light green, purple and light purple pigmentations were observed for 64.29 %, 26.79 % and 8.93 % of the genotypes, respectively. Regarding leaf sheath pubescence, majority of the germplasm accessions (60.71 %) were recognized with dense pubescence, 26.79 % of the accessions were observed to be with sparse pubescence and 12.50 % of the accessions were glabrous in nature. Leaf blade pubescence was perceived to be dense for 51.79 % of the genotypes while 42.81 % of the accessions exhibited sparse leaf blade pubescence. With regard to leaf angle, a total of 35 and 21 genotypes were observed to be semi erect and erect accounting for about 62.50 % and 37.50 % respectively. In connection with leaf colour, more than half of the accessions (53.58 %) were observed to have dark green leaves whereas remaining genotypes were discerned to have light green leaves. Among the germplasm, appreciable amount of variation was detected for the presence of prop roots. Prop roots were confined to 1 – 2 basal nodes in most of the genotypes (67.86 %) whereas in 23.21 % of genotypes, it was found to extend up to 6 – 8 basal nodes and only in five genotypes, they were present around 3 – 4 basal nodes accounting 8.93 %. Branching refers to the number of secondary tillers arising from a single culm. In most of the genotypes (80.36 %), only few tillers arise, while 19.64 % of the genotypes were recorded with high tillering. The traits, panicle colour, bristle colour, node pigmentation, internode pigmentation, position of branches and indentation of leaf margin exhibited no variation among the genotypes. With reference to bristle length, medium, short and long bristles were found to be exhibited by 58.93 %, 37.50 %, and 3.57 % of the accessions, respectively. Node pubescence was identified to be present in majority of the

Table 1. Details of 56 Napier grass germplasm accessions employed in the study

S. No	Genotypes	Identity of species and variety	Origin
1.	FD 426	*Pennisetum purpureum*	
2.	FD 430	*P.purpureum* Merker, 337620	
3.	FD 431	*P.purpureum* Merker, 365733	
4.	FD 432	*P.purpureum* Merker, 365134	
5.	FD 433	*P.purpureum* Merker	
6.	FD 434	*P.purpureum* Merker, J.2	
7.	FD 435	*P.purpureum* Merker, P.R.	
8.	FD 436	*P.purpureum* Merker, Panama	Puerto Rico
9.	FD 437	*P.purpureum* Merker, Hybrid 69	
10.	FD 438	*P.purpureum* Merker, Hybrid 70	
11.	FD 439	*P.purpureum* Merker, P.R. 169	
12.	FD 440	*P.purpureum* Merker, Dwarf	
13.	FD 441	*P.purpureum* Merker, Lif. 3245	
14.	FD 442	*P.purpureum* Merker, Lif 532	
15.	FD 443	*P.purpureum* Merker, Z – 12	
16.	FD 444	*P.purpureum* Merker, GA (Tift)	
17.	FD 445	*P.purpureum* Tift, N-22	
18.	FD 446	*P.purpureum* Tift, N-43	
19.	FD 447	*P.purpureum* Tift, N-24.8.	USA
20.	FD 448	*P.purpureum* Tift. N-19	
21.	FD 449	*P.purpureum* Merker,Gold cost 52303	
22.	FD 450	*P.purpureum* U.Hairless 5782	
23.	FD 451	*P.purpureum* 52504	
24.	FD 452	*P.purpureum* 5519	
25.	FD 453	*P.purpureum* 5182	
26.	FD 454	*P.purpureum* Uganda 56349	
27.	FD 455	*P.purpureum K* 5517	
28.	FD 456	*P.purpureum* Congo kinshalsha 54197	
29.	FD 457	*P.purpureum* kabete 52440	
30.	FD 458	*P.purpureum* Uganda 52305	Kenya
31.	FD 459	*P.purpureum* 54874	
32.	FD 460	*P.purpureum* Uganda 52507	
33.	FD461	*P.purpureum* Cameroon 52507	
34.	FD 462	*P.purpureum* Songhoi 54256	
35.	FD 463	*P.purpureum* Machakos 58175	
36.	FD 464	*P.purpureum* Nigeria 5379	
37.	FD 465	*P.purpureum* Nigeria 5380	
38.	FD 466	*P.purpureum* Congo kinshalsha	
39.	FD 467	*P.purpureum* 56351	
40.	FD 468	*P.purpureum* 56347	
41.	FD 470	*P.purpureum* 20360 Cameroon strain 21	
42.	FD 471	*P.purpureum* 20365 Cameroon strain 49	
43.	FD472	*P.purpureum* 20365 Uganda	
44.	FD 473	*P.purpureum* 20456 Kakamega	
45.	FD 474	*P.purpureum* Rostermanuville	
46.	FD 476	*P.purpureum* 20463 sel.27	
47.	FD 477	*P.purpureum* 20464 sel.49	Australia
48.	FD 478	*P.purpureum* 7839 Capum elefante var “B”	
49.	FD 479	*P.purpureum* 7838 Capum elefante	
50.	FD 480	*P.purpureum* 66926 Cumano	
51.	FD 481	*P.purpureum* 66928 Minevio	
52.	FD 482	*P.purpureum* 66929 Taiwan	
53.	FD 483	*P.purpureum* 66931 Hybrid 534	
54.	FD 485	*P.purpureum* Capricon	
55.	FD 455/1	*P.purpureum*	India
56.	FD 453/1	*P.purpureum*	

