# Studies on Genetic diversity, Variability and Contribution of Traits for Green Fodder Yield and Quality Traits in Napier grass (*Pennisetum purpureum* L. Schumach.)

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## ABSTRACT

Napier grass, being robust, quick growing perennial allotetraploid fodder crop with repeated cutting ability gains significance for sustaining the animal population and maintaining its productivity. Fifty six Napier grass genotypes were evaluated for character association and diversity analysis during *Kharif* 2020. The genotypes were significantly different for all the characters, which indicated scope for further genetic studies. High estimates of PCV and GCV were observed for PHT, LBH, LWT, CFT, ASH, DMY and GFY. Moderate estimates of PCV and GCV were observed for NOT, NOL, NON, ILH, SWT, ADF, CPN, DMC. High heritability along with high genetic advance as percent of mean was recorded for PHT, NOT, NOL, NON, ILH, LLH, LBH, SGH, LWT, SWT, ADF, CPN, CFT, ASH, DMC, DMY and GFY indicating the predominance of additive gene effects in the inheritance of these characters except LSR, NDF and CFR. Traits like PHT, NOT, NOL, LLH, LBH, SGH, LWT, SWT, LSR, CPN, CFT, ASH, DMC and DMY had positive and significant correlation at genotypic level with GFY and the selection based on these traits will result in enhanced GFY. Most of the yield contributing traits like DMY, SWT and LSR exhibited positive direct effect on GFY. Genetic diversity among the genotypes was assessed based on Mahalanobis's $D^2$ statistics clustering approach. Based on Tocher's method, the genotypes were classified into 10 clusters. The highest inter cluster distance was observed between cluster VIII and VII (29.76) followed by VII and IV (28.96), X and VII (28.19) and cluster IX and VII (27.54). Therefore, the genotypes from the above clusters *viz.*, FD 453/1, FD 467, FD 435, FD 446 and FD 445 could be used as parents for the development of high yielding Pearl millet Napier hybrids.

## KEY WORDS

*Napier grass (Pennisetum purpureum L. Schumach.); Variability; Correlation; Path analysis; Genetic diversity; Mahalanobis's $D^2$ analysis.*

## INTRODUCTION

As per 20th livestock census the total livestock population in India is 535.78 million which is 4.6% increase over the 19th livestock census. 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 the 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 that could yield more green fodder per unit area. Napier grass is one of the forage crops that 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 $C_4$ 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. Besides, it also serves as one of the parents of the most successful and highest biomass yielding Pearl millet Napier hybrid grass.

The existence of genetic diversity in crop species is considered a gift from nature. Scientific understanding about the presence and extent of genetic diversity generally helps the breeder to select superior genotypes and avoid redundancy of genotypes and identify distantly related genotypes to form a most heterotic cross combination in hybridization especially in Pearl millet Napier hybrids. Since the studies on genetic diversity in Napier grass are very limited the present study was carried out to assess the extent of genetic variability in the domestic gene pool to exploit it effectively.

## MATERIAL AND METHODS

The present investigation was carried out using 56 Napier grass domestic germplasm accessions being maintained vegetatively at the Department of Forage Crops, Tamil Nadu Agricultural University, Coimbatore, India. Each accession was grown in two rows of four meter length with a spacing of 60 cm x 50 cm laid out in Randomized Block Design (RBD) with two replications. All the recommended agronomic package of practices were followed to raise a good crop and five competitive plants were randomly selected from each genotype in each replication avoiding border plants.

Plants to be selected were tagged before initiation of flowering for recording the observations at the time of days to 50 per cent flowering stage on quantitative and qualitative traits *viz.,* PHT (cm), NOT, NOL, NON, ILH (cm), LLH (cm), LBH (cm), SGH (cm), LWT (g), SWT (g), LSR, DMY (g), GFY (g), DMC

(%), CPN (%), CFT (%), ASH (%), CFR (%), ADF (%), NDF content (%). For CPN, CFT, ASH and CFR estimation, plant samples were collected at the time of panicle initiation. The samples were chopped, air dried and finally oven dried at 60°C for two days. The oven dried samples were ground and sieved using different sieve sizes. A sieve size of 0.5 mm was used for estimation of CFR, ADF, NDF and 0.1 mm sieve size was used for CPN, CFT and ASH estimation. CPN was estimated by Kjeldahl"s method and CFT was estimated with the soxhlet method using petroleum ether while CFR estimation was done through digestion with sulphuric acid, sodium hydroxide solution and ADF, NDF was estimated by using CFR apparatus. Mean values were used to compute the genetic parameters and statistical data analysis was carried out for each character (Panse and Sukhatme 1967). Genotypic and phenotypic coefficient of variation was estimated as suggested by Burton (1952). The correlation coefficients were calculated using the formulae of Falconer (1964) and path coefficient analysis was carried out following Dewey and Lu (1959). 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.

## RESULT AND DISCUSSION

### Estimates of genetic variability, heritability and genetic advance

In the napier grass germplasm accessions studied, high PCV and high GCV were noticed for seven characters *viz.,* PHT (23.904, 22.527), LBH (32.524, 28.801), LWT (26.711, 26.158), CFT (37.148, 35.633), ASH (23.841, 22.183), DMY (46.882, 45.467) and green fodder yield (39.776, 38.573) (Table 1). Similar results for PHT have been reported by Kapoor (2017), Santhosh *et al.* (2017) in Napier grass. Moderate PCV and moderate GCV were noticed for eight characters *viz.,* NOT (19.323, 18.410), NOL (19.982, 18.707), NON (17.886, 16.327), ILH (16.485, 13.709), SWT (16.171, 15.833), ADF (14.099, 13.198), NDF (10.557, 10.004), CPN (15.717, 14.795) and DMC(14.345, 12.382) (Table 1). Similar results have been reported by Santhosh *et al.* (2017) in Napier grass. The characters *viz.,* LSR, CFR recorded low level of PCV and GCV. This indicated the higher environment influence in the expression of traits and selection may not be effective for these traits. High PCV and moderate GCV were observed for LLH (20.283, 19.818) and SGH (22.379, 19.373). The PCV was slightly higher than GCV indicating limited influence of environment on the expression of characters.

