

# Comparison of Gene Finding Tools in the Context of *Trichoderma* Genomes

Committee members: Dave Schneider, Tony Kusalik, Matthew  
Links, Leon Kochian

Connor Burbridge

May 31, 2023

# Background: *Trichoderma*

What is *Trichoderma*?

- ▶ *Trichoderma* is an opportunistic symbiotic fungi
- ▶ *Trichoderma* strains have been shown to provide benefits to the host plant it colonizes
  - ▶ Increased resistance to abiotic and biotic stressors
  - ▶ Facilitating nutrient uptake
  - ▶ Increased germination rates
- ▶ These benefits have resulted in *Trichoderma* being used in manufacturing processes for antibiotics and other materials

## Background: Previous GIFS Work

Two strains have been sequenced in previous work within GIFS:

- ▶ These strains have been named DC1 and Tsth20
- ▶ Strains from the prairie regions of Canada, including Alberta and Saskatchewan
- ▶ One of these strains has been shown to improve crop tolerance to soils with high salt content. The other shows potential as a bioremediation agent for soils contaminated with hydrocarbons
- ▶ How exactly do these processes work?
- ▶ We must sequence and annotate these strains to find out!

# Research Problem

These sequenced strains offer an opportunity to assemble and annotate them:

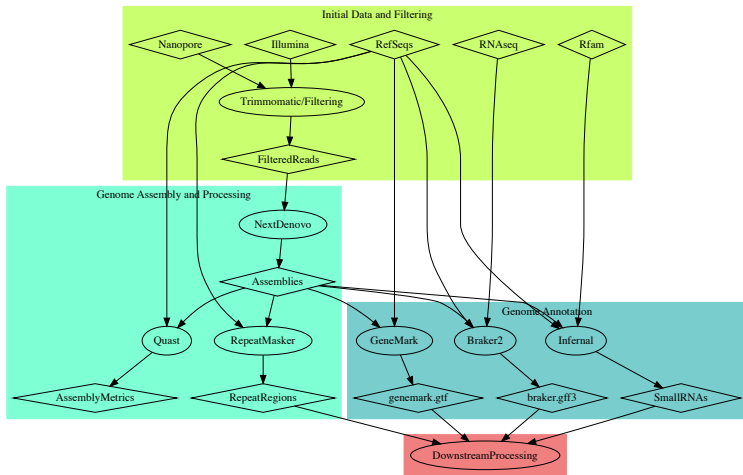
- ▶ Genome assembly is 'relatively' straight-forward
- ▶ **However, the choice of a tool for gene finding or annotation is uncertain**
- ▶ There has been relatively little comparative analysis for gene finding tools in fungi, and even fewer for *Trichoderma*
- ▶ **This raises questions. How do different gene finding tools perform in fungi and *Trichoderma* in particular?**

# Project Goal

**This project aims to evaluate several different gene finding tools in the context of *Trichoderma* genomes**

- ▶ Gene finding tools currently selected are GeneMark-ES and Braker2
- ▶ The selected tools aim to include a mix of *ab initio*, evidence-based and hybrid gene finding methods
- ▶ This list is not final and will include at least one more tool for comparison

# Methodology



# Downstream Analysis of Gene Finding Predictions

- ▶ A plan for evaluating and comparing the selected tools is in development
- ▶ Results for five total genomes will be considered
- ▶ Current metrics for comparison will include both quantitative and qualitative observations

# Quantitative Metrics

- ▶ Total genes predicted
- ▶ Total transcripts predicted
- ▶ Genes predicted in repetitive regions
- ▶ Analysis of low GC content regions
- ▶ Genes overlapping small RNAs
- ▶ Length of gene models predicted
- ▶ Comparison to genes predicted in other fungal species (Yeast)
- ▶ Run times and memory usage



# Qualitative Metrics

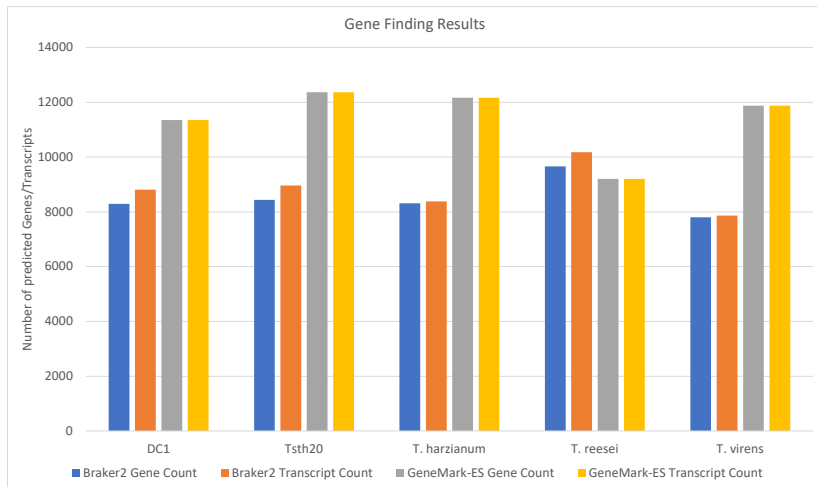
- ▶ Features of the gene finding tools
- ▶ Ease of software installation and their dependencies
- ▶ Ease of use
- ▶ Popularity among other research