genotypes accounting to 87.50 % and absent in seven genotypes accounting to 12.50 %. Thus, characterization of the germplasm accessions implies the prevalence of significant amount of variation for most of the traits studied. Thus, characterization of the germplasm revealed significant variation for most of the traits studied except

Table 2. List of 17 qualitative traits observed with details of score, phenotype and per cent frequency recorded among 56 Napier grass germplasm accessions

S. No.	Character	Score	Phenotype	Per cent frequency
1.	Early plant vigour	1	Poor	17.86
		2	Good	62.50
		3	Very good	21.43
2.	Plant growth habit	1	Erect	19.64
		2	Semi – erect	80.36
		3	Prostrate	-
3.	Leaf sheath pigmentation	1	Light green	64.29
		2	Green	-
		3	Dark green	-
		4	Light purple	8.93
		5	Purple	26.79
		9	Others (Specify)	-
4.	Leaf sheath pubescence	1	Glabrous	12.50
		2	Sparsely	26.79
		3	Densely	60.71
5.	Leaf blade pubescence	1	Glabrous	-
		2	Sparsely	42.81
		3	Densely	51.79
6.	Leaf angle	1	Erect	37.50
		2	Semi – erect	62.50
		3	Drooping	-
		9	Others (Specify)	-
7.	Leaf colour	1	Light green	46.43
		2	Green	-
		3	Dark green	53.58
		9	Others (Specify)	-
8.	Presence of prop roots	1	Confined to 1 -2 basal nodes	67.86
		2	Up to 3 – 5 basal nodes	8.93
		3	Up to 6 -8 basal nodes	23.21
9.	Position of branches	1	None	-
		2	Few	80.36
		3	High	19.64
10.	Panicle colour	1	Light yellow	100.00
		2	Golden yellow	-
		3	Light purple	-
		4	Deep purple	-
		9	Others (specify)	-
11.	Bristle colour	1	Green	-
		2	Yellow	100.00
		3	Tan	-
		4	Brown	-
		9	Others (specify)	-
12.	Node pigmentation	1	Light green	100.00
		2	Green	-
		3	Dark green	-
		4	Light purple	-
		5	Purple	-
		9	Others (specify)	-
13.	Internode pigmentation	1	Light green	100.00
		2	Green	-
		3	Dark green	-
		4	Light purple	-
		5	Purple	-
		9	Others (specify)	-
14.	Position of branches	1	More at stem top	100.00
		2	More at stem base	-
		3	Random distribution	-
15.	Indentation of leaf margin	1	Smooth/ hair like	-
		2	Curved /bent	-
		3	Stiff and sharp	100.00
16.	Bristle length	1	Short	37.50
		2	Medium	58.93
		5	Long	3.57
17.	Node pubescence	0	Absent	12.50
		1	Present	87.50

node pigmentation, internode pigmentation, position of branches, bristle colour and indentation of leaf margin.

Analysis of variance revealed significant difference for all the 13 quantitative traits studied among 56 Napier grass accessions (**Table 3**). All the 56 Napier grass accessions were grouped into 11 clusters based on Mahalanobis's D^2 value (Tocher's cut off value: 331.68) and shown in **Table 4 and Fig.1**. Cluster I was the largest and turned out to be an accommodative for maximum number of genotypes. Similar results were reported by Shanmuganathan *et al*. (2006) in pearl millet, Ramakrishnan *et al*. (2013) in guinea grass, Krishna *et al*. (2014) in forage oat and Damor *et al*. (2017) in forage sorghum. It consisted of 31 genotypes followed by Cluster II and cluster VI with 11 and 6 genotypes respectively. Clusters III, IV, V, VII, VIII, IX, X and XI were the smallest, with one genotype each. The results of cluster analysis revealed the non correspondence of geographic origin with genetic diversity owing to the fact that the genotypes from different centres of diversity were grouped to the same cluster. Similar findings were reported by Dave and Joshi (1991) in pearl millet, Yadav (1994) in pearl millet, Ramakrishnan *et al*.