Heritability and genetic gain are the two important parameters, of which, former is used to estimate the expected genetic gain through selection. Their relative comparison gives an idea about the nature of gene action governing a particular character. Therefore, it is essential to partition the observed variability into heritable and non-heritable components. High heritability with high genetic advance as per cent of mean was observed for PHT (0.888, 43.733), NOT (0.908, 36.131), NOL (0.876, 36.076), NON (0.833,30.704), ILH (0.692, 23.485), LLH (0.955, 39.891), LBH (0.784, 52.539), SGH (0.749, 3.549), LWT (0.959, 52.769), SWT (0.959, 31.934), ADF (0.876, 25.450), CPN (0.886, 28.689), CFT (0.920, 70.411), ASH (0.866, 42.520), DMC(0.745, 22.015), DMY (0.941, 90.836) and GFY (0.940, 77.057) in Napier grass accessions Table 1. This indicated the lesser influence of

environment in the expression of these characters and the prevalence of additive gene action in their inheritance, facilitating effective selection. The obtained results were in accordance with the results on the number of leaves per plant by Sharma *et al.* (2003) in pearl millet.

High heritability and high genetic advance for LWT, SWT, LSR and CPN content were reported by Suthamani and Stephen Dorairaj (1995) in pearl millet. For GFY, similar results were reported by Sharma *et al.* (2003) and Vidyadhar*et al.* (2007) in pearl millet, Jain and Patel (2012) in fodder sorghum and Vinodhana*et al.* (2013) in pearl millet.

High values for desirable variability, heritability and genetic advance were observed for traits namely PHT, LBH, LWT, CFT, ASH, DMY and green fodder yield. It represents that selection based on these characters is effective since it is governed by additive gene action. LLH and GFY exhibited high heritability with moderate genetic advance as per cent of mean in Napier grass accessions which inferred that selection would be effective for these characters when a favorable environment prevails (table 1).

### Association of different traits with Green fodder yield

In a forage crop, the green fodder yield, is influenced by the number of vegetative plant characters. For achieving rational improvement in fodder yield and its components, knowledge of the mechanism of association, cause and effect relationship provides a basis for formulating suitable selection indices for the yield components. Results indicated that all the yield contributing traits had highly significant positive correlation at genotypic and phenotypic levels with GFY except NON, intermodal length, ADF, NDF and CFR Table 2. Among them, NON had positive significant correlation at the genotypic as well as phenotypic level and ILH had a positive and highly significant correlation at the genotypic level and positive significant correlation at phenotypic level and thereby selection based on these traits would result in enhanced green fodder yield in Napier.

On the contrary, two quality traits evaluated *viz.,* ADF and NDF exhibited a negative and highly significant correlation with GFY. In contrast CFR had a highly negative significant correlation at the genotypic level and negative non significant correlation at phenotypic level with GFY. The highest value of positive and significant correlation was observed between GFY and CPN (0.9975, 0.9566) followed by PHT (0.9945, 0.9278), DMY (0.9828, 0.9719). Amongst the six quality parameters studied only three traits *viz.,* CPN, CFT, and crude ASH exhibited positive and significant correlation with GFY whereas the other three traits *viz.,* CFR, ADF and NDF exhibited negative and significant correlation with GFY. Similar results were reported by Kapoor (2017) in Napier grass.

Traits like PHT, NOT, NOL, LLH, LBH, SGH, LWT, SWT, LSR, CPN, CFT, ASH, DMC, DMY showed positive and highly significant correlation amongst each other but exhibited negative and highly significant correlation with quality parameters *viz.,* ADF, NDF and CFR.

### Direct and indirect effect of traits on Green fodder yield

Path analysis partitions the total correlation coefficient into direct and indirect effects and measures the relative importance of the causal factor (Dewey and Lu, 1959). In the present study, green fodder yield was considered as a dependent character and other characters were taken as independent characters. The results of path analysis are presented in Table 3. The component of the residual effect of path analysis was 0.0311. The lower residual effect indicated that the characters chosen for path analysis were adequate and appropriate.

The characters such as NOT (0.1948), NOL (0.0088), LBH (0.0744), SWT (0.6210), LSR (0.3664), CFR (0.0575), NDF (0.0290), CPN (0.1846), ASH (0.0739) had positive direct effect on GFY. Among them DMY had a very high positive direct effect (1.3941) on GFY indicating that there is always scope for enhancement of fodder yield by selecting this trait. The present results are in agreement with the findings of Bahadur and Lodhi (2009) and Jain and Patel (2012).The traits, PHT (-0.0270), NON (-0.0231), ILH (-0.0028), LLH (-0.3426), SGH (-0.1635), LWT (-0.8733), ADF (-0.0037), CFT (-0.0762) and DMC (-0.4745) had a negative direct effect on GFY.

Among the traits, PHT (1.3939), NOT (1.3551), NOL (1.3309), LLH (1.3720), SGH (1.2668), LWT (1.3669), SWT (1.3439), LSR (1.3501), CPN (1.3841), CFT (1.3457), ASH (1.3766), DMC (1.1554) and DMY (1.3941) had very high positive indirect effect on green fodder yield through DMY. ADF (0.3223) and NDF (0.3395) had a high positive indirect effect on green fodder yield through LLH. ADF (0.8392), NDF (0.8595) had high positive indirect effect on green fodder yield through LWT. PHT (0.6240), NOT (0.5950), NOL (0.6094), LLH (0.5994), LBH (0.6021), SGH (0.5566), LWT (0.6157), LSR (0.6101), CPN (0.6124), CFT (0.6104), ASH (0.6146), DMC (0.5319), DMY (0.5986) had high positive indirect effect on GFY through SWT. PHT (0.3650), NOT (0.3526), NOL (0.3573), LLH (0.3600), LBH (0.3471), SGH (0.3193), LWT (0.3654), SWT (0.3599), CPN (0.3535), CFT (0.3537), ASH (0.3680), DMC (0.3013), DMY (0.3548) had high positive indirect effect on GFY through LSR. ADF (0.3451), NDF(0.3978) had high positive indirect effect on green fodder yield through DMC. The NON (0.5459), ILH (0.4971) had a high positive indirect effect on green fodder yield through DMY. The NON (0.2293) had a moderate positive indirect effect on GFY through SWT. This was in accordance with the findings of Iyanar*et al.* (2010).

