

Draft genomes and comparative analyses of binucleate *Rhizoctonia* isolates

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The *Rhizoctonia* species complex in the family Ceratobasidiaceae is commonly associated with its pathogenic lifestyle causing diseases in crops of economic importance. However, this family comprises saprobes and mycorrhizal symbionts associated with orchids. Based on hyphal recognition, anastomosis groups are distinguished within 2 major groups: multinucleate and binucleate, which differ in genome sizes, host specificity and number of secreted proteins, suggesting differences in pathogenesis or plant associations. While genomes of multinucleate anastomosis groups have been assembled and their pathogenicity mechanisms studied, binucleate isolates have not been equally described. Given this diversity and lack of information for binucleate isolates to date, studying the genome of multiple anastomosis groups remains necessary for a better understanding of the species. We present 4 draft genomes from binucleate *Rhizoctonia* isolates from Arkansas, Alabama and Louisiana obtained with Nanopore sequences. Assemblies were 72.8 to 82 Mb long. Completeness of the genomes showed >75% complete ortholog genes based on BUSCO content. Between 17,223 to 19,452 genes with average length of 2,108 nucleotides were annotated. Pairwise comparisons of read alignments were carried out to understand sequence similarities and around 10,000 carbohydrate active enzymes (CAZys) were identified per sample. These preliminary genomic resources provide a framework for future comparative analyses.