Table 3. Analysis of variance for 13 quantitative traits among 56 Napier grass germplasm accessions

Source of variation	Mean Square													
	DF	PHT	NOT	NON	NOL	LLH	LBH	SGH	ILH	LWT	SWT	LSR	GFY	DMC
Treatment	55	1919.49**	15.01**	6.03**	4.66**	272.55**	0.80**	2.35**	3.01**	226343.74**	293221.50**	0.24**	841602.12**	50.52**
Replication	1	25.75	17.94	1.23	2.83	17.14	0.04	0.47	2.36	463.25	70.98	0.03	171.57	12.64
Error	55	103.73	5.50	0.67	0.77	18.24	0.06	0.15	0.96	13314.50	23448.17	0.02	41242.56	3.85

*Significant at 5 % level of significance
PHT – Plant height (cm)
NOT – Number of tillers per plant
NON – Number of nodes on main tiller
NOL – Number of leaves per tiller
LLH – Leaf length (cm)
LBH – Leaf breadth (cm)

**Significant at 1 % level of significance
SGH – Stem girth (cm)
ILH – Internodal length (cm)
LWT – Leaf weight (g)
SWT – Stem weight (g)
LSR – Leaf to stem ratio
GFY – Green forage yield per plant (g)
DMC – Dry matter content (%)

Table 4. Clustering pattern of 56 Napier grass germplasm accessions by Tocher's method and agglomerative hierarchical clustering method

Cluster	Tocher's method		Agglomerative hierarchical clustering method	
	Number of genotypes	Name of genotypes	Number of genotypes	Name of genotypes
I	31	FD 430, FD 434, FD 443, FD 441, FD 439, FD 436, FD 460, FD 455, FD 455/1, FD 454, FD 445, FD 452, FD 450, FD 478, FD 479, FD 449, FD 457, FD 442, FD 451, FD 446, FD 480, FD 431, FD 458, FD 477, FD 448, FD 472, FD 433, FD 453/1, FD 453, FD 483, FD 456	3	FD 426, FD 437, FD 462
II	11	FD 447, FD 481, FD 467, FD 438 , FD 464 , FD 465, FD 485 , FD 463 , FD 466, FD 440, FD 482	5	FD 430, FD 434, FD 442, FD 468, FD 483
III	1	FD 432	3	FD 431, FD 479, FD 480
IV	1	FD 437	4	FD 432, FD 441, FD 472, FD 453/1
V	1	FD 459	5	FD 433, FD 435, FD 440, FD 473, FD 482
VI	6	FD 470, FD 474, FD 471, FD 461, FD 473, FD 476	10	FD 436, FD 439, FD 443, FD 445, FD 449, FD 450, FD 453, FD 455, FD 456, FD 458
VII	1	FD 444	16	FD 438, FD 444, FD 446, FD 447, FD 448, FD 451, FD 452, FD 454, FD 457, FD 463, FD 465, FD 467, FD 478, FD 481, FD 485, FD 455/1
VIII	1	FD 462	5	FD 459, FD 460, FD 464, FD 466, FD 477
IX	1	FD 435	3	FD 461, FD 470, FD 471
X	1	FD 426	1	FD 474
XI	1	FD 468	1	FD 476

