

# Assembly and Investigation of *Trichoderma* Strains Conferring Resistance to Soils with High Salt and Hydrocarbon Content

Connor Burbridge

November 22, 2021

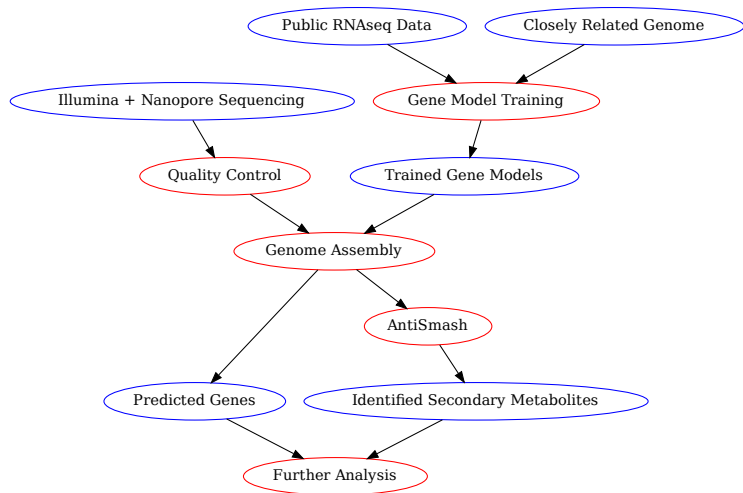
# Background on *Trichoderma*

- ▶ *Trichoderma* is an opportunistic symbiotic fungi that colonizes plant roots
- ▶ This fungus has been shown to provide several benefits to plants including:
  - ▶ Increased resistance to abiotic and biotic stressors
  - ▶ Facilitating nutrient uptake
  - ▶ Increased germination rates
- ▶ We seek to understand the mechanisms behind these benefits

# What is unique to this work?

- ▶ Two interesting strains have been identified in the prairie regions of Canada
- ▶ These strains are DC1 and Tsth20
- ▶ Have been shown to increase crop tolerance to soils with high salt and high hydrocarbon content
- ▶ We would like to know more about these strains by identifying important secondary metabolites such as polyketides, non-ribosomal peptide synthetases as well as effector and signalling peptides
- ▶ However, we do not have assemblies for these strains and they have yet to be truly classified

# Proposed Methods



# Preliminary Results

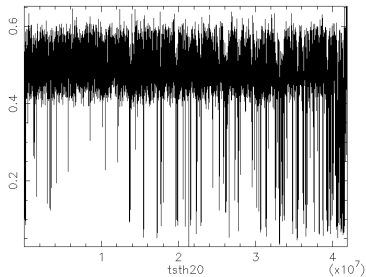
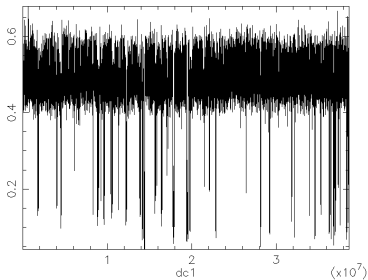
- ▶ We currently have preliminary results from Illumina data only
- ▶ Nanopore data is ready but has not been processed yet
- ▶ Results will be shown for Illumina assembly's of DC1 and Tsth20 along with preliminary annotation results

# Results: Assembly Metrics

Strain	Total Contigs	Total Length	Largest Contig	GC%	N50	L50
Tsth20	815	41.67 Mb	1.63 Mb	47.30	478.22 Kb	26
DC1	416	38.60 Mb	1.71 Mb	47.95	229.00 Kb	47
<i>T. asp.</i>	419	37.46 Mb	3.82 Mb	47.34	2.12 Mb	7
<i>T. atr.</i>	29	36.14 Mb	5.62 Mb	49.75	2.01 Mb	6
<i>T. cit.</i>	533	33.21 Mb	3.29 Mb	52.44	1.84 Mb	7
<i>T. gam.</i>	172	37.90 Mb	1.83 Mb	48.95	679.39 Kb	18
<i>T. har.</i>	532	40.98 Mb	4.08 Mb	47.61	2.41 Mb	7
<i>T. ree.</i>	77	33.39 Mb	3.75 Mb	52.82	1.21 Mb	9
<i>T. vir.</i>	93	39.02 Mb	3.45 Mb	49.25	1.83 Mb	8

# Results: Interesting Regions of Low GC Content

- ▶ Low GC content means low diversity of amino acids
- ▶ Why do these regions exist? Do they code for anything?



# Results: Annotation of Signalling and Effector Proteins

- ▶ Initial annotation of these strains shows a promising number of effector and signalling proteins
- ▶ Current annotation is an awkward mapping of different annotation programs including InterProScan, SignalP and EffectorP
- ▶ However, future work will include a more robust annotation approach using AntiSmash



# Future Work

- ▶ With newly generated Nanopore sequencing, re-run everything from the beginning
- ▶ Large amount of new RNAseq data on NCBI can be utilized for more accurate/robust annotation
- ▶ Hybrid assemblies should be more contiguous and complete
- ▶ Annotation of secondary metabolites via AntiSmash will provide more valuable information
- ▶ Comparative analysis with closely related *Trichoderma* strains
- ▶ Open to other ideas as well!

# Computer Science MSc.

- ▶ How is this related to computer science?
- ▶ Plan to identify gaps in existing procedures where improvements could be made
- ▶ Potentially generate a pipeline for similar automated analyses

Questions, comments, thoughts?

- ▶ Other things to discuss:
  - ▶ Courses for next term
  - ▶ Potential other committee members