# Genetic diversity in Napier grass (*Cenchrus purpureus*) collections and progeny plants: potential-duplicates and unique genotypes

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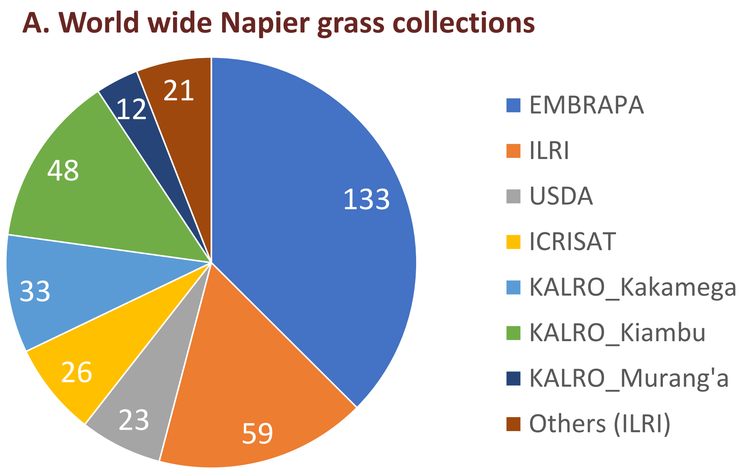
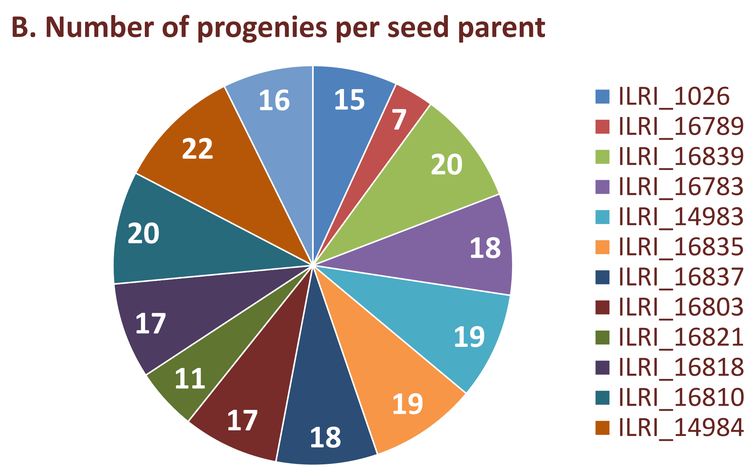
## I. Introduction

Napier grass (*Cenchrus purpureus* syn. *Pennisetum purpureum*) is a perennial grass widely cultivated as forage in tropical and subtropical dairy systems. Napier grass is known for its high biomass and high dry matter production that can reach up to 78 tons of dry matter/ha/year. Its high biomass production also makes it one of the potential grasses to produce biofuels, such as alcohol, ethanol, butanol, and methane. Although Napier grass is strictly out crossing and self-incompatible, attributes that ensure its high genetic variation, it has a limited global diversity mainly due to its vegetative propagation. In this study, we analyzed and compared the among and within genetic diversity in worldwide collections and progeny plants raised from seeds with the aim of enhancing the genetic diversity in the Napier grass collections maintained in the ILRI forage genebank and generating information useful for designing breeding strategies for the species.

## II. Napier grass populations used in the study

**Figure 1**. A total of 574 Napier grass plants composed from worldwide collections (A) and progenies raised from 13 ILRI accessions (B) were used in the genetic diversity study. The number of accessions per collection ranged from 12 in KALRO_Murang'a to 133 in EMBRAPA (A); while the number of progeny plants per accession ranged from 7 in ILRI_16789 to 22 in ILRI_14984.




## III. Genome-wide high-density SNP and SilicoDArT markers generated on the population

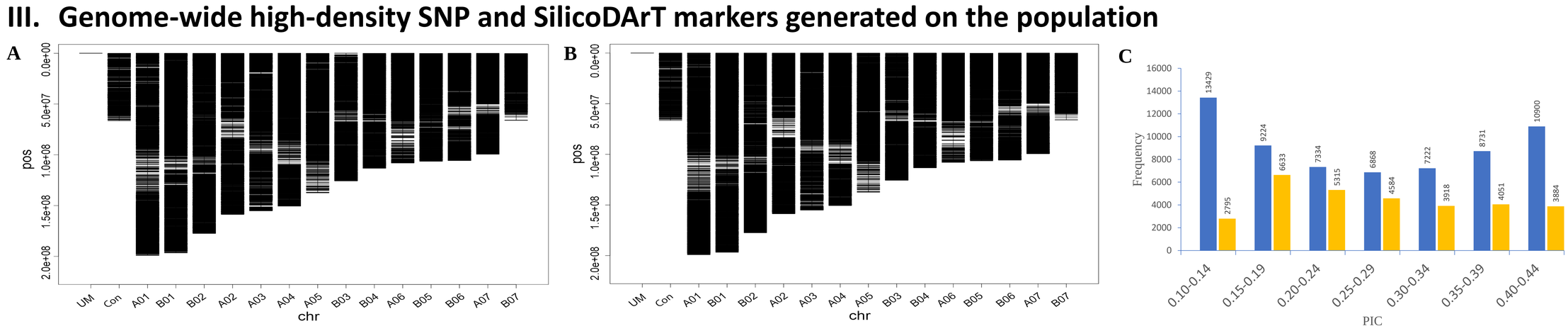



**Figure 2**. The Napier grass collections and progeny plants genotyped by the DArTseq platform and genome-wide high-density markers were generated. The distribution of SNP (A) and SilicoDArT (B) markers across the fourteen chromosomes of the Napier grass genome is shown. The markers that were not mapped are indicated by a "UM", and those markers that were mapped onto different contigs are indicated by an "Con". In (C) the distribution of polymorphic information content (PIC) values for the SilicoDArT (orange) and SNP (blue) markers is shown

