



5th IMPB

INTERNATIONAL
MEETING ON PLANT
BREEDING

INTEGRATED DATA ANALYSIS AS A TOOL TO REVOLUTIONIZE PLANT BREEDING

GENOMICS INSIGHTS FROM THE FIRST CHROMOSOME-SCALE GENOME OF THE SOURGRASS SMUT FUNGUS USING OXFORD NANOPORE READS

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Introduction

Commonly called sourgrass, *Digitaria insularis* (L.) Fedde is a perennial weed with invasive behavior and has gained relevance in recent years due to its high tolerance to Glyphosate, generating high production cost for farmers. Sourgrass is also a host to the smut fungi *Sporisorium panici-leucophaei* that infects seedlings of *Digitaria insularis*, responsible for the sourgrass smut disease. Symptomatically, the disease resembles another one caused by *S. scitamineum* in sugarcane, producing a whip-like structure from the apex of the plants where sporogenesis takes place. Despite similarities with sugarcane smut, genomic information is scarce about this pathosystem.

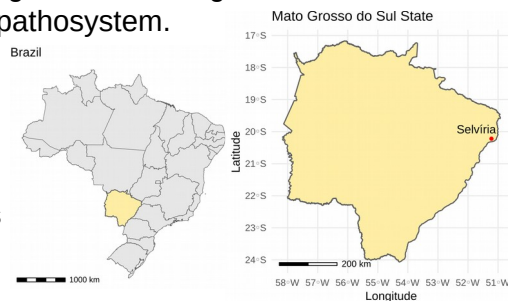
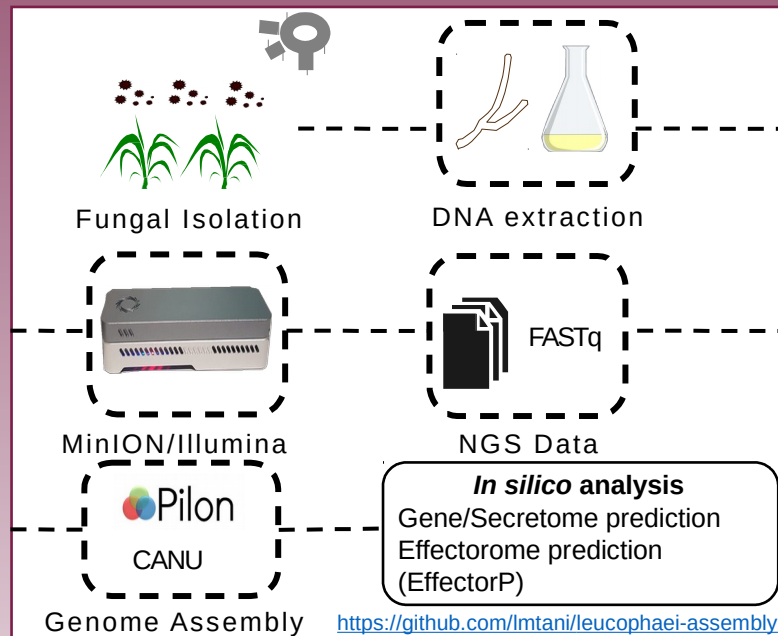


Fig. 1. Fungal spores were isolated in Selvíria, MS, Brazil.

Objective

The objective of our project was to sequence, for the first time, the complete genome of *S. panici-leucophaei* using Nanopore long reads and predict the fungi effector repertoire.

Materials and methods



Results and discussion

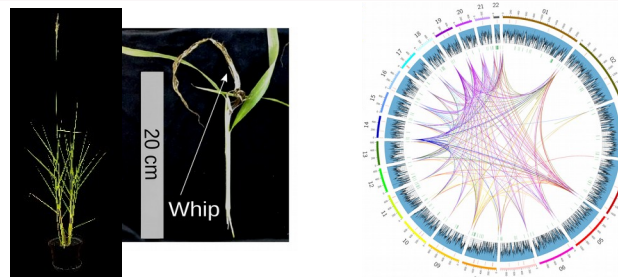


Table 1. Summary of the genome sequencing, assembly and annotation statistics

Feature	<i>Sporisorium panici-leucophaei</i>
Raw data (Nanopore) (Mbp)	417
Raw data (Illumina) (Mbp)	418
Assembly software	Canu
Genome (bp)	18,915,934
Total sequence coverage	32x
Number of chromosomes	22
Largest chromosomes (bp)	2,102,384
Smallest chromosome (bp)	152,803
Mitochondrial genome (bp)	78,051
Mitochondrial contigs	1
Genome N50 (bp)	969,070
GC content (%)	53.99
BUSCO completeness (genome mode) (%)	97.7
BUSCO completeness (protein mode) (%)	97.2
Repeat elements (%)	2.71
Number of predicted protein-encoding genes	6,402
Number of predicted secreted proteins	388
Number of predicted effectors	68

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Conclusion

To the best of our knowledge, this is the first smut and also *S. panici-leucophaei* genome sequence assembled with nanopore reads. The complete genome of this poorly studied fungus will provide a valuable resource for future studies as a biocontrol agent against *D. insularis*.

Acknowledgments

