

# Genome sequencing and Annotation of *Lentinus* Section Tigrini

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## Introduction

*Lentinus tigrinus* is a white rot fungus commonly found across Europe and parts of North America, growing on riverbeds and partially submerged logs. *L. tigrinus* exhibits an enigmatic phylogenetic divergence between North American and European populations. This study presents preliminary genomic analysis of *L. tigrinus* from both groups in addition to two other species within the section Tigrini, including a possibly novel species of *Lentinus* in the section Tigrini from Guyana, offering further insights into the diversity of this clade.

## Methodology

### Genetic analysis

Genome sequencing for eight specimens from section Tigrini, two *L. tigrinus* from the “North American” group, two from the “European” group, two *L. glabratus* and two possibly novel *Lentinus* sp. collected from Guyana in South America, was performed using 150x150 Illumina Novoseq6000. Genomes were assembled using MegaHit v1.2.9. We used Funannotate (version) to perform genome annotation and comparison against the an of *L. tigrinus* reference genome, Lenti7.

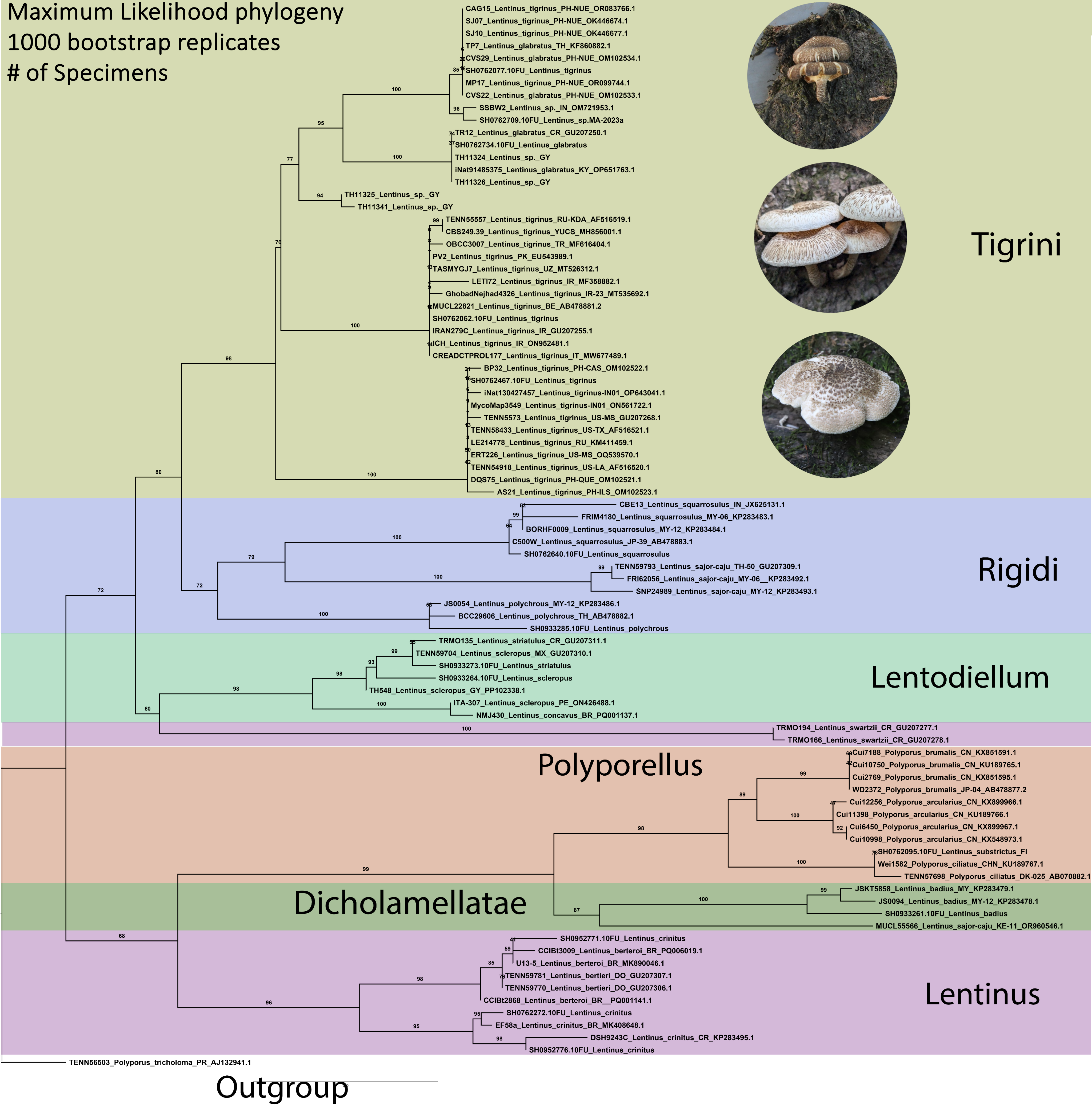
### Phylogenetic Analysis

Curated ITS dataset from UNITE species hypotheses and GenBank accessions across the genus *Lentinus*. Dataset was modeled around the genus-level *Lentinus* analysis performed in Seelan et al. 2015. Alignments were done in MAFFT v7.525; phylogenetic tree was constructed and bootstrapped in IQ-TREE v2.3.6.

## Works cited

Citations here