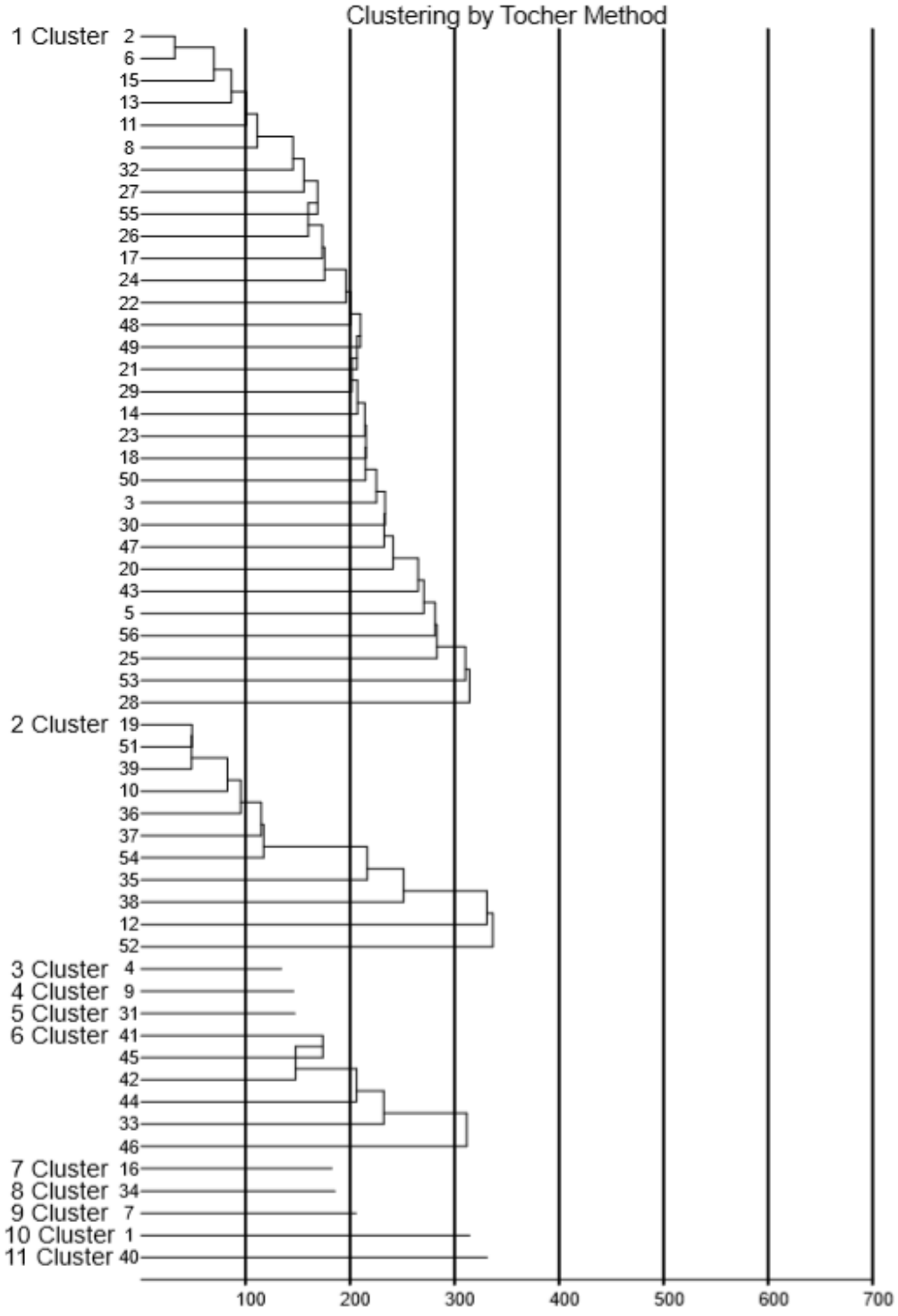

Fig. 1. Clustering of 56 Napier grass germplasm accessions by Tocher's method

(2013) in guinea grass, Doijad *et al.* (2016) in sorghum and Damor *et al*. (2017) in forage sorghum.

The average inter and intra cluster distances were given in **Table 5.** The inter cluster D^2 values ranged from 14.35 to 67.82 and intra cluster D^2 values ranged from 0 to 17.28. The values of inter cluster distance was relatively higher than that of intra cluster distance. The above results were in agreement with the results of Suthamathi and Durairaj (1994) in Napier grass, Ramakrishnan *et al*. (2013) in guinea grass, Krishna *et al*. (2014) in forage oat, Mali *et al*. (2014) in Napier grass, Damor *et al*. (2017) in forage sorghum and Kumari *et al.* (2019) in oats. The maximum intra cluster distance was observed for cluster VI (17.28) followed by clusters I and II with 15.68 each, thereby indicating substantial level of genetic diversity among the genotypes of this cluster. Hybridization between genotypes belonging to two clusters isolated by greater statistical distance would produce good heterotic effects and highly variable population in the segregating generations. Furthermore, selection of diverse parents forms an important obligation to a plant breeder to initiate any hybridization programme, thereby producing promising hybrids in F_1 and transgressive seggregants in the ensuing generations. The highest inter cluster distance was observed between cluster X and VI (67.82) followed by cluster VI and IV (57.63) and cluster VIII and VI (52.48) indicating existence of wider genetic diversity among the genotypes of these clusters, thereby, implying that the genetic makeup of one cluster is markedly different from that of the other cluster. Therefore, the genotypes from these clusters FD 426, FD 470, FD 474, FD 471, FD 461, FD 473, FD 476, FD 437 and FD 462 could very well be utilized in future breeding programme (**Table 3**). The lowest inter cluster distance was observed between cluster IX and VII (14.35) followed by clusters VIII and IV (15.57) indicating that the genotypes of these clusters are comparatively homogenous and less diverse.

