Committee meeting for Connor Burbridge

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

Connor Burbridge

November 15, 2022

Project Proposal Outline

- Background
- Research Problem
- Current Progress
- Timeline
- Deliverables

Background: *Trichoderma*

What is *Trichoderma*?

- *Trichoderma* is an opportunistic symbiotic fungi, which can colonize the roots of plants
- *Trichoderma* strains have been shown to provide several benefits to the host plant it colonizes, those generally being:
  - 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
- How exactly do these processes work? Which genes are included in these processes?
- To answer these questions, both strains were sequenced with Illumina and Nanopore technologies

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, GenomeThreader, and Braker2
- These tools include a mix of *ab initio*, evidence-based and hybrid gene finding methods
- This list is not final and may include more tools if desired or necessary

Evaluation of Gene Finding Tools

A methodology for evaluating and comparing the selected tools needs to be developed. Metrics for comparison will include:

- Efficiency of selected gene finding tools
- Requirements of selected gene finding tools and ease of installation
- Comparison and validation of called genes with existing RNASeq data if available
- Identification of small RNAs and genes in repetitive and AT-rich regions
- Distribution of lengths of called genes (particularly in the case of *ab initio* gene finders)

Current Progress

Preliminary assemblies for both DC1 and Tsth20 are ready

- Two assemblies for each strain using both SPAdes and MaSuRCA
- Both assemblers use a hybrid assembly approach

Assembly Metrics

SPAdes

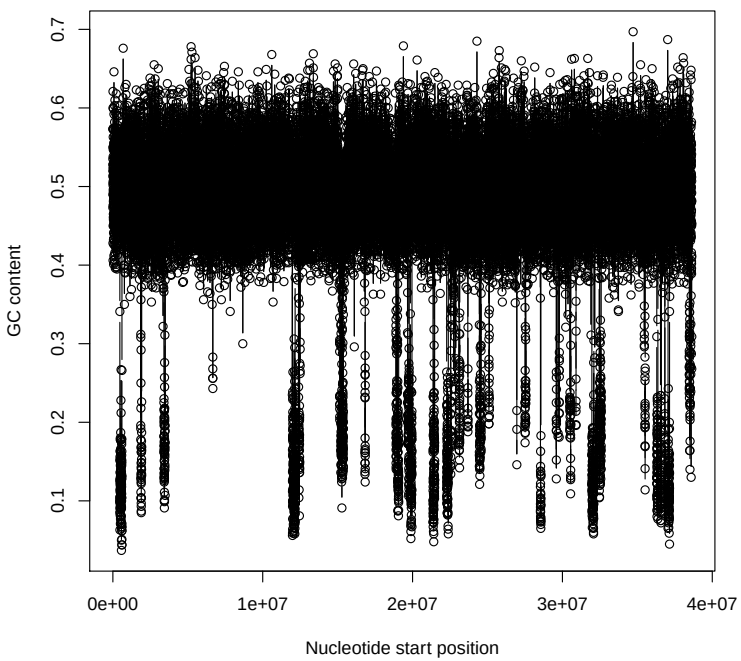
Strain	Total Contigs	Total Length	Largest Contig	GC%	N50	L50
Tsth20	611	41.88 Mb	2.44 Mb	47.28	1.17 Mb	14
DC1	181	38.60 Mb	1.85 Mb	47.95	807.44 Kb	17

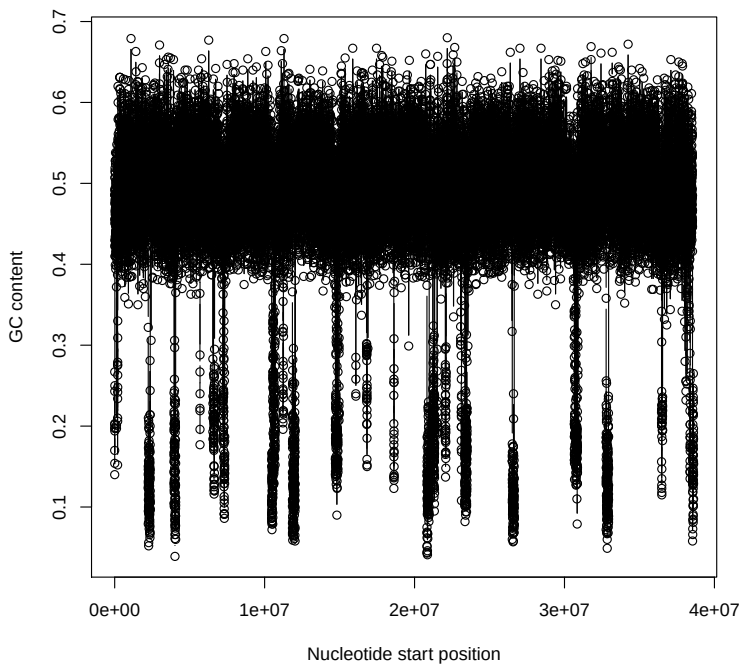
MaSuRCA

Strain	Total Contigs	Total Length	Largest Contig	GC%	N50	L50
Tsth20	8	41.52 Mb	9.97 Mb	47.36	4.96 Mb	3
DC1	13	38.60 Mb	7.36 Mb	47.96	4.06 Mb	4

Existing Progress Cont.

