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Presenter Information

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Genetic variability in Napier grass (*Pennisetum purpureum*) germplasm conserved at ICRISAT genebank

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Introduction

Napier grass or elephant grass [*Pennisetum purpureum* Schum.] is an important forage crop in tropical and sub-tropical regions valued for its high biomass production, perennial nature, pest resistance, and forage quality. It is a unique grass species with high dry matter, which sustains its utilization for direct animal grazing and as a feed complement during drought periods. It has additional advantages like preventing soil erosion and improving soil fertility. Napier grass also has potential for bioenergy production and conversion to alcohol or methane due to its rapid growth and degradable biomass characteristics. The present study was planned to assess the genetic variability among *purpureum* germplasm conserved at ICRISAT genebank, Patancheru for their potential utilization in development of forage varieties and bajra-napier hybrids.

Materials and Methods

The present study comprised of 48 accessions of *purpureum* assembled from six different countries. They were tested in a replicated trial using alpha design at ICRISAT, Patancheru. Data was recorded for quantitative traits like green forage yield (t/ha), leaf: stem ratio, dry matter content (%), dry matter yield (t/ha), plant height (cm), no. of tillers/plant, no. of leaves/plant, leaf length (cm), leaf width (mm), stem thickness (mm), and eight forage quality traits *viz.*, DM, Ash, NDM, NDFDM, ADFDM, ADLDM, ME, IVOMD. Data on qualitative traits like leaf hairiness, stem hairiness, tillering attitude, and green forage yield potential on scale basis were also recorded. Data on quantitative traits was analyzed by following Residual Maximum Likelihood method (REML; Patterson and Thompson, 1971); variance components due to genotype (σ^2_g), replicates, replicates x blocks, and its standard errors were estimated. Best linear unbiased predictors (BLUPs) for each genotype for all the traits were estimated. Range, mean, and genetic parameters like heritability in broad sense (h^2_{bs}), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), genetic advance (GA), and genetic advance as per cent mean (GAM) were estimated. Principal component analysis (PCA) was performed using GENSTAT 14th ed. Cluster analysis was performed using scores of principal components (PCs). The Shannon-Weaver diversity index (H') (Shannon and Weaver, 1949) was computed and used to measure and compare phenotypic diversity for each trait in *purpureum* germplasm.

Results and Discussion

Significant variation for forage yield and its eight component traits was observed among the *purpureum* germplasm, except dry matter content. However, among eight forage quality traits significant variation was observed only for ADFDM showing narrow variability for majority of the forage quality traits. Majority of the forage yield and component traits showed higher heritability (h^2_{bs}), PCV, GCV, and GAM, except dry matter content (%) (Table 1). However, forage quality traits showed low to moderate heritability, lower PCV, GCV, and GAM. Green forage yield showed significant positive correlation with dry matter yield, leaf length, leaf width, stem thickness, plant height, dry matter content, and ADFDM, but significant negative correlation with leaf: stem ratio (Table 2). ADFDM showed significant positive correlation with traits like DM, NDFDM, green forage yield, and dry matter yield, but significant negative correlation with ash content and leaf: stem ratio. Principal component analysis revealed seven PCs explaining almost 90% of the variation in the *purpureum* germplasm. The biplot was drawn using two major PCs explaining almost 55% of the variation which revealed interrelations among the traits. Cluster analysis grouped 48 accessions of *purpureum* into four major clusters based on dissimilarity. Grouping of the accessions was irrespective of the source country. However, Lowe *et al.* (2003) could differentiate 48 accessions of *purpureum* germplasm into five sub-groups based on region (East Africa, Southern Africa, USA1, USA2 and Miscellaneous) using RAPD markers. Similarly, Sousa Azevedo *et al.* (2012)

