Characterizing a Novel Fungal Lineage in Boreal Soil

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Introduction

Mycology

- Fungi do a variety of essential tasks for their environment
- Alaska treeless without fungal symbionts (8)
- including giving plants mineral nutrients and water, and decomposing plant matter (2)(5)
- Fungi play a pivotal role in carbon stability
- Mycology is in its cataloging phase: Of an estimated 1.5 million fungal species only 5% have been formally described. (1)

Detection of Divergence in a Novel Fungal Lineage in Boreal Forest

- Lineage highly divergent from known taxa.
- Of five novel lineages found previously discovered by Dr. Lee Taylor, we further characterized the diversity within one of the five novel lineage.

Research Questions

1. Is there diversity within this lineage?

Methods

Ran a whole Genome Amplification of .25 gram of soil core sample
Cloned specific fungal lineage

Plot 6 core locations from 2003

Used Sequencher along with BLAST Trim Vector to clean up DNA sequences.
Constructed a phylogeny of clone samples

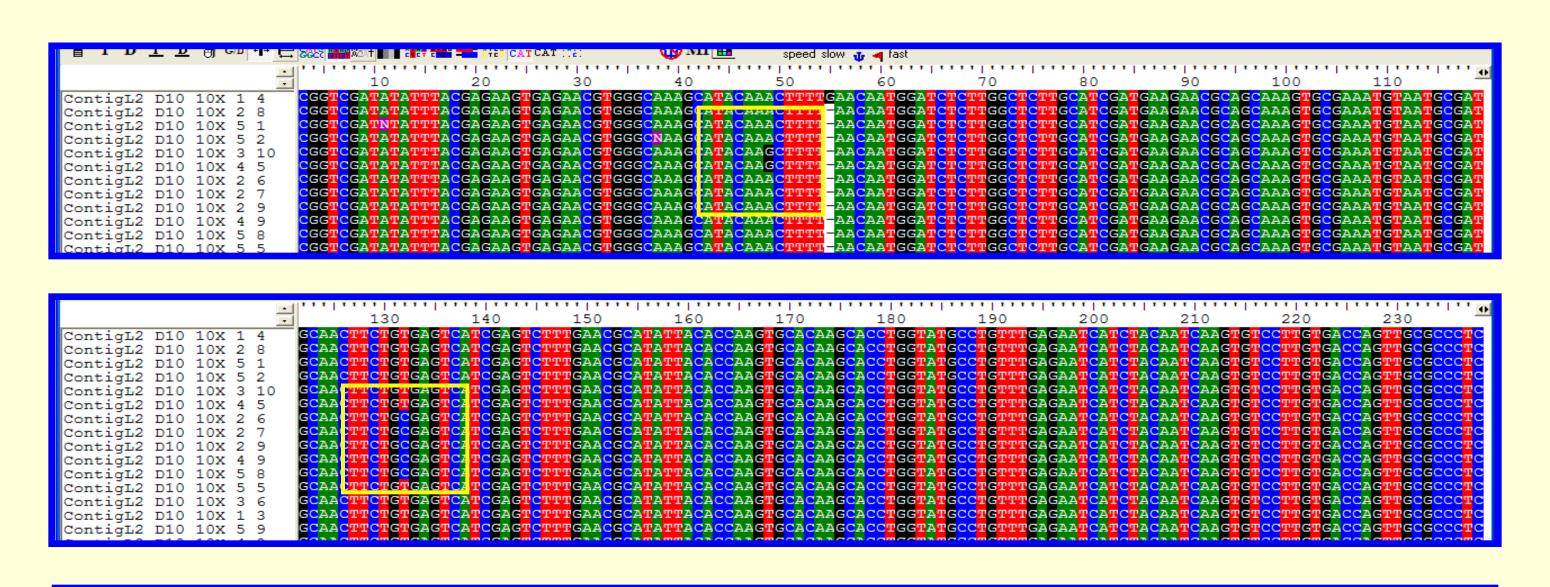


Figure 2. Clone Sequences from single soil core. Note: Transition mutations in yellow boxes.

Results

•Appears to be three different taxa in .25 gram soil core. (See Fig 3)

Number of clones within each clade is 26, five, and two.

- The intraspecific sequence similarity of these clones is 99.66%.
- From the original sequence of the same site there was a 98.3% sequence similarity.
- •The base pair mutations in these taxa are transitions: the group of five having a C instead of T and the group of two having an A instead of G as compared to the original sequence. (See fig 2)

Note: The branches of the phylogenetic tree do not represent time in this diagram but instead mutational divergence. The biological time it took for these mutations is unknown and impractical to illustrate for our purposes.