ADF (-1.3047) and NDF (-1.4049) had a very high negative indirect effect on GFY through DMY. PHT (-0.3447), NOT (-0.3354), NOL (-0.3249), LBH (-0.3171), LWT (-0.3375), SWT (-0.3307), LSR (-0.3367), CPN (0.3374), CFT (0.3263), ASH (-0.3424), DMY (-0.3372), had a high negative indirect effect on GFY through LLH. PHT (-0.8837), NOT (0.8436), NOL (0.8526), NON (0.3069), LLH (-0.8602), LBH (-0.8484), SGH (0.7803), SWT (-0.8658), LSR (0.8709), CPN (-0.8638), CFT (-0.8578), ASH (0.8768), DMC (-0.7209), DMY (-0.8562), had a high negative indirect effect on GFY through LWT. ADF (-0.5938, -0.3467), NDF (-0.5992, -0.3586) had a high negative indirect effect on GFY through SWT and LSR. PHT (-0.4005), NOT (-0.4007), NOL (0.4008), LLH (-0.3846), LBH (-0.3682), SGH (0.3425), LWT (-0.3917), SWT (-0.4064), LSR (-0.3902), CPN (-0.3768), CFT (-0.3610), ASH (-0.3856), DMY (-0.3932), had a high negative indirect effect on GFY through dry matter content. CFR (-0.4563) had a high negative indirect effect on GFY through DMY. DMC (-0.2777) had a moderate negative indirect effect on GFY through LLH. ILH (-0.2733) had a moderate negative indirect effect on GFY through LWT. DMC had a moderate negative indirect effect on GFY through DMC.

*Diversity study*

All the fifty six Napier grass accessions were grouped into 10 clusters based on Mahalanobis's D²value (Tocher's cut off value: 262.89) and depicted in Table 4 and Fig.1. Cluster I was the largest and turned out to be accommodative for maximum number of genotypes viz., FD 457, FD 473, FD 463, FD 454, FD 479, FD 485, FD 480, FD 430, FD 462, FD 453, FD 440, FD 447, FD 452, FD 470, FD 458, FD 461, FD 450, FD 451, FD 433, FD 436, FD 459, FD 439, FD 474, FD 426, FD 460, FD 478. Similar results were reported by Damor*et al*. (2017) in forage sorghum. Cluster I consisted of 26 genotypes followed by Cluster II with 16 genotypes whereas cluster III, had 7 genotypes each. Clusters IV, V, VI, VII, VIII IX, X were the smallest and each contained one genotype. Similar findings were reported by Doijad*et al.* (2016) in sorghum. The average inter and intra cluster distances were given in Table 5**.** The inter cluster D²values ranged from 10.59 to 29.76 and intra cluster D²values ranged from 7.94 to 8.65. The values of inter cluster distance were relatively higher than that of intra cluster distance. The above results were in agreement with the results of Mali *et al*. (2014) in Napier grass, Kumari *et al.* (2019) in oats and Natchiar *et al*. (2020).

The maximum intra cluster distance was observed for cluster II (8.65) followed by clusters III and I with 8.07, 7.94 respectively thereby indicating the substantial level of genetic diversity among the genotypes in these clusters. Furthermore, the selection of diverse parents forms an important task to a plant breeder to initiate any hybridization program, thereby producing promising hybrids and transgressive segregants. The highest inter cluster distance was observed between clusters VIII and VII (29.76) followed by clusters VII and IV (28.96), cluster X and VII (28.19) and clusters IX and VII (27.54) indicating the 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 453/1, FD 467, FD 435, FD 446 and FD 445 could be utilized in synthesizing diverse hybrids of pearl miller Napier hybrids with higher heterotic potential (Table 3). The lowest inter cluster distance was observed between clusters V and IV (10.59) followed by clusters VI and I (10.99), V and II (11.42) indicating that the genotypes of these clusters are comparatively homogenous and less diverse. Clustering the genotypes by way of cluster means of different quantitative and qualitative traits paves the way to identify suitable genotypes with an appropriate trait of interest.

*Mean values*

The mean values for 20 quantitative traits for 10 clusters obtained by Tocher's clustering method are given in Table 6. A perusal of the results of Tocher's method reveals that there a was considerable amount of inter cluster variation among the cluster means for all the traits studied. Cluster VIII evinced the highest mean values for PHT (330.23), NOT (22.20), ILH (13.35), LLH (110.16), LWT (1546.00), SWT (2050.00), CPN (11.09), ASH (10.49) and GFY (3276.00). Cluster X recorded highest mean values for NOL (25.70), LBH (5.95), LSR (0.43), CFT (8.98) and DMY (883.00). Clusters I, II, III, IV, VII, IX recorded the highest mean values for CFR (30.32), NON (9.13), ADF (49.51), DMC (34.40) NDF (67.29) and SGH (7.62) respectively. Hence, the genotypes FD 453/1, FD 445 from the above mentioned clusters could be selected to evolve Pearl millet napier hybrids with improvement in respective

traits. Cluster VII showed the lowest mean values for PHT (153.66), NOT (10.90), NOL (10.90), LLH (56.30), SGH (3.14), LWT (527.00), SWT (1056.00), LSR (0.33), CPN (6.03), CFT (1.70), and ASH (4.13), DMC(20.18) , DMY (178.00), GFY (886.50), whereas cluster III depicted the lowest mean value for LBH (1.91). Clusters V, VIII, IX, X depicted the lowest mean values for CFR (25.70), ADF (31.29), ILH (7.76) and NDF (49.30). The percentage contribution of each trait towards total genetic divergence was estimated by Tocher's method Table 7. Among the traits studied, LLH (20.26%) contributed most towards genetic divergence followed by the NON (18.83%), NOT (12.79%) and SWT (11.88%). Hence, 63.76 per cent of total genetic divergence was contributed by the above four traits. Hence, the diverse genotypes, thus identified, could be utilized for the development of high biomass yielding Pearl millet Napier interspecific hybrids in future breeding programmes.

## CONCLUSION

The present investigation indicates that the highest inter cluster distance was observed between clusters VIII and VII followed by VII and IV, X and VII, IX and VII. In these clusters, the genotypes viz., FD 453/1, FD 467, FD 435, FD 446, FD 445 recorded high green fodder yield and it could be used as parents to enhance green fodder yield in the pearl millet Napier grass hybrid development. Variability and association studies revealed that the traits viz., PHT, NOT, NOL, LBH, LWT, SWT, DMY, CPN, CFT, ASH and DMC were highly heritable and exhibited significant positive direct on GFY. It was concluded that, the utilization of these diverse genotypes for synthesising diverse and heterotic pearl millet Napier hybrid combination and the selection of hybrids based on the green fodder yield contributing traits viz., PHT, NOT, NOL, LBH, LWT, SWT, DMY, CPN, CFT, ASH and DMC would be effective in the development of pearl millet Napier grass hybrids (Table 8).

