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Abstract for poster presentation

Genome sequencing of the sugarcane orange rust pathogen *Puccinia kuehnii*

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Puccinia kuehnii, the causal agent of orange rust, is a fungal pathogen that causes damaging losses to the sugarcane crop in Florida since 2007. During plant infection, rust fungi deliver effector proteins into host tissues using a specialized feeding structure called a haustorium, to manipulate plant functions and promote parasitic growth. Identification of these effectors is therefore an essential step to understand host-pathogen interactions and to develop new control methods. In this study, two isolates of *P. kuehnii* from Florida were used for genome sequencing and effector discovery based on sequence features. Genomic DNA was extracted from spores of *P. kuehnii* 1040 and *P. kuehnii* 2143 that were collected from sugarcane cultivars CL 85-1040 and CP 89-2143, respectively. Short Illumina DNAseq and long read Pacbio sequencing was performed and a hybrid assembly was obtained for the genome of each isolate of *P. kuehnii*. These assemblies will be used as genomic resources for gene calling and proteome prediction.