## IV. Genetic diversity among the collections and progenies

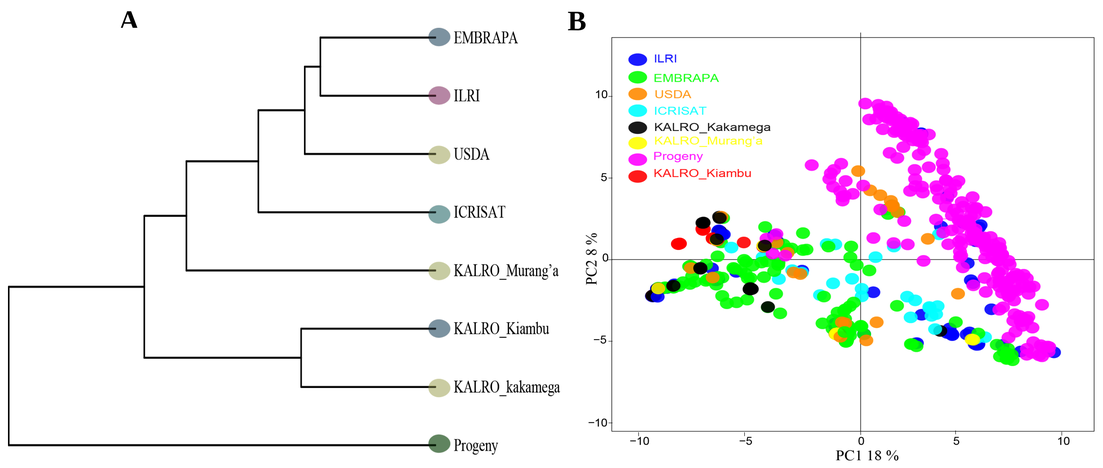



**Figure 3**. The collections and progeny plants were subjected to genetic diversity analysis using a subset of the genome-wide markers. UPGMA dendrogram (A) and PCA plot (B) depicting the genetic relationships among the collections and progeny plants. The progeny plants clustered separately from the other collections and were scattered across the PCA plot, suggesting the presence of a unique genetic makeup in progeny plants.

## V. Genetic diversity within the collections and progenies

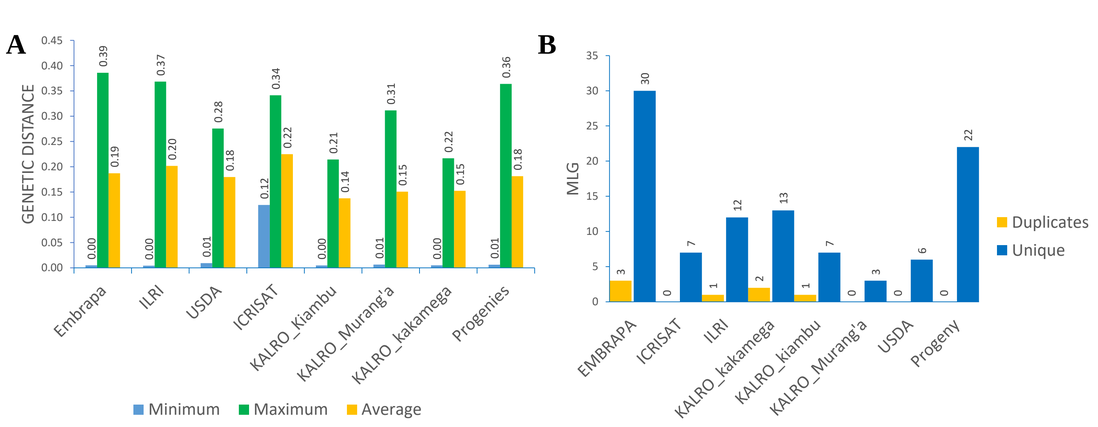



**Figure 4.** In (A), the range and average of genetic diversity within each collection and progenies are shown. In (B), the number of unique genotypes (blue, at a threshold of 0.2 Nei's pairwise genetic distance) and potential duplicates (orange, at a threshold of 0.005 Nei's pairwise genetic distance), detected by using multilocus genotype (MLG) analysis, are shown. A large number of unique genotypes were identified in EMBRAPA collection, followed by progenies.

## VI. Conclusions

- The genetic diversity analysis revealed the existence of a substantial amount of variation within the collections and progeny plants and identified some unique genotypes and potential duplicates.
- The progeny plants clustered separately from the collection, suggesting crossing and analyzing the progenies as a potential breeding strategy to increase the genetic diversity in Napier grass.
- The results of this study provide useful information for the Napier grass breeding strategy and enhancement of genetic diversity in the ILRI collection.

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**Abbreviations:**
EMBRAPA = Brazilian Agricultural Research Corporation; ICRISAT = International Crop Research Institute for the Semi Arid Tropics; ILRI = International Livestock Research Institute; USDA = United States Department of Agriculture; KALRO = Kenya Agricultural & Livestock Research Organization



## VII. References

- Yan et al. 2020. doi.org/10.1111/1755-0998.13271
- Muktar et al., 2019. doi.org/10.1038/s41598-019-43406-0
- Negawo et al., 2017. doi.org/10.3390/agronomy7020028

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