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**Figure 1.Clustering of 56 Napier grass germplasm accessions by Tocher's method**
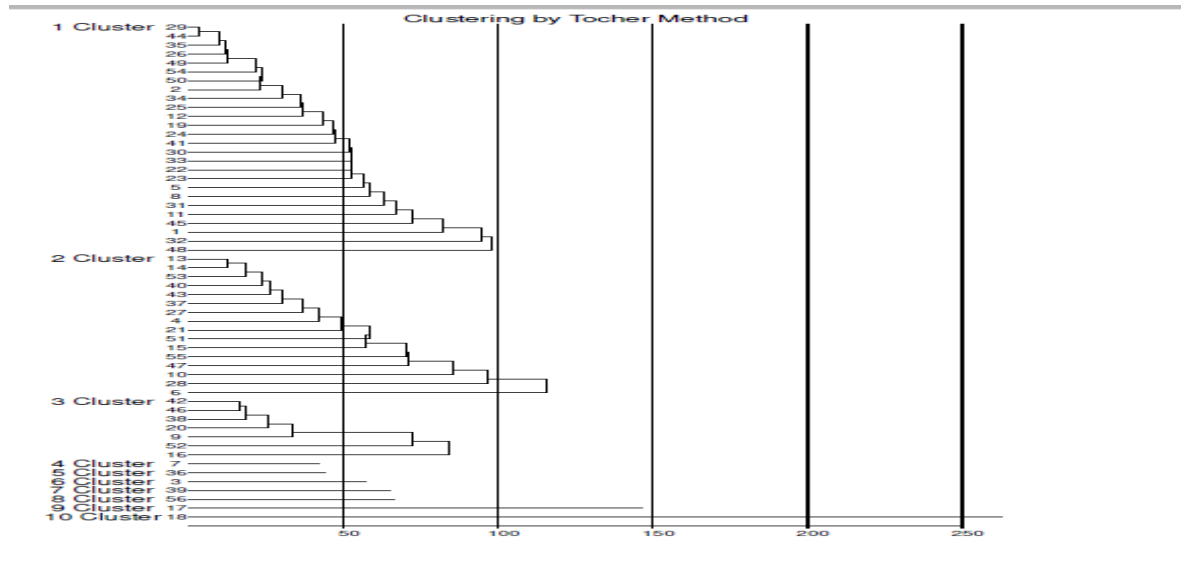
Table 1.Estimates of genetic variability analysis in Napier grass germplasm accessions

| S. No. | Traits | PV | GV | PCV | GCV | H² | GA | GAM |
|---|---|---|---|---|---|---|---|---|
| 1. | Plant height(cm) | 3142.525 | 2790.870 | 23.904 | 22.527 | 0.888 | 102.558 | 43.733 |
| 2. | No of tillers per plant | 10.354 | 9.398 | 19.323 | 18.410 | 0.908 | 6.016 | 36.131 |
| 3. | No of leaves per tiller | 14.462 | 12.674 | 19.982 | 18.707 | 0.876 | 6.866 | 36.076 |
| 4. | No of nodes on main tiller | 2.086 | 1.738 | 17.886 | 16.327 | 0.833 | 2.479 | 30.704 |
| 5. | Internodal  length(cm) | 2.567 | 1.775 | 16.485 | 13.709 | 0.692 | 2.283 | 23.485 |
| 6. | Leaf  length(cm) | 276.572 | 264.053 | 20.283 | 19.818 | 0.955 | 32.708 | 39.891 |
| 7. | Leaf width (cm) | 1.097 | 0.860 | 32.524 | 28.801 | 0.784 | 1.692 | 52.539 |
| 8. | Stem girth (cm) | 1.478 | 1.108 | 22.379 | 19.373 | 0.749 | 1.877 | 34.549 |
| 9. | Leaf weight(g) | 80598.570 | 77293.836 | 26.711 | 26.158 | 0.959 | 560.852 | 52.769 |
| 10. | Stem weight(g) | 70307.648 | 67398.594 | 16.171 | 15.833 | 0.959 | 523.621 | 31.934 |
| 11. | Leaf to stem ratio | 0.001 | 0.001 | 7.628 | 7.158 | 0.881 | 0.054 | 13.840 |
| 12. | Crude fibre content (%) | 8.022 | 3.666 | 9.791 | 6.619 | 0.457 | 2.666 | 9.216 |
| 13. | Acid detergent fibre content (%) | 33.226 | 29.114 | 14.099 | 13.198 | 0.876 | 10.405 | 25.450 |
| 14. | Neutral detergent fibre content (%) | 38.338 | 34.427 | 10.557 | 10.004 | 0.898 | 11.454 | 19.530 |

| 15. | Crude protein content (%) | 1.775 | 1.573 | 15.717 | 14.795 | 0.886 | 2.432 | 28.689 |

| Traits | | PHT | NOT | NOL | NON | ILH | LLH | LBH | SGH | LWT | SWT | LSR | CFR | ADF | NDF | CPN | CFT | ASH | DMC | DMY | GFY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PHT | $r_g$ | 1.0000 | 0.9878** | 0.9691** | 0.3571** | 0.3559** | 0.9861** | 0.9916** | 0.8807** | 0.9720** | 0.9347** | 0.9964** | -0.2434 | -0.9840** | -0.9957** | 0.9871** | 0.9529** | 0.9277** | 0.8442** | 0.9999** | 0.9945** |
| | $r_p$ | 1.0000 | 0.8829** | 0.9053** | 0.2889* | 0.2865* | 0.9411** | 0.8538** | 0.7667** | 0.9564** | 0.9393** | 0.9203** | -0.1988 | -0.8872** | -0.9138** | 0.9091** | 0.9175** | 0.8934** | 0.6681** | 0.9254** | 0.9278** |
| NOT | $r_g$ | | 1.0000 | 0.9462** | 0.4118** | 0.3539** | 0.9790** | 0.9110** | 0.9178** | 0.9660** | 0.9581** | 0.9625** | -0.2487 | -0.9076** | -0.9771** | 0.9923** | 0.9419** | 0.9157** | 0.8445** | 0.9720** | 0.9538** |
| | $r_p$ | | 1.0000 | 0.8649** | 0.3290* | 0.2808* | 0.9533** | 0.8297** | 0.7769** | 0.9345** | 0.9325** | 0.8772** | -0.0857 | -0.8587** | -0.9154** | 0.9356** | 0.9029** | 0.9474** | 0.7356** | 0.9329** | 0.9139** |