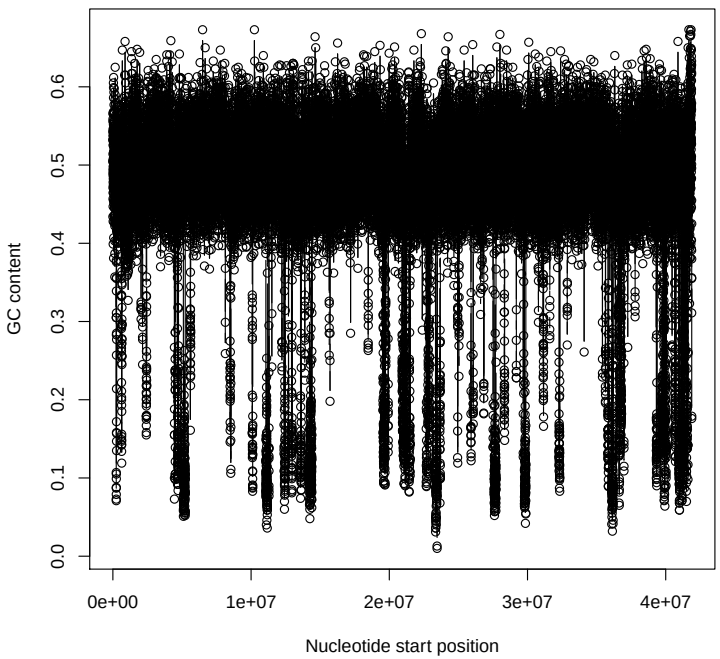
AT-rich regions of assembled DC1 genomes (SPAdes left, MaSuRCA right):

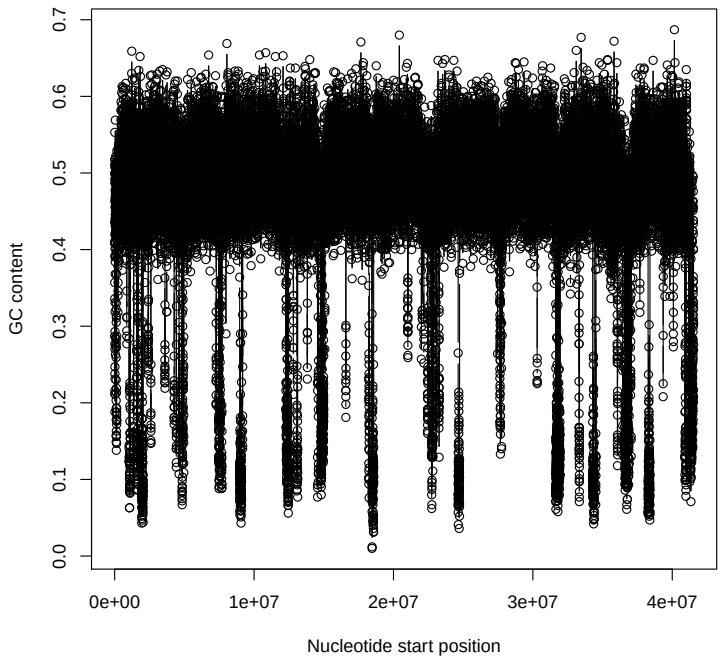




Existing Progress Cont.