Table 5. Average intra (in bold) and inter cluster D^2 distances for 56 Napier grass germplasm accessions

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**15.68**	23.83	18.86	23.15	21.77	43.47	19.16	21.74	25.18	33.18	28.36
II		**15.68**	29.56	37.34	20.95	29.24	25.21	31.03	30.37	47.18	22.84
III			**0.00**	27.75	18.11	45.65	28.40	30.51	34.65	38.30	29.00
IV				**0.00**	36.99	57.63	21.62	15.57	23.14	17.74	38.59
V					**0.00**	34.61	29.79	32.68	36.01	45.70	22.93
VI						**17.28**	46.37	52.48	49.43	67.82	25.22
VII							**0.00**	16.83	14.35	28.69	32.62
VIII								**0.00**	20.43	21.87	36.17
IX									**0.00**	25.69	35.03
X										0.00	48.41
XI											0.00

Clustering the genotypes by way of cluster means of different quantitative traits paves the way to identify suitable genotype with appropriate trait of interest (Krishna *et al*., 2014). The mean values for 13 quantitative traits for 11 clusters obtained by Tocher's method and agglomerative hierarchical clustering method are given in (**Table 6)**. Perusal of results of Tocher's method reveals that, there was considerable amount of inter cluster variation among the cluster mean for all the traits studied. The cluster X evinced the highest mean values for number of nodes in main tiller (11.07), number of leaves per tiller (15.16) and leaf breadth (4.99). Cluster V recorded highest mean values for leaf weight (1667.7), stem weight (1682.1), green forage yield per plant (3349.8) and dry matter content (54.85). Cluster XI recorded the highest mean values for number of tillers per plant (20.74) and internodal length (14.05). Cluster III and cluster IX exhibited highest mean values for leaf length (111.7) and leaf to stem ratio (1.15), respectively. Cluster IV and VII exhibited the highest mean values for plant height (285.95) and stem girth (7.12), respectively. Hence, the genotypes namely, FD 432, FD 437, FD 459, FD 444, FD 435, FD 426, FD 468 from the above mentioned clusters could be selected in order to evolve varieties with improvement in respective traits. In addition to that, cluster I recorded relatively higher cluster mean value for leaf to stem ratio (0.82) and dry matter content (50.37) and comparatively average cluster mean values for majority of the traits and genotypes from these cluster may also be considered for utilizing in future crop improvement programme. Cluster VI showed the lowest mean values for green forage yield per plant (1120.18), leaf breadth (2.15), stem girth (4.15) and leaf length (72.98) whereas cluster IX depicted lowest mean values for dry matter content (30.1) and stem weight (552.78). The lowest mean value for leaf to stem ratio (0.5) and leaf weight (400) was exhibited by cluster IV. Cluster VII depicted lowest mean values for number of nodes on main tiller (5.3) and plant height (161.84) whereas cluster II showed lowest mean values for number of tillers per plant (13.71) and number of leaves per tiller (10.56). Cluster V recorded lowest mean value for intermodal length (9.32).

The percentage contribution of each trait towards total genetic divergence was estimated by Tocher's method and presented in **Table 7**. Among the traits studied, leaf breadth (48.64%) contributed most towards genetic divergence followed by leaf length (17.34%) and stem girth (14.94%). Hence, 80.92 per cent of total genetic divergence was contributed by the above three traits.

Table 6. Cluster mean for 13 biometrical traits in 56 Napier grass germplasm accessions

