IMPROVING THE USE OF GENOMIC TOOLS IN TROPICAL FORAGE GRASS BREEDING WITH DIPLOID RUZIGRASS AS A REFERENCE

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Beef production in Brazil is based on planted pastures, with most of the area occupied by species of *Urochloa*. Breeding in the genus relies on intra- and inter-specific crosses within an agamic complex including three *Urochloa* species, which compose a mixture of sexual diploids and polyploids, among facultative or obligate apomicts. One of these species, ruzigrass (*Urochloa ruziziensis*), is a diploid tropical forage grass known for its high nutritional quality. Ruzigrass plays a crucial role in brachiaria grass breeding as a sexual female parent that can be crossed with apomicts, once its chromosome number is doubled with colchicine. In *Urochloa*, it is estimated that the development and release of a new cultivar can take up to 10 years. There is room for significant improvement in rates of genetic gain by using more efficient breeding methods and reducing breeding cycles. While marker-assisted selection and genomic prediction would be valuable tools for this goal, use of genomic information in tropical grass forage breeding is still limited. Application of molecular tools for QTL mapping, genome sequencing and assembly or marker-assisted selection is rare or non-existent. Our group has focused on acquiring genomic information in diploid ruzigrass, in order to provide useful tools for *Urochloa* breeding and genetics. Previous studies based on shallow Illumina sequencing allowed the development of the first microsatellite markers for the species, assessments of germplasm diversity and structure, assembly and annotation of complete plastid genomes for four *Urochloa* species, as well as characterization of their phylogenetic divergence. Next, we assembled a draft genome for ruzigrass C69 heterozygous clone using PacBio Sequel single-molecule real-time sequencing. The current assembly obtained with FALCON contains 7,628 primary contigs, with NG50 of 412 kbp. Assessment of genome completeness using BUSCO showed 80.7% complete genes, 21.7% of which were duplicated. In addition, RNA-seq data was obtained using Illumina NovaSeq, totaling approximately 500 million reads and 30 Gbp of raw data. Initial transcriptome assemblies obtained with Trinity, SOAPdenovo-Trans, rnaSPAdes, and Velvet/Oases, totaling 11 million transcripts, were used as input for EvidentialGene-R pipeline to generate a high-quality gene set. This produced 108,000 transcripts, which will be used for gene model prediction and genome annotation. Further steps include the optimization of assembly quality parameters, haplotype phasing and polishing, haplotig deduplication, 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 and closely related species. In addition, ongoing research is also focused on establishing the necessary foundations for genomic selection in ruzigrass.

PRESENTER BIO: Dr. Pessoa-Filho is a Research Scientist at Embrapa, applying genomics to improve the use of plant genetic resources by breeding programs. He has experience with the development and use of molecular tools in genetics and breeding of crops such as rice, soybean, cassava and ruzigrass.