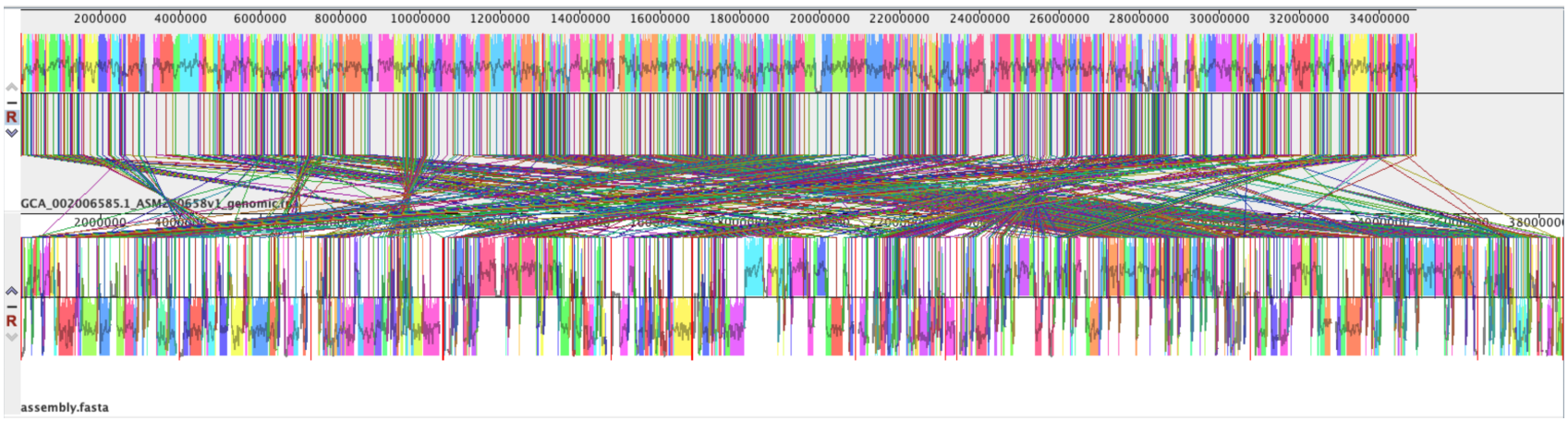
AT-rich regions of assembled Tsth20 genomes (SPAdes left, MaSuRCA right):





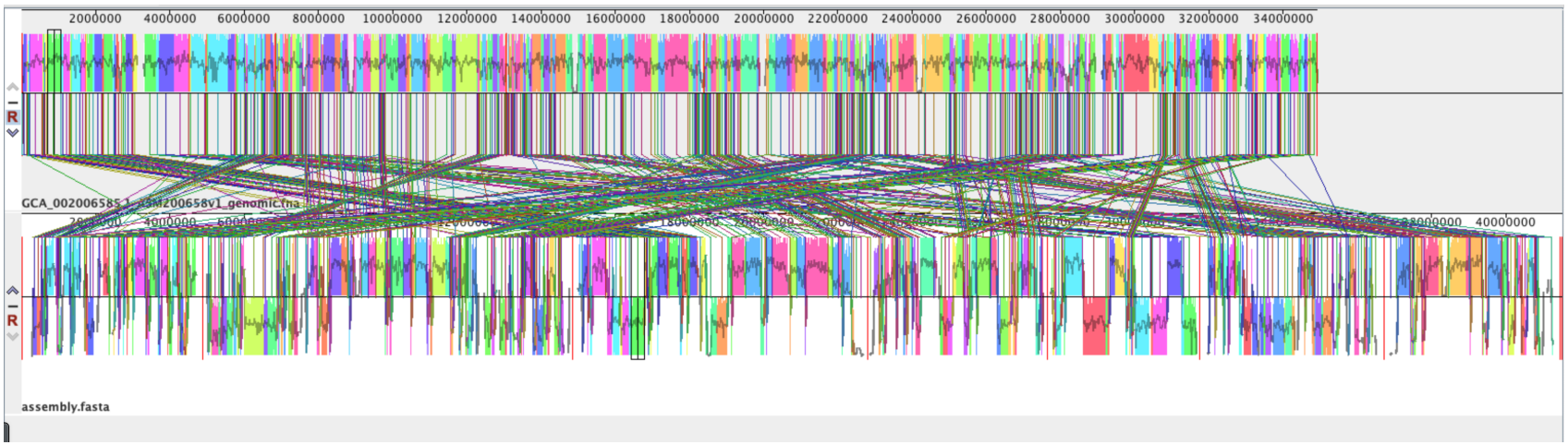
Existing Progress Cont.

Mauve Alignments for DC1 MaSuRCA Assembly:



Existing Progress Cont.

Mauve Alignments for Tsth20 MaSuRCA Assembly:



Next Steps

- Finish assemblies of DC1 and Tsth20
- Identify repetititve regions of selected assemblies
- Identify non-coding RNAs in selected assemblies
- Apply gene finders to selected assemblies and evaluate

Deliverables

- Assemblies of both Tsth20 and DC1
- Lists of potential genes for each *Trichoderma* assembly considered
- A consensus or core gene set for genes called by all gene finders
- Repetitive regions identified in all *Trichoderma* genomes considered
- Potential true positives supported by RNAseq evidence and existing annotations
- Final comparative tables including the evaluation metrics described previously

Timeline

- Finishing assemblies of DC1 and Tsth20 assemblies (2 weeks)
- Collection of existing genome assemblies (1 week)
- Application of gene finding tools to selected genomes (1-2 months)
- Downstream analysis of gene finding results (1-2 months)

Questions and/or comments