Clusters	Cluster mean values of 11 clusters for 13 biometrical traits by Tocher's method												
	PHT	NOT	NON	NOL	LLH	LBH	SGH	ILH	LWT	SWT	LSR	GFY	DMC
I	200.55	14.56	7.82	12.60	103.79	3.55	6.52	11.71	742.86	968.96	0.82	1711.82	50.37
II	169.27	13.71	5.58	10.56	92.40	3.07	5.18	10.61	614.26	797.79	0.84	1412.05	49.70
III	220.30	15.56	8.50	13.81	111.17	2.90	7.01	12.69	985.74	1674.65	0.61	2660.39	52.67
IV	285.95	19.65	8.66	14.73	109.57	3.94	6.59	12.73	400.00	802.08	0.50	1202.08	42.77
V	194.05	19.25	7.51	12.70	97.04	2.96	5.82	9.32	1667.70	1682.10	1.00	3349.80	54.85
VI	181.99	16.80	7.28	11.25	72.98	2.15	4.15	12.28	472.57	647.61	0.84	1120.18	51.49
VII	161.84	15.20	5.30	12.80	95.04	3.91	7.12	11.49	564.51	664.51	0.85	1229.02	42.74
VIII	237.25	17.80	6.30	14.00	101.43	4.36	5.26	10.21	733.01	1182.06	0.62	1915.06	46.91
IX	188.20	14.70	7.72	11.65	100.96	3.91	6.07	11.34	638.04	552.78	1.15	1190.82	30.10
X	257.65	20.00	11.07	15.16	108.07	4.99	7.03	12.07	1317.05	1308.25	1.01	2625.30	38.05
XI	280.44	20.74	8.81	12.30	81.89	2.62	5.21	14.05	1044.50	1177.09	0.89	2221.59	48.55
Clusters	Cluster mean values of 11 clusters for 13 biometrical traits by Agglomerative hierarchical clustering method												
	PHT	NOT	NON	NOL	LLH	LBH	SGH	ILH	LWT	SWT	LSR	GFY	DMC
I	260.28	19.15	8.69	14.63	106.35	4.43	6.29	11.67	816.69	1097.46	0.71	1914.15	42.58
II	230.10	17.60	8.24	12.94	101.74	3.11	6.01	12.95	880.50	1157.58	0.79	2038.07	48.15
III	189.67	16.92	6.27	10.72	103.80	3.39	5.64	11.84	618.78	1430.71	0.44	2049.49	50.11
IV	205.53	14.25	7.45	13.28	102.75	3.65	7.27	12.30	1071.86	1633.25	0.67	2705.11	49.99
V	202.82	13.88	6.83	11.20	94.56	3.11	4.92	12.63	632.18	691.24	1.04	1323.43	41.86
VI	209.56	14.22	9.41	13.46	102.67	3.73	7.00	11.34	783.79	862.68	0.97	1646.47	50.85
VII	174.26	13.26	6.21	11.41	98.49	3.34	5.98	10.89	461.54	643.44	0.76	1104.97	50.45
VIII	173.22	16.48	6.18	11.61	97.55	3.19	5.76	10.14	1312.14	1280.41	1.07	2592.55	53.45
IX	187.29	16.79	7.73	10.39	79.32	2.08	3.56	12.51	351.88	652.08	0.52	1003.96	51.06
X	211.80	20.50	8.77	14.55	59.42	2.02	4.95	12.34	515.51	839.82	0.62	1355.33	58.87
XI	136.45	15.47	5.16	10.60	66.49	2.40	4.34	11.49	459.80	261.15	1.76	720.95	50.81

Table 7. Percentage of contribution of various traits towards divergence for 56 Napier grass germplasm accessions by Tocher's method

Trait	No. of first rank	Contribution (%)
PHT	10	0.65 (%)
NOT	0	0.00 (%)
NON	14	0.91 (%)
NOL	29	1.88 (%)
LLH	267	17.34 (%)
LBH	749	48.64 (%)
SGH	230	14.94 (%)
ILH	65	4.22 (%)
LWT	0	0.00 (%)
SWT	10	0.65 (%)
LSR	43	2.79 (%)
GFY	60	3.90 (%)
DMC	63	4.09 (%)

Therefore, the above characters could be used as selection criteria in either selection or hybridization in order to evolve high yielding cultivars.

Dissimilarity among the 56 germplasm accessions by agglomerative hierarchical clustering based on Euclidean with complete linkage method (Cut off value at 5.2 Euclidean diatance) against Tocher's method was given in **Table 4 and Fig. 2**. The results from this method classified the genotypes into 11 clusters.