differentiated 107 Napier grass accessions from Embrapa-BAGCE in to three major clusters comprising of wild accessions, pearl millet x napier hybrids and purpleum germplasm, respectively using selected microsatellite markers. The Shannon-Weaver diversity index (H') estimated for qualitative (4) and quantitative (18) traits revealed higher phenotypic diversity in quantitative (0.554) compared to qualitative traits (0.407). Wide phenotypic diversity was observed for majority of the quantitative traits including IVOMD (0.619), ash (0.612), leaf length (0.611), stem thickness (0.604), and ME (0.600), while green fodder potential (0.607) among the qualitative traits. Similarly, Wanjala *et al.* (2013) while assessing genetic diversity among 281 accessions of purpleum from Eastern Africa and ILRI germplasm observed moderate genetic differentiation among the germplasm using AFLP markers. Genetic diversity across all accessions was found to be fairly high (Shannon's diversity index 0.306) and thus the collection probably represents a wide genetic base for this species. Among 48 accessions, seven accessions recorded significantly higher, while 14 accessions recorded numerically superior green forage yield compared to control Pusa giant napier. Identified high yielding purpleum germplasm with better leaf: stem ratio need to be further evaluated for their potential as a forage variety or in hybridization programme to develop superior bajra-napier hybrids.

Table 1. Genetic components for forage yield, its components and forage quality traits

| Sl. | Trait | Range | Mean | H _{bs} (%) | GCV (%) | PCV (%) | GA | GAM (%) |
|-----|---------------------------|----------------|--------|---------------------|---------|---------|-------|---------|
| 1 | Green forage yield (t/ha) | 7.64 - 61.65 | 23.51 | 85.56 | 55.18 | 59.66 | 24.72 | 105.15 |
| 2 | Leaf stem ratio | 0.61 - 2.11 | 1.05 | 87.20 | 37.25 | 39.95 | 0.75 | 71.55 |
| 3 | Dry matter (%) | 31.19 - 33.93 | 32.43 | 14.68 | 5.71 | 14.91 | 1.46 | 4.51 |
| 4 | Dry matter yield (t/ha) | 2.56 - 22.69 | 7.91 | 84.46 | 63.08 | 68.64 | 9.45 | 119.42 |
| 5 | Plant height (cm) | 89.75 - 213.42 | 144.96 | 87.72 | 21.61 | 23.08 | 60.45 | 41.70 |
| 6 | Tillers/plant | 6.39 - 16.22 | 9.29 | 60.40 | 27.15 | 34.93 | 4.04 | 43.46 |
| 7 | No. of leaves /plant | 69.63 - 201.35 | 112.08 | 75.70 | 33.22 | 38.18 | 66.74 | 59.54 |
| 8 | Leaf length (cm) | 29.62 - 87.55 | 61.22 | 91.78 | 21.61 | 22.56 | 26.11 | 42.65 |
| 9 | Leaf width (mm) | 8.27 - 29.68 | 18.35 | 93.52 | 30.77 | 31.82 | 11.25 | 61.31 |
| 10 | Stem thickness (mm) | 4.42 - 20.16 | 11.83 | 92.58 | 30.89 | 32.10 | 7.24 | 61.22 |
| 11 | DM | 87.82 - 89.41 | 88.91 | 34.19 | 0.71 | 1.21 | 0.76 | 0.85 |
| 12 | ASH | 16.01 - 17.80 | 16.86 | 25.32 | 4.40 | 8.75 | 0.77 | 4.56 |
| 13 | NDM | 1.11 - 1.25 | 1.15 | 28.19 | 3.89 | 7.78 | 0.05 | 4.01 |
| 14 | NDFDM | 64.74 - 67.62 | 66.41 | 40.47 | 1.53 | 2.41 | 1.33 | 2.01 |
| 15 | ADFDM | 28.98 - 36.28 | 34.74 | 47.19 | 5.51 | 8.02 | 2.71 | 7.79 |
| 16 | ADLDM | 3.95 - 4.37 | 4.22 | 26.25 | 3.43 | 6.66 | 0.15 | 3.65 |
| 17 | ME | 6.28 - 6.73 | 6.57 | 24.37 | 2.64 | 5.32 | 0.18 | 2.69 |
| 18 | IVOMD | 45.15 - 48.13 | 47.15 | 23.21 | 2.60 | 5.39 | 1.22 | 2.58 |

