

Genetic diversity in Napier grass (*Cenchrus purpureus*) collections as revealed by genotyping by sequencing method of the DArTseq platform



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I. Introduction

Napier grass, also called elephant grass, is an important tropical forage grass primarily used as cut-and-carry feed and of growing potential as an energy crop. The ILRI genebank holds a diverse set of Napier grass accessions and a collection from the Brazilian Agricultural Research Corporation (EMBRAPA). One-hundred-five accessions were subjected to genotyping by sequencing (GBS) using DArTseq, which generated high-density genome-wide SilicoDArT and SNP markers. Diversity analysis showed the existence of a substantial amount of variation in the collections and a few accessions that represent the diversity were selected with the objective of distributing subsets of a manageable size for further evaluation. LD (linkage disequilibrium) analyses revealed a fast LD-decay in the overall population and showed variation in LD between the ILRI compared to the EMBRAPA collection.

II. Genome-wide high density SilicoDArT and SNP markers

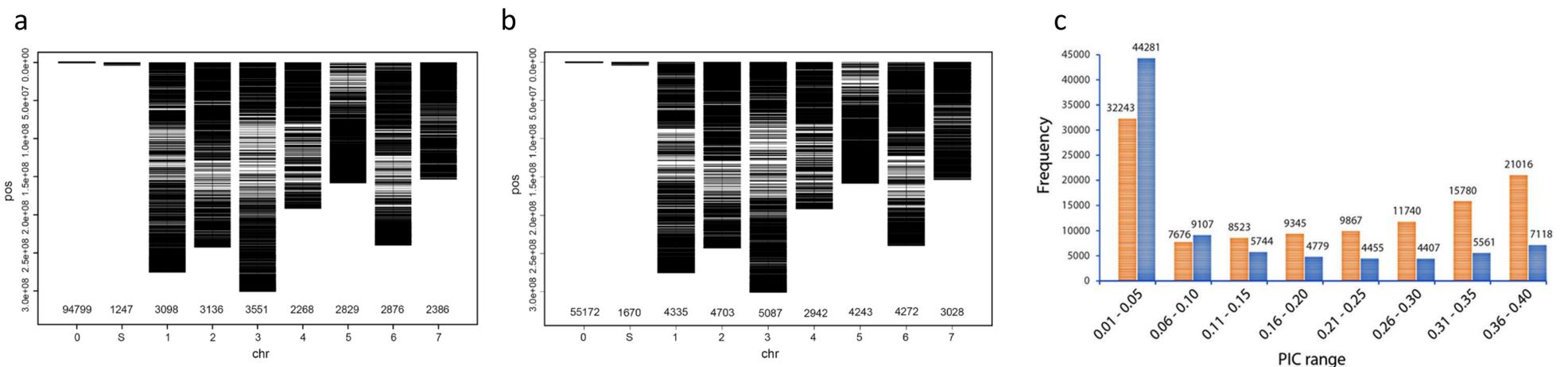


Figure 1. Genome-wide distribution of SilicoDArT (a) and SNP (b) markers across the seven chromosomes of the pearl millet genome. The markers that were not mapped are indicated by a 0, and those markers that were mapped onto different scaffolds are indicated by an S. The number of markers mapped per chromosome is shown on the x-axis. In (c) the distribution of polymorphic information content (PIC) values for the SilicoDArT (orange) and SNP (blue) markers is shown