| 16. | Crude fat content (%) | 3.404 | 3.132 | 37.148 | 35.633 | 0.920 | 3.497 | 70.411 |
| 17. | Ash content (%) | 2.788 | 2.413 | 23.841 | 22.183 | 0.866 | 2.978 | 42.520 |
| 18. | Dry matter content (%) | 16.66 3 | 12.41 4 | 14.345 | 12.382 | 0.745 | 6.265 | 22.015 |
| 19. | Dry matter yield(g) | 58677.79 3 | 55190.31 3 | 46.882 | 45.467 | 0.941 | 469.346 | 90.836 |
| 20. | Green fodder yield per plant (g) | 487601.719 | 458552.406 | 39.776 | 38.573 | 0.940 | 1352.769 | 77.057 |

PV- Phenotypic variance GV- Genotypic variance PCV- Phenotypic coefficient of variation GCV- Genotypic coefficient of variation $h^2$- heritability(broad sense) GA- Genetic advance  GAM- Genetic advance as percent of mean

**Table 2. Genotypic ($r_g$) and Phenotypic ($r_p$) correlation coefficients among twenty characters in Napier grass**

| Trait | Stat | NOL | NON | ILH | LLH | LBH | SGH | LWT | SWT | LSR | CFR | ADF | NDF | CPN | CFT | ASH | DMC | DMY | GFY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NOL | rg | 1.0000 | 0.3586** | 0.3211* | 0.9482** | 0.9635** | 0.8701** | 0.9763** | 0.9813** | 0.9753** | -0.1601 | -0.9178** | -0.9577** | 0.9596** | 0.9743** | 0.9865** | 0.8448** | 0.9546** | 0.9486** |
|  | rp | 1.0000 | 0.2897* | 0.2419 | 0.8960** | 0.8318** | 0.7714** | 0.9277** | 0.9185** | 0.8817** | -0.1212 | -0.8353** | -0.8710** | 0.8815** | 0.8977** | 0.8731** | 0.6671** | 0.8992** | 0.9006** |
| NON | rg |  | 1.0000 | 0.4366** | 0.3849** | 0.3523* | 0.4006** | 0.3515* | 0.3692** | 0.3578* | 0.2685* | -0.3435** | -0.4238** | 0.3994* | 0.3431** | 0.3765** | 0.3915* | 0.3566** | 0.3307* |
|  | rp |  | 1.0000 | 0.3311* | 0.3101* | 0.2415 | 0.2585 | 0.2988* | 0.3031* | 0.3092* | 0.1429 | -0.2582 | -0.3341* | 0.2812* | 0.2481 | 0.2756* | 0.3319 | 0.2755* | 0.2652* |
| ILH | rg |  |  | 1.0000 | 0.3653** | 0.3773** | 0.3905** | 0.3130* | 0.3017* | 0.2801* | -0.1236 | -0.3571** | -0.3249* | 0.3852** | 0.3521* | 0.4101** |  | 0.3566** | 0.4025** |
|  | rp |  |  | 1.0000 | 0.2952* | 0.2804* | 0.2821* | 0.2557 | 0.2320 | 0.2395 | -0.0323 | -0.2933* | -0.2520 | 0.2886* | 0.2721* | 0.2876* |  | 0.2755* | 0.3064 |
| LLH | rg |  |  |  | 1.0000 | 0.9255** | 0.8561** | 0.9850** | 0.9652** | 0.9827** | -0.3037 | -0.9405** | -0.9908** | 0.9849** | 0.9522** | 0.9994** | 0.8106** | 0.9841** | 0.9752** |
|  | rp |  |  |  | 1.0000 | 0.8594** | 0.7600** | 0.9712** | 0.9591** | 0.9130** | -0.1725 | -0.9021** | -0.9567** | 0.9498** | 0.9368** | 0.9584** | 0.7087** | 0.9644** | 0.9583** |
| LBH | rg |  |  |  |  | 1.0000 | 0.8888** | 0.9715** | 0.9695** | 0.9474** | -0.2383 | -0.9872** | -0.9480** | 0.9770** | 0.9958** | 0.9481** | 0.7761** | 0.9640** | 0.9754** |
|  | rp |  |  |  |  | 1.0000 | 0.7397** | 0.8969** | 0.9009** | 0.8466** | -0.0175 | -0.8698** | -0.8450** | 0.8828** | 0.8871** | 0.8603** | 0.6591** | 0.8760** | 0.8796** |
| SGH | rg |  |  |  |  |  | 1.0000 | 0.8935** | 0.8963** | 0.8715** | -0.2357 | -0.8976** | -0.8897** | 0.9377** | 0.9249** | 0.9328** | 0.7219** | 0.9086** | 0.9169** |
|  | rp |  |  |  |  |  | 1.0000 | 0.7749** | 0.7898** | 0.6842** | -0.1228 | -0.7355** | -0.7683** | 0.8132** | 0.7993** | 0.7679** | 0.5003** | 0.7884** | 0.8115** |
| LWT | rg |  |  |  |  |  |  | 1.0000 | 0.9914** | 0.9973** | -0.2232 | -0.9610** | -0.9842** | 0.9891** | 0.9823** | 0.9640** | 0.8255** | 0.9805** | 0.9762** |
|  | rp |  |  |  |  |  |  | 1.0000 | 0.9808** | 0.9676** | -0.1226 | -0.9111** | -0.9413** | 0.9408** | 0.9564** | 0.9453** | 0.7160** | 0.9550** | 0.9538** |
| SWT | rg |  |  |  |  |  |  |  | 1.0000 | 0.9824** | -0.1544 | -0.9562** | -0.9649** | 0.9862** | 0.9829** | 0.9897** | 0.8566** | 0.9640** | 0.9532** |
|  | rp |  |  |  |  |  |  |  | 1.0000 | 0.9168** | -0.0820 | -0.9197** | -0.9262** | 0.9449** | 0.9626** | 0.9406** | 0.7558** | 0.9461** | 0.9373** |
| LSR | rg |  |  |  |  |  |  |  |  | 1.0000 | -0.1707 | -0.9462** | -0.9789** | 0.9649** | 0.9656** | 0.9746** | 0.8225** | 0.9684** | 0.9608** |
|  | rp |  |  |  |  |  |  |  |  | 1.0000 | -0.0750 | -0.8422** | -0.8866** | 0.8669** | 0.8829** | 0.8849** | 0.6952** | 0.8948** | 0.8829** |
| CFR | rg |  |  |  |  |  |  |  |  |  | 1.0000 | 0.2202 | 0.3120* | -0.2625 | -0.2729* | -0.2476 | 0.1131 | -0.3273* | -0.3779** |
|  | rp |  |  |  |  |  |  |  |  |  | 1.0000 | 0.1303 | 0.1158 | -0.1495 | -0.1874 | -0.1200 | 0.1717 | -0.1972 | -0.2627 |
| ADF | rg |  |  |  |  |  |  |  |  |  |  | 1.0000 | 0.9353** | -0.9589** | -0.9645** | -0.9546** | -0.7274** | -0.9358** | -0.9525** |
|  | rp |  |  |  |  |  |  |  |  |  |  | 1.0000 | 0.8612** | -0.9063** | -0.9192** | -0.8967** | -0.6423** | -0.8908** | -0.9019** |
| NDF | rg |  |  |  |  |  |  |  |  |  |  |  | 1.0000 | -0.9912** | -0.9601** | -0.9902** | -0.8385** | -0.0977** | -0.9916** |
|  | rp |  |  |  |  |  |  |  |  |  |  |  | 1.0000 | -0.9262** | -0.9025** | -0.9120** | -0.7009** | -0.9498** | -0.9378** |
| CPN | rg |  |  |  |  |  |  |  |  |  |  |  |  | 1.0000 | 0.9930** | 0.9905** | 0.7941** | 0.9928** | 0.9975** |
|  | rp |  |  |  |  |  |  |  |  |  |  |  |  | 1.0000 | 0.9453** | 0.9590** | 0.6799** | 0.9481** | 0.9566** |
| CFT | rg |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.0000 | 0.9755** | 0.7627** | 0.9652** | 0.9820** |
|  | rp |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.0000 | 0.9357** | 0.6396** | 0.9244** | 0.9515** |
| ASH | rg |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.0000 | 0.8127** | 0.9874** | 0.9843** |
|  | rp |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.0000 | 0.6857** | 0.9306** | 0.9342** |
| DMC | rg |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.0000 | 0.8288** | 0.7264** |
|  | rp |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.0000 | 0.7642** | 0.6122** |
| DMY | rg |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.0000 | 0.9828** |
|  | rp |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.0000 | 0.9719** |