Table 2. Correlation among forage yield, its components and forage quality traits

| Trait | TLP | LFN | LFL | LFW | STT | GFY | LSR | DMC | DMY | DM | ASH | NDM | NDFDM | ADFDM | ADLDM | ME | IVOMD |
|-------|-------|--------------|---------------|---------------|---------------|--------------|---------------|---------------|---------------|--------|--------|---------------|---------------|---------------|---------------|---------------|---------------|
| PHT | 0.117 | 0.355 | 0.032 | -0.005 | -0.184 | 0.409 | -0.305 | 0.142 | 0.398 | 0.244 | -0.053 | -0.348 | 0.322 | 0.358 | 0.277 | 0.105 | 0.090 |
| TLP | | 0.852 | -0.308 | -0.349 | -0.357 | -0.116 | 0.271 | -0.161 | -0.137 | 0.159 | -0.076 | -0.333 | -0.076 | -0.091 | 0.107 | 0.119 | 0.065 |
| LFN | | | -0.460 | -0.526 | -0.553 | -0.091 | 0.284 | -0.217 | -0.114 | 0.145 | -0.054 | -0.407 | 0.090 | -0.022 | 0.203 | 0.040 | -0.014 |
| LFL | | | | 0.853 | 0.840 | 0.688 | -0.643 | 0.317 | 0.677 | 0.161 | 0.030 | 0.153 | -0.143 | 0.133 | -0.151 | 0.090 | 0.120 |
| LFW | | | | | 0.827 | 0.546 | -0.614 | 0.426 | 0.568 | 0.072 | -0.035 | 0.193 | -0.015 | 0.136 | -0.121 | 0.074 | 0.106 |
| STT | | | | | | 0.457 | -0.515 | 0.202 | 0.444 | 0.152 | -0.053 | 0.209 | -0.136 | 0.127 | -0.129 | 0.197 | 0.212 |
| GFY | | | | | | | -0.608 | 0.343 | 0.982 | 0.240 | 0.039 | -0.128 | 0.173 | 0.343 | 0.122 | 0.178 | 0.194 |
| LSR | | | | | | | | -0.470 | -0.607 | -0.130 | -0.039 | 0.029 | -0.207 | -0.291 | -0.078 | -0.035 | -0.058 |
| DMC | | | | | | | | | 0.481 | -0.262 | 0.203 | 0.012 | 0.012 | -0.075 | -0.193 | -0.141 | -0.123 |
| DMY | | | | | | | | | | 0.162 | 0.074 | -0.089 | 0.163 | 0.291 | 0.074 | 0.137 | 0.158 |
| DM | | | | | | | | | | | -0.277 | 0.046 | -0.048 | 0.759 | 0.186 | 0.857 | 0.873 |
| ASH | | | | | | | | | | | | 0.132 | -0.281 | -0.358 | -0.208 | -0.422 | -0.349 |
| NDM | | | | | | | | | | | | | -0.542 | -0.173 | -0.554 | 0.052 | 0.133 |
| NDFDM | | | | | | | | | | | | | | 0.493 | 0.775 | -0.044 | -0.059 |
| ADFDM | | | | | | | | | | | | | | | 0.531 | 0.688 | 0.711 |
| ADLDM | | | | | | | | | | | | | | | | 0.144 | 0.132 |
| ME | | | | | | | | | | | | | | | | | 0.990 |

In bold, significant values at the level of significance alpha=0.050 (two-tailed test)

PHT- Plant height (cm); TLP- Tillers/plant; LFN- No.of leaves/plant; LFL- Leaf length; LFW- Leaf width; STT- Stem thickness; GFY- Green forage yield (t/ha); LSR- Leaf:Stem ratio; DMC- Dry matter content; DMY- Dry matter yield (t/ha)

Conclusion

Enormous genetic diversity was observed among purpleum germplasm conserved at ICRISAT Genebank. The identified high yielding purpleum germplasm need to be further evaluated for their potential as a forage variety and also involve them in hybridization programme towards developing superior bajra-napier hybrids.

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