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Genetic Diversity in Napier Grass (*Cenchrus purpureus*) Collections as Revealed by Genotyping-by-Sequencing Method of the DArTseq Platform

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Abstract

Napier grass is one of the most important fodder crops, particularly in Eastern and Central African countries and used as a cut-and-carry feed with high potential as a biofuel crop. The ILRI (International Livestock Research Institute) genebank holds a diverse set of Napier grass accessions and also has a collection contributed by the Brazilian Agricultural Research Corporation (EMBRAPA). One hundred and five accessions were subjected to genotyping by sequencing using the DArTseq platform, which generated 116,190 SilicoDArT and 85,452 SNP high-density and polymorphic markers together with short sequence reads. The short sequence reads, with an average of 54 nucleotides, were mapped to the pearl millet reference genome, which is the closest related species to Napier grass. Around 17 % of the SNP and 33 % of the SilicoDArT markers were mapped and, based on the map position, the closest genes aligned with the markers were identified and the corresponding annotation information extracted. In turn, these data were used to select candidate genes for important forage traits based on functional annotations and sequence similarity. A total of 980 highly polymorphic SNP markers distributed across the genome and mostly independent were used to assess population structure and diversity. Up to seven subgroups were identified using phylogenetic analysis and the major ones were supported by the admixture model in STRUCTURE and principal component analysis (PCA). A few representative Napier grass accessions were subsetted from the diversity with the objective to distribute a representative subset of a manageable size for adaptation/evaluation in different production systems and agroecological conditions. Genome-wide linkage disequilibrium (LD) analyses revealed a fast LD-decay, on average at about 2.54 kbp, in the overall population with the LD-decay slower in the ILRI material compared to the EMBRAPA collection. This genotyping initiative generated high-density markers with a reasonable distribution across the genome. The diversity analysis revealed the existence of a substantial amount of variation, particularly in the ILRI collection and identified some unique materials from the EMBRAPA collection, demonstrating the suitability of the overall population for further genetic and marker-trait association studies.

Keywords: DArTseq, diversity analysis, elephant grass, forage, genebank, linkage disequilibrium

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