# Assembly Metrics

## NextDenovo

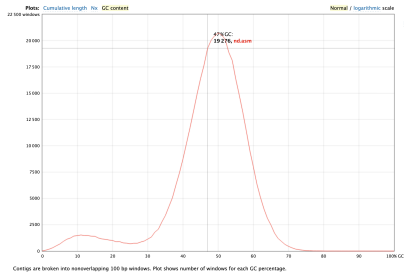
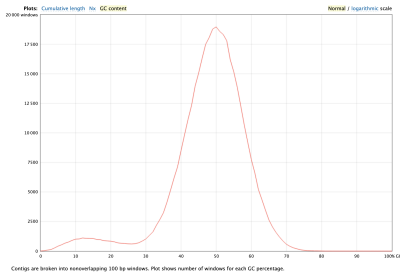
Strain	Total Contigs	Total Length	Largest Contig	GC%	N50	L50
DC1	8	38.53 Mb	11.47 Mb	47.96	5.67 Mb	3
Tsth20	7	41.48 Mb	8.0 Mb	47.32	6.50 Mb	3
<i>T. harzianum</i>	532	40.98 Mb	4.08 Mb	47.61	2.41 Mb	7
<i>T. virens</i>	93	39.02 Mb	3.45 Mb	49.25	1.83 Mb	8
<i>T. reesei</i>	77	33.39 Mb	3.75 Mb	52.82	1.21 Mb	9

# Initial Gene Finding Results

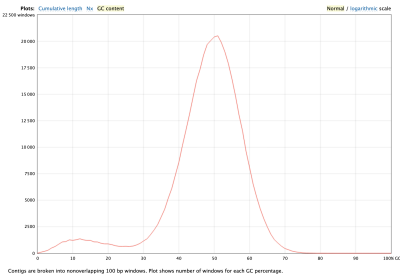
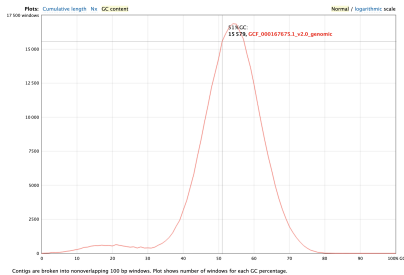


## Low GC Content in *Trichoderma* Genomes

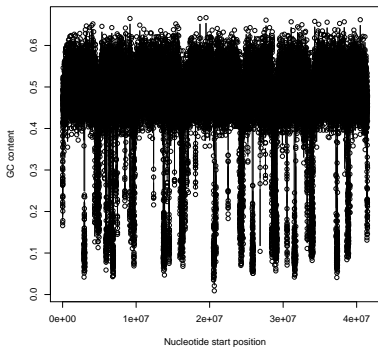
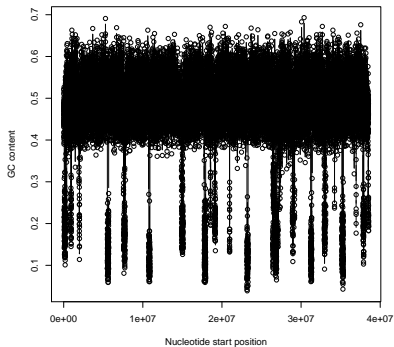
- ▶ Low GC content of some *Trichoderma* genomes
  - ▶ Example of DC1 and Tsth20 GC content



# Low GC content in *T. reesei* and *T. harzianum*



# Low GC Content Regions in *Trichoderma* (DC1 and Tsth20)



# Why is this useful to RSMI/GIFS?

- ▶ Assemblies and statistics of novel *Trichoderma* strains DC1 and Tsth20 made available
- ▶ Multiple sets of gene calls, sRNAs and repeat annotations made available
- ▶ Analysis of GC content in combination with gene calls and repeat regions
- ▶ Unfortunately, I can't tell you which genes are responsible for resistance to high salt content soils and bioremediation. At least not yet!

# What Next?

- ▶ Genes predicted in repetitive regions
- ▶ Genes overlapping smallRNAs
- ▶ Length of gene models predicted
- ▶ Comparison to genes predicted in other fungal species (Yeast)
- ▶ Run times and memory usage
- ▶ Annotation of small RNAs using Infernal
- ▶ Annotation with another gene finding tool (possibly NCBI)



# Acknowledgements

- ▶ Committee members - Dave, Tony, Leon and Matthew
- ▶ Brendan Ashby - Sequencing and initiation of this project
- ▶ Dr. Shayeb Shahariar - Additional lab work and processing for DC1 and Tsth20 with tomato plants

Questions?