PHT – Plant height (cm), NOT – Number of tillers per plant, NOL – Number of leaves per tiller, NON – Number of nodes on main tiller, ILH – Internodal length (cm), LLH – Leaf length (cm), LBH- Leaf breath (cm), SGH – Stem girth (cm), LWT – Leaf weight (g), SWT – Stem weight (g), LSR – Leaf to stem ratio, CFR – Crude fibre (%), ADF – Acid detergent fibre (%), NDF- Neutral detergent fibre (%), CPN – Crude protein (%), CFT – Crude fat (%), ASH – Ash (%), DMC – Dry matter content (%), DMY- Dry matter yield (g), GFY – Green fodder yield (g)

### Table 3. Path coefficient analysis of different characters with green fodder yield per plant in Napier grass

| Traits | PHT | NOT | NOL | NON | ILH | LLH | LBH | SGH | LWT | SWT | LSR | CFR | ADF | NDF | CPN | CFT | ASH | DMC | DMY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PHT | **-0.0270** | -0.0267 | -0.0262 | -0.0096 | -0.0096 | -0.0272 | -0.0268 | -0.0238 | -0.0273 | -0.0271 | -0.0269 | 0.0066 | 0.0266 | 0.0269 | -0.0272 | -0.0271 | -0.0278 | -0.0228 | -0.0270 |
| NOT | 0.1924 | **0.1948** | 0.1843 | 0.0802 | 0.0689 | 0.1907 | 0.1775 | 0.1788 | 0.1882 | 0.1867 | 0.1875 | -0.0484 | -0.1768 | -0.1903 | 0.1933 | 0.1835 | 0.1979 | 0.1645 | 0.1894 |
| NOL | 0.0086 | 0.0084 | **0.0088** | 0.0032 | 0.0028 | 0.0084 | 0.0085 | 0.0077 | 0.0086 | 0.0087 | 0.0086 | -0.0014 | -0.0081 | -0.0085 | 0.0085 | 0.0086 | 0.0087 | 0.0075 | 0.0084 |
| NON | -0.0083 | -0.0095 | -0.0083 | **-0.0231** | -0.0101 | -0.0089 | -0.0081 | -0.0093 | -0.0081 | -0.0085 | -0.0083 | -0.0062 | 0.0079 | 0.0098 | -0.0092 | -0.0079 | -0.0079 | -0.0110 | -0.0091 |
| ILH | -0.0010 | -0.0010 | -0.0009 | -0.0012 | **-0.0028** | -0.0010 | -0.0011 | -0.0011 | -0.0009 | -0.0008 | -0.0008 | 0.0003 | 0.0010 | 0.0009 | -0.0011 | -0.0010 | -0.0011 | -0.0003 | -0.0010 |
| LLH | -0.3447 | -0.3354 | -0.3249 | -0.1319 | -0.1251 | **-0.3426** | -0.3171 | -0.2933 | -0.3375 | -0.3307 | -0.3367 | 0.1041 | 0.3223 | 0.3395 | -0.3374 | -0.3263 | -0.3424 | -0.2777 | -0.3372 |
| LBH | 0.0738 | 0.0678 | 0.0717 | 0.0262 | 0.0281 | 0.0689 | **0.0744** | 0.0661 | 0.0723 | 0.0721 | 0.0705 | -0.0177 | -0.0735 | -0.0705 | 0.0727 | 0.0741 | 0.0706 | 0.0578 | 0.0717 |
| SGH | -0.1440 | -0.1500 | -0.1422 | -0.0655 | -0.0638 | -0.1399 | -0.1453 | **-0.1635** | -0.1461 | -0.1465 | -0.1425 | 0.0385 | 0.1467 | 0.1454 | -0.1533 | -0.1512 | -0.1525 | -0.1180 | -0.1485 |
| LWT | -0.8837 | -0.8436 | -0.8526 | -0.3069 | -0.2733 | -0.8602 | -0.8484 | -0.7803 | **-0.8733** | -0.8658 | -0.8709 | 0.1949 | 0.8392 | 0.8595 | -0.8638 | -0.8578 | -0.8768 | -0.7209 | -0.8562 |
| SWT | 0.6240 | 0.5950 | 0.6094 | 0.2293 | 0.1873 | 0.5994 | 0.6021 | 0.5566 | 0.6157 | **0.6210** | 0.6101 | -0.0959 | -0.5938 | -0.5992 | 0.6124 | 0.6104 | 0.6146 | 0.5319 | 0.5986 |
| LSR | 0.3650 | 0.3526 | 0.3573 | 0.1311 | 0.1026 | 0.3600 | 0.3471 | 0.3193 | 0.3654 | 0.3599 | **0.3664** | -0.0625 | -0.3467 | -0.3586 | 0.3535 | 0.3537 | 0.3680 | 0.3013 | 0.3548 |
| CFIB | -0.0140 | -0.0143 | -0.0092 | 0.0154 | -0.0071 | -0.0175 | -0.0137 | -0.0136 | -0.0128 | -0.0089 | -0.0098 | **0.0575** | 0.0127 | 0.0180 | -0.0151 | -0.0157 | -0.0142 | 0.0065 | -0.0188 |