Cluster VII was the largest with 16 genotypes namely FD 438, FD 444, FD 446, FD 447, FD 448, FD 451, FD 452,

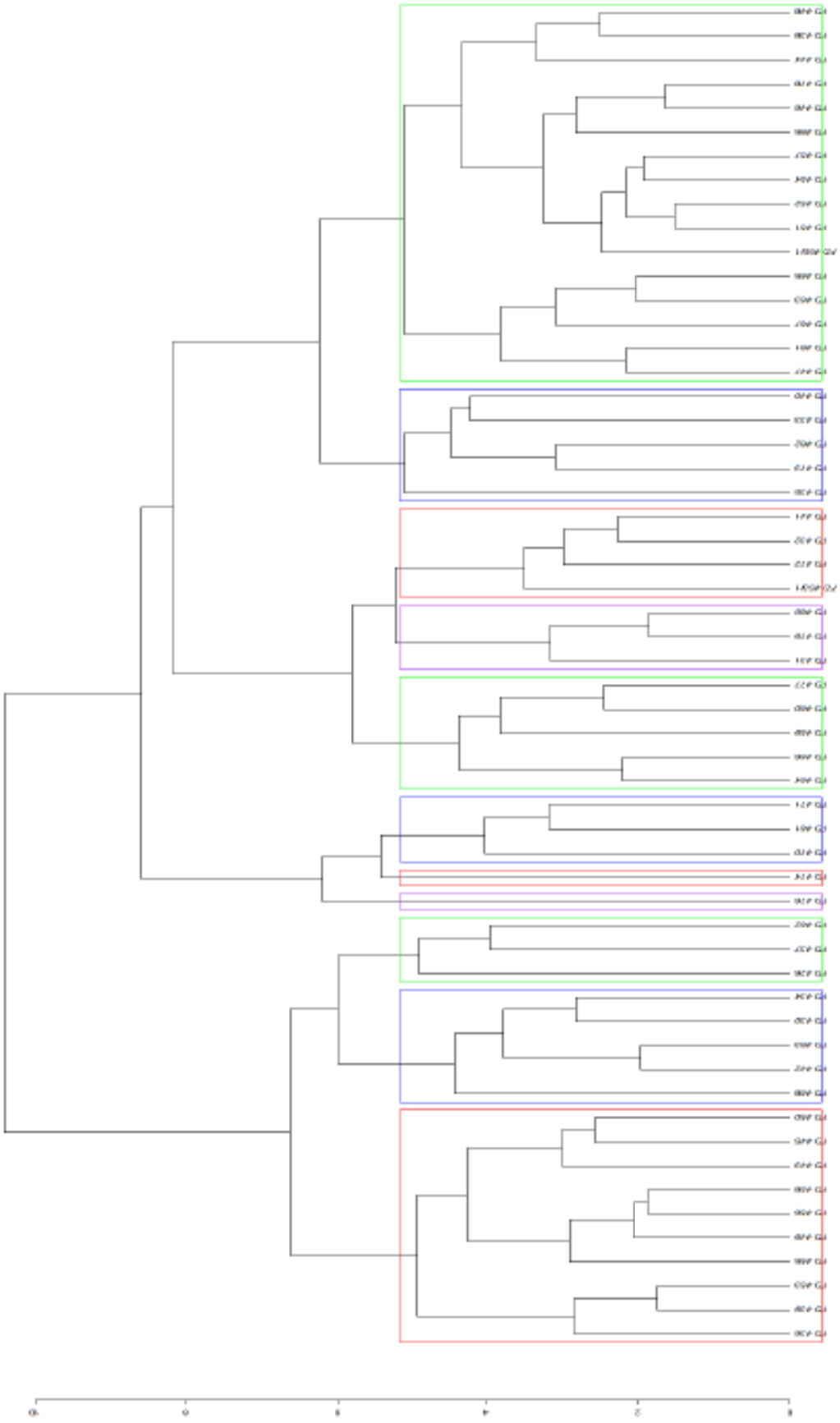

Fig. 2. Clustering of 56 Napier grass germplasm accessions by agglomerative hierarchical cluster method

FD 454, FD 457, FD 463, FD 465, FD 467, FD 478, FD 481, FD 485, and FD 455/1. The genotypes in this cluster were partly similar to those found in the cluster I and cluster II generated through Tocher's method. Cluster VII was followed by Cluster VI with 10 genotypes *viz*., FD 436, FD 439, FD 443, FD 445, FD 449, FD 450, FD 453, FD 455, FD 456, and FD 458. The genotypes in this cluster entirely coincides with the cluster I genotypes classified by the previous method.

Cluster II, V and VIII were circumscribed each with five genotypes and cluster IV was comprised with four genotypes. Among these, in cluster II and cluster IV, most of the genotypes matched with the genotypes of cluster I grouped by earlier method.

Cluster I, III and IX were encompassed each with three genotypes. The genotypes in the cluster III and cluster IX perfectly concorded with the genotypes in cluster I and cluster VI respectively of former classification by Tocher's method. Clusters X and cluster XI were observed to be mono genotypic.