III. Diversity in the Napier grass populations

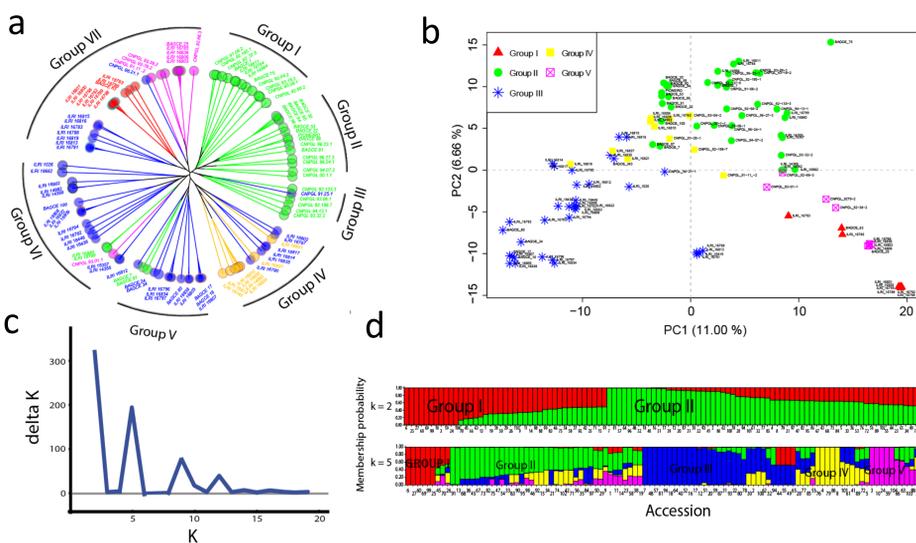


Figure 2. Clusters of the Napier grass accessions (a) UPGMA tree showing seven groups; (b) PCA plot for PC1 and PC2; (c) The delta K suggesting two major groups and up to 5 subgroups; (d) Bar plots based on the admixture model in STRUCTURE, for K = 2 and K = 5. The colors in (a) and (b) are according to the STRUCTURE analysis with k = 5

VI. Conclusions and Outlook

- GBS using the DArTseq platform generated high-density and genome-wide distributed dominant and co-dominant markers, which are suitable for marker-trait association analysis
- The diversity analysis revealed the presence of considerable variation in the collections and showed the suitability of the population for marker-trait association studies
- Subsets of Napier grass accessions that represent the genetic and phenotypic diversity held in the collections have been identified. These subsets are of a manageable size and act as a reference set for distribution and evaluation in different agro-ecologies and production systems
- A fast rate of LD-decay was observed across the Napier grass A' genome and the LD decay was slower in the ILRI when compared to the EMBRAPA collection, suggesting the materials from ILRI contain long haplotype blocks, in which a large amount of variation may be stacked which could potentially be released by crossing

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IV. Representative subsets of the collection

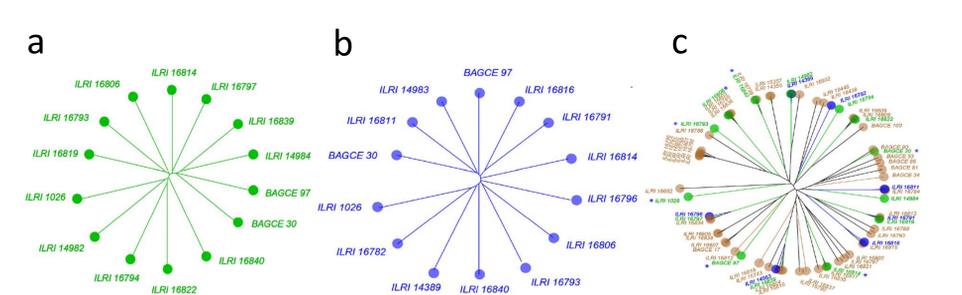


Figure 3. UPGMA tree for the subsets under optimal-water (a) and water-deficit (b) conditions. In (c), the positions of the subsets in the whole collection is shown by different colours. The subsets were selected using selected genome-wide SNP markers that complemented with phenotypic traits collected from optimal-water (OW) and water-deficit (WD) plots

V. Genome-wide linkage disequilibrium

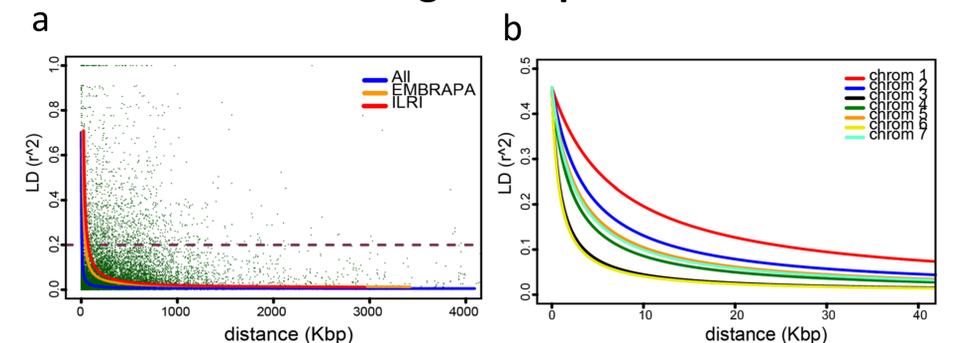


Figure 4. Estimated linkage disequilibrium decay (LD-decay) in the overall Napier grass collections (blue), 45 EMBRAPA accessions (orange) and 59 ILRI accessions (red) (a). In (b), the LD-decay per chromosome is shown

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