| ADF | 0.0036 | 0.0033 | 0.0034 | 0.0013 | 0.0013 | 0.0034 | 0.0036 | 0.0033 | 0.0035 | 0.0035 | 0.0035 | -0.0008 | **-0.0037** | -0.0034 | 0.0035 | 0.0035 | 0.0035 | 0.0027 | 0.0034 |
| NDF | -0.0289 | -0.0283 | -0.0278 | -0.0123 | -0.0094 | -0.0287 | -0.0275 | -0.0258 | -0.0285 | -0.0280 | -0.0284 | 0.0090 | 0.0271 | **0.0290** | -0.0287 | -0.0278 | -0.0287 | -0.0243 | -0.0292 |
| CPN | 0.1859 | 0.1831 | 0.1771 | 0.0737 | 0.0711 | 0.1818 | 0.1803 | 0.1731 | 0.1826 | 0.1820 | 0.1781 | -0.0485 | -0.1770 | -0.1829 | **0.1846** | 0.1833 | 0.1828 | 0.1466 | 0.1832 |
| CFT | -0.0764 | -0.0718 | -0.0743 | -0.0262 | -0.0268 | -0.0726 | -0.0759 | -0.0705 | -0.0749 | -0.0749 | -0.0736 | 0.0208 | 0.0735 | 0.0732 | -0.0757 | **-0.0762** | -0.0744 | -0.0581 | -0.0736 |
| ASH | 0.0759 | 0.0750 | 0.0729 | 0.0278 | 0.0303 | 0.0738 | 0.0700 | 0.0689 | 0.0742 | 0.0731 | 0.0742 | -0.0183 | -0.0705 | -0.0731 | 0.0732 | 0.0721 | **0.0739** | 0.0600 | 0.0729 |
| DMC | -0.4005 | -0.4007 | -0.4008 | -0.2266 | -0.0589 | -0.3846 | -0.3682 | -0.3425 | -0.3917 | -0.4064 | -0.3902 | -0.0537 | 0.3451 | 0.3978 | -0.3768 | -0.3619 | -0.3856 | **-0.4745** | -0.3932 |
| DMY | 1.3939 | 1.3551 | 1.3309 | 0.5459 | 0.4971 | 1.3720 | 1.3440 | 1.2668 | 1.3669 | 1.3439 | 1.3501 | -0.4563 | -1.3047 | -1.4049 | 1.3841 | 1.3457 | 1.3766 | 1.1554 | **1.3941** |
| GFY | 0.9945** | 0.9538** | 0.9486** | 0.3307* | 0.4025** | 0.9752** | 0.9754** | 0.9169** | 0.9762** | 0.9532** | 0.9608** | -0.3779** | -0.9525 ** | -0.9916** | 0.9975** | 0.9820** | 0.9843** | 0.7264** | 0.9828** |

Residual effect of path analysis : 0.0311

Table 4.Clustering pattern of 56 Napier grass germplasm accessions by Tocher·s method

| Cluster | Number of genotypes | Name of genotypes |
|---|---|---|
| I | 26 | FD 457,FD 473, FD 463, FD 454, FD 479, FD 485,FD 480, FD 430,FD 462, FD 453, FD 440, FD 447,FD 452, FD 470, FD 458, FD 461, FD 450, FD 451, FD 433, FD 436, FD 459, FD 439, FD 474, FD 426, FD 460, FD 478 |
| II | 16 | FD 441, FD 442, FD 483, FD 468, FD 472, FD 465, FD 455, FD 432, FD 449, FD 481, FD 443, FD 455/1, FD 477, FD 438, FD 456, FD 434 |
| III | 7 | FD 471, FD 476, FD 466, FD 448,FD FD 437, FD 482, FD 444 |
| IV | 1 | FD 435 |
| V | 1 | FD 464 |
| VI | 1 | FD 431 |
| VII | 1 | FD 467 |
| VIII | 1 | FD 453/1 |
| IX | 1 | FD 445 |
| X | 1 | FD 446 |

Table 5.Average intra (in bold) and inter cluster D² distances for Napier grass germplasm accessions

| Cluster | I | II | III | IV | V | VI | VII | VIII | IX | X |
|---|---|---|---|---|---|---|---|---|---|---|
| I | 7.94 | 13.32 | 13.13 | 15.03 | 14.15 | 10.99 | 21.02 | 15.99 | 14.00 | 18.74 |
| II | | 8.65 | 20.33 | 11.56 | 11.42 | 15.96 | 26.75 | 11.62 | 19.23 | 17.92 |
| III | | | 8.07 | 20.90 | 18.66 | 14.69 | 12.74 | 23.09 | 19.26 | 24.15 |
| IV | | | | 0.00 | 10.59 | 16.30 | 28.96 | 15.34 | 19.67 | 22.40 |
| V | | | | | 0.00 | 12.52 | 25.08 | 14.53 | 20.60 | 21.85 |
| VI | | | | | | 0.00 | 22.13 | 18.61 | 17.32 | 21.01 |
| VII | | | | | | | 0.00 | 29.76 | 27.54 | 28.19 |
| VIII | | | | | | | | 0.00 | 20.23 | 17.73 |
| IX | | | | | | | | | 0.00 | 18.91 |
| X | | | | | | | | | | 0.00 |