The mean performance of clusters for various traits based on agglomerative hierarchical clustering approach was shown in Table 6. Cluster I which encompassed the genotypes, FD 426, FD 437 and FD 462 showed the highest mean values for plant height (260.28), number of leaves per plant (14.63), leaf length (106.35) and leaf breadth (4.43). Similarly, in Tocher's method of clustering, the genotype FD 437 of cluster IV was depicted with the highest cluster mean for plant height (285.95) and the genotype FD 426 of cluster X with the highest mean values for number of leaves per tiller (15.16) and leaf breadth (4.99).

The maximum mean values for stem weight (1633.25), green forage yield per plant (2705.11) and stem girth (7.27) was displayed by Cluster IV whereas the maximum mean value for internodal length (12.95) and number of nodes on main tiller (9.41) were observed in cluster II and VI respectively. The cluster X was observed to have maximum mean values for number of tillers per plant (20.50) and dry matter content (58.87). Cluster XI showed highest mean value for leaf to stem ratio. Cluster VIII which encompassed the genotypes FD 459, FD 460, FD 464, FD 466, FD 477 recorded the highest mean value for leaf weight (1312.14). Similarly, in Tocher's method of clustering also, the genotype FD 459 of cluster V recorded the highest mean value for the same (1667.70). The cluster VII with the following genotypes FD 438, FD 444, FD 446, FD 447, FD 448, FD 451, FD 452, FD 454, FD 457, FD 463, FD 465, FD 467, FD 478, FD 481, FD 485 and FD 455/1 was observed to have the lowest cluster mean value for number of tillers per plant (13.26). Similarly, in Tocher's method also, the genotypes FD 438, FD 447, FD 463, FD 465, FD 467, FD 481 and FD 485 of cluster II were recorded with poor performance for number of tillers per plant (13.71). Cluster X with the genotype FD 474 was observed to have the lowest cluster mean value for leaf length (59.42) and leaf breadth (2.02). Analogously, the same genotype FD 474 which was grouped in cluster VI by Tocher's method exhibited the lowest cluster mean for leaf length (72.98) and leaf breadth (2.15). The genotypes of cluster IX *viz*., FD 461, FD 470 and FD 471 evinced the lowest cluster mean value for stem girth (3.56). Identically, the same genotypes FD 470 and FD 471 of cluster VI grouped by Tocher's method also depicted the lowest cluster mean for stem girth (4.15). In a similar manner, the genotypes FD 459, FD 476 and FD 435 grouped under various clusters by both the methods were recorded with lowest mean values for internodal length, green fodder yield and dry matter content respectively. Thus, the results from both the clustering methods comparatively correspond with each other and stand evident to the prevalence of genetic diversity in the germplasm studied. Characterization of the Napier grass germplasm revealed significant variation for majority of the morphological traits studied, implying prevalence of genetic diversity among the accessions. The traits like presence of prop roots, leaf sheath pigmentation and bristle length evinced highest variation ranging from 8.93 % - 67.86 %, 8.93 % - 64.29 % and 3.57 % - 58.93 % respectively . Cluster analysis by Tocher's method classified the genotypes into 11 clusters and revealed existence of significant amount of genetic diversity among the 56 Napier grass germplasm. The analysis revealed that the highest inter cluster distance was between cluster X and VI (67.82) followed by cluster VI and IV (57.63) and cluster VI and VIII (52.48). Hence the genotypes from these diverse clusters IV, VI, X and VIII *viz*., FD 437, FD 470, FD 474, FD 471, FD 461, FD 473, FD 476, FD 426, FD 462 could be chosen in future breeding programmes in order to attain higher heterosis and better recombinants in segregating generations. In addition to that, diverse genotypes may also be selected from clusters with higher cluster mean value for the desired trait in order to enhance the trait of interest. Hence based on cluster mean, genotypes from clusters, V, X and XI *viz*., FD 459, FD 426 and FD 468 were found to be complementary for majority of the traits studied and could be selected for use in upcoming crop improvement programmes. Clustering by agglomerative hierarchical clustering approach also classified the genotypes into 11 clusters. The outcome from the both the methods relatively commensurate with each other and satisfactory to explain the existence of genetic diversity among the population but clustering by hierarchical approach was able to dissociate the clusters into sub clusters at appropriate cut off levels and provided additional advantage for selection of genotypes. Hence, the diverse genotypes, thus identified, could be utilized for the development of high biomass yielding Pearl millet Napier interspecific hybrids in the future breeding programmes.

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