PE1184 A Phased Diploid Genome Assembly for the Forage Grass Urochloa Ruziziensis Based on Single-Molecule Real-Time Sequencing

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Body

Ruzigrass (*Urochloa ruziziensis*) is a diploid, tropical forage grass native to Africa, widely planted in Brazil, known for its high nutritional quality. It is closely related to important forage species of *Urochloa*, and plays a crucial role in the breeding program of brachiaria grasses, mostly focused on inter-specific hybirds. Previous studies from our group based on shallow Illumina sequencing resulted in the development of the first molecular markers for the species (Silva et al., 2013 (http://dx.doi.org/10.1186/1471-2164-14-17)), as well as in assessments of germplasm diversity and structure (Pessoa-Filho et al., 2015 (http://dx.doi.org/10.2135/cropsci2015.02.0096)). Assembly and analysis of complete plastid genomes for four *Urochloa* species allowed the characterization of their phylogenetic divergence (Pessoa-Filho et al., 2017 (http://dx.doi.org/10.1186/s12864-017-3904-2)). Here, we present a near-complete phased diploid genome assembly of the heterozygous ruzigrass clone C69. We used PacBio Sequel to generate over 13.3 million long reads (mean size 6.5 kbp), adding up to 87.5 Gbp of raw data (~142x coverage). The current diploid assembly using FALCON-Unzip contains ~603 Mbp in 3,539 primary contigs, with NG50 of 286 kbp, and covers 98.2% of the estimated haploid genome size of 615 Mbp for ruzigrass. In addition, 82% of the assembly could be phased as separate haplotypes, with ~500 Mbp resolved as haplotigs. Assessment of assembly completeness showed 95.2% BUSCO matches as complete, and 83.3% as complete single-copy. Ongoing research includes transcriptome assembly to aid gene prediction and annotation, anchoring of contigs in linkage maps, and Hi-C scaffolding. A high-quality, chromosome-scale genome assembly for ruzigrass will aid research groups in the development and application of genomic tools in breeding and genetics of brachiaria grasses.