Table 6.Cluster mean for 20 quantitative and qualitative traits in 56 Napier grass germplasm accessions

| Clusters | PHT | NOT | NOL | NON | ILH | LLH | LBH | SGH | LWT | SWT | LSR | CFR | ADF | NDF | CPN | CFT | ASH | DMC | DMY | GFY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | 212.77 | 15.57 | 17.77 | 8.11 | 9.55 | 75.41 | 2.91 | 5.04 | 960.71 | 1570.50 | 0.38 | 30.32 | 42.52 | 61.26 | 8.02 | 4.37 | 6.45 | 28.03 | 409.10 | 1428.92 |
| II | 290.44 | 19.96 | 22.36 | 9.13 | 10.39 | 100.18 | 4.04 | 6.38 | 1345.03 | 1887.88 | 0.42 | 27.81 | 35.45 | 52.22 | 9.79 | 6.64 | 8.68 | 31.58 | 778.19 | 2467.63 |
| III | 157.43 | 12.41 | 13.99 | 6.69 | 9.35 | 59.79 | 1.91 | 4.16 | 664.64 | 1219.00 | 0.35 | 28.01 | 49.51 | 66.14 | 6.76 | 2.25 | 4.74 | 23.16 | 216.71 | 930.50 |
| IV | 279.77 | 20.90 | 22.90 | 7.50 | 7.94 | 99.10 | 3.65 | 5.48 | 1309.00 | 1857.50 | 0.41 | 25.88 | 45.25 | 51.97 | 9.42 | 6.07 | 8.33 | 34.40 | 800.50 | 2335.50 |
| V | 302.49 | 20.50 | 23.20 | 5.50 | 7.80 | 102.96 | 3.86 | 6.56 | 1375.00 | 1923.50 | 0.41 | 25.70 | 33.47 | 51.15 | 9.75 | 6.50 | 8.54 | 30.38 | 760.50 | 2503.50 |
| VI | 247.37 | 12.50 | 17.90 | 6.00 | 8.92 | 75.56 | 2.77 | 4.25 | 1066.50 | 1637.50 | 0.40 | 29.10 | 41.53 | 62.17 | 7.07 | 4.63 | 6.00 | 28.58 | 380.00 | 1327.00 |
| VII | 153.66 | 10.90 | 10.90 | 7.20 | 8.86 | 56.30 | 2.05 | 3.14 | 527.00 | 1056.00 | 0.33 | 26.25 | 46.10 | 67.29 | 6.03 | 1.70 | 4.13 | 20.18 | 178.00 | 886.50 |
| VIII | 330.23 | 22.20 | 25.70 | 7.00 | 13.35 | 110.16 | 4.86 | 7.47 | 1546.00 | 2050.00 | 0.43 | 27.50 | 31.29 | 49.60 | 11.09 | 8.81 | 10.49 | 24.65 | 805.50 | 3276.00 |
| IX | 227.42 | 17.40 | 21.70 | 7.10 | 7.76 | 69.54 | 3.70 | 7.62 | 1053.00 | 1684.50 | 0.38 | 29.60 | 40.63 | 61.58 | 8.52 | 5.80 | 7.00 | 31.42 | 522.00 | 1659.00 |
| X | 310.56 | 17.20 | 25.70 | 8.30 | 9.56 | 96.04 | 5.95 | 7.45 | 1494.00 | 2042.50 | 0.43 | 26.40 | 31.90 | 49.30 | 10.45 | 8.98 | 7.88 | 27.77 | 883.00 | 3178.00 |

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

| S. No. | Traits | Number of times ranked first | Contribution (%) |
|---|---|---|---|
| 1. | Plant height(cm) | 18 | 1.17 |
| 2. | No of tillers per plant | 197 | 12.79 |
| 3. | No of leaves per tiller | 6 | 0.39 |
| 4. | No of nodes on main tiller | 290 | 18.83 |
| 5. | Internodal length(cm) | 50 | 3.25 |
| 6. | Leaf length(cm) | 312 | 20.26 |
| 7. | Leaf breath(cm) | 16 | 1.04 |
| 8. | Stem girth (cm) | 37 | 2.40 |
| 9. | Leaf weight(g) | 37 | 2.40 |
| 10. | Stem weight(g) | 183 | 11.88 |
| 11. | Leaf to stem ratio | 18 | 1.17 |
| 12. | Crude fibre content | 28 | 1.82 |
| 13. | Acid detergent fibre content (%) | 73 | 4.74 |
| 14. | Neutral detergent fibre content (%) | 8 | 0.52 |
| 15. | Crude protein content (%) | 6 | 0.39 |
| 16. | Crude fat content (%) | 122 | 7.92 |
| 17. | Ash content (%) | 62 | 4.03 |
| 18. | Dry matter content (%) | 16 | 1.04 |
| 19. | Dry matter yield(g) | 26 | 1.69 |
| 20. | Green fodder yield(g) | 35 | 2.27 |

Table 8. Per se performance for superior traits in napier grass germplasm accessions

| S.No | Genotypes identified | Per se performance for superior traits | | | | | Cluster occupied |
|------|----------------------|----------------------------------|-----|-----|-----|-----|------------------|
| | | Number of tillers per plant | Number of leaves per plant | Dry matter yield (g) | Crude protein (%) | Green fodder yield (g) | |
| 1. | FD 453/1 | 22.20 | 25.70 | 805.26 | 11.08 | 3275.56 | VIII |
| 2. | FD 446 | 17.20 | 25.70 | 883.08 | 10.45 | 3177.90 | X |
| 3. | FD 435 | 20.90 | 22.90 | 800.27 | 9.42 | 2335.48 | IV |
| 4. | FD 445 | 17.40 | 21.70 | 521.74 | 8.52 | 1659.09 | IX |
| 5. | FD 467 | 10.90 | 10.90 | 177.99 | 6.03 | 886.49 | VII |