

Deciphering the Genome Diversity of Wheat Pathogen Pyrenophora tritici-repentis

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Introduction

- Pyrenophora tritici-repentis (Ptr) is a fungal necrotrophic plant pathogen that causes tan spot, a destructive foliar disease of wheat.
- Genomics of the *Ptr* pathogen has shown it to have a complex genome with many repetitive sequences, and several smallsecreted proteins (SSPs). The pathogen genome encoded host selective effectors (HSEs) in Ptr, specifically the necrosis-inducing effector gene (ToxA) and the chlorosisinducing effector genes (ToxB and ToxC) are the major virulence factors expressed in the wheat host, yet the contribution of other genomic regions is important for host adaptation.
- Our genomics-enabled research targets to study structural variations present in the pathogen genome related to virulence encoding regions under selection pressure to enhance the pathogen fitness on its diverse hosts.

REU-Learning Goals

Understanding of Wheat-*Ptr* model, bioinformatics learning, and **collaboration:** We used 25 diverse isolates collected from wheat, rye, and triticale in this study.

Bioinformatics Objective: Compare different De Novo assemblers, genome assembly, and genome comparison – Illumina and Oxford Nanopore MinION datasets.

Open Science – Data and Codes

Data and associated metadata files will be deposited in NCBI SRA.

- Tools:
- Shovill with SPAdes, Shovill with MEGAHIT, SPAdes, SOAPdenovo2 and Platanus
- Genome ribbon, CLC Workbench
- Code reconfiguration for analysis – Will be hosted in GitHub

Illumina:



rted gene_name.bestTree o gene_name.newick and \ aded to MEGA11 for tree visualiza

Nanopore:

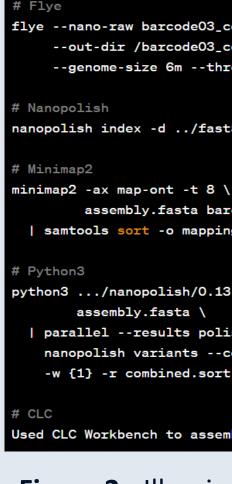


Figure 2 - Illumina code to the left and Nanopore code above.



Figure 1 - (A) (B) Chlorotic symptoms on wheat leaf.

Necrotic symptoms

Software benchmarking and contig assembly of 25 diverse isolates – Illumina short re

De Novo Assembler	Isolate Number	Size (MB)	Contig	GC %	N50 (bp)
Platanus	3	0.233	70	46.79	1246
Shovill with SPAdes	3	36.065	3844	50.95	21607

De Novo Assembler	Isolate Number	Size (MB)	Contig	GC %	N50 (bp)	L50 (b
Flye - Unfiltered	26	36.007	133	50.74	2186992	
Flye - Unfiltered	27	38.289	474	50.74	1503834	
Flye - Unfiltered	28	36.482	68	50.68	2869119	
CLC	26	36.0	30	50.7	2329755	
CLC	27	39.09	154	50.75	558505	
CLC	28	36.04	18	50.65	3083327	



Conclusions

 Shovill with SPAdes works better for our dataset. • Genome re-arrangements are frequent in the

pathogen population.

Ongoing Work

Gene Annotation and Pangenome Construction.

enome-size 6m --threads 10 --trestle

opolish index -d ../fast5/ barcode03_combined.fastq

assembly.fasta barcode03_combined.fastq samtools sort -o mappings/combined.sort.bam

oython3 .../nanopolish/0.13.2/scripts/nanopolish_makerange.py \ parallel --results polish_out/nanopolish.results -P 20 nanopolish variants --consensus -o polish_out/polished.{1}.vc: -w {1} -r combined.sort.bam -g assemblv.fasta

Used CLC Workbench to assemble and create a genome ribbon



Results

Acknowledgement

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South Dakota Wheat Commission

SDSU's Genomics Sequencing Facility





read	data	

Region	Host
South Dakota	Triticosecale
South Dakota	Triticosecale
South Dakota	T. aestivum
South Dakota	Secale cereale
Canada	T. aestivum
Canada	T. aestivum
Canada	T. aestivum
South Dakota	T. aestivum
ROMANIA	T. aestivum
ROMANIA	T. aestivum
LATVIA	T. aestivum
LATVIA	T. aestivum
LITHUANIA	T. aestivum
LITHUANIA	T. aestivum
NEBRASKA	T. aestivum
NEBRASKA	T. aestivum
South Dakota	T. aestivum
South Dakota	T. aestivum
South Dakota	T. aestivum
Latvia	T. aestivum
South Dakota	T. aestivum

