



A draft genome assembly for the forage grass *Urochloa ruziziensis* based on single-molecule real-time sequencing

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ABSTRACT:

Ruzigrass (*Urochloa ruziziensis*) is a diploid, tropical forage grass native to Africa, widely planted in Brazil, and known for its high nutritional quality. It is closely related to other important forage species of *Urochloa*, playing a crucial role in the breeding program of brachiaria grasses, which is mostly focused on inter-specific hybrids. Previous studies from our group based on shallow Illumina sequencing resulted in the development of the first molecular markers for the species, as well as in assessments of germplasm diversity and structure. Assembly and analysis of complete plastid genomes for four *Urochloa* species allowed the characterization of their phylogenetic divergence. Here, we strengthen the set of genomic tools for tropical forage grasses by assembling long reads into a first draft for the nuclear genome of the heterozygous clone C69. We used PacBio Sequel to generate over 13.3 million raw reads (mean size 6.5 kbp), adding up to 87.5 Gbp of raw data (~142x coverage). The current assembly using FALCON contains ~1.02 Gbp in 7,628 primary contigs, with NG50 of 412 kbp. It covers almost twice the size of the estimated haploid genome size of 615 Mbp for ruzigrass, indicating that haplotypes were assembled separately. In addition, RNA-seq data was obtained, totaling 258 million reads and 26 Gbp of raw data. These will allow transcriptome characterization for different tissues and aid gene prediction and annotation. Ongoing research includes haplotype phasing, polishing, assembly curation and Hi-C scaffolding. A high-quality genome assembly for ruzigrass will aid research groups in the development and application of genomic tools in breeding and genetics of brachiaria grasses.

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