Figure 3. Chytridiomycota - Chytridiales - eucarpic thallus of *Rhizophydium*

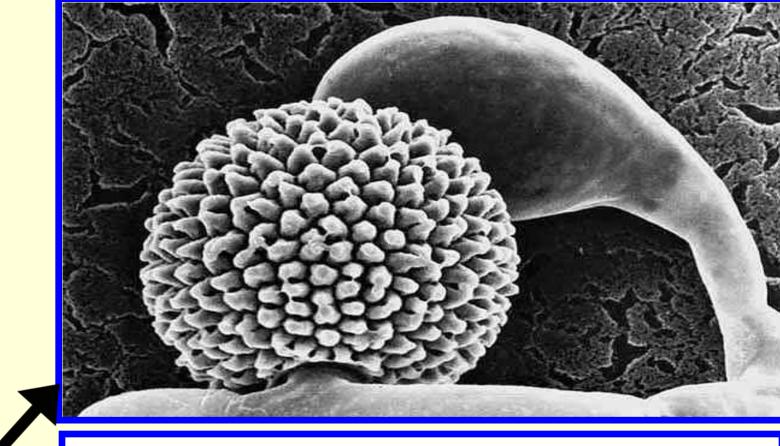


Figure 4. Zygo Spore: Zygomycetes

ontigL2_D10_10X_2_1 ontigL2D1010X1_2 ontigL2_D10_10X_3_9 ontigL2_D10_10X_5_2 ontigL2_D10_10X_5_1 ontigL2_D10_10X_4_4 ontigL2_D10_10X_5_9 ContigL2_D10_10X_3_5 ontigL2D1010X1_6 ontigL2_D10_10X_3_7 ontigL2_D10_10X_4_3 ContigL2_D10_10X_4_1 ontigL2_D10_10X_2_4 ontigL2_D10_10X_3_2 ContigL2_D10_10X_4_8 ontigL2_D10_10X_3_8 ContigL2_D10_10X_6 ontigL2_D10_10X_2 ontigL2D1010X1_7 ontigL2_D10_10X_5_5 ContigL2_D10_10X_4_2 ontigL2_D10_10X_3_6 ontigL2_D10_10X_1_3 ontigL2_D10_10X_2_8 ontigL2_D10_10X_1_4

Figure 5. Phylogeny constructed from a single soil core clone library. Different clades represent same taxon represented by multiple clones.

Conclusion

•Singles Core variation: leads to believe more diversity within site(s)

Future Direction: test for diversity in other 9 sites (See fig 1)

Multiple clones for each taxon: not likely Taq error

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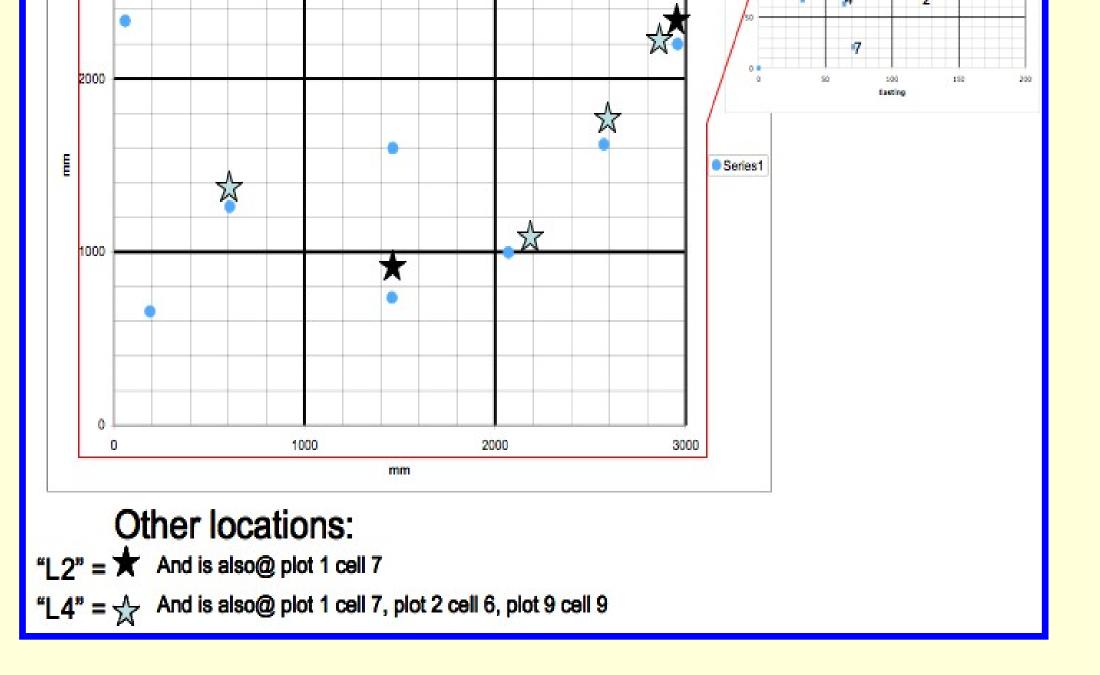


Figure 1. Black Spruce site, black stars represent our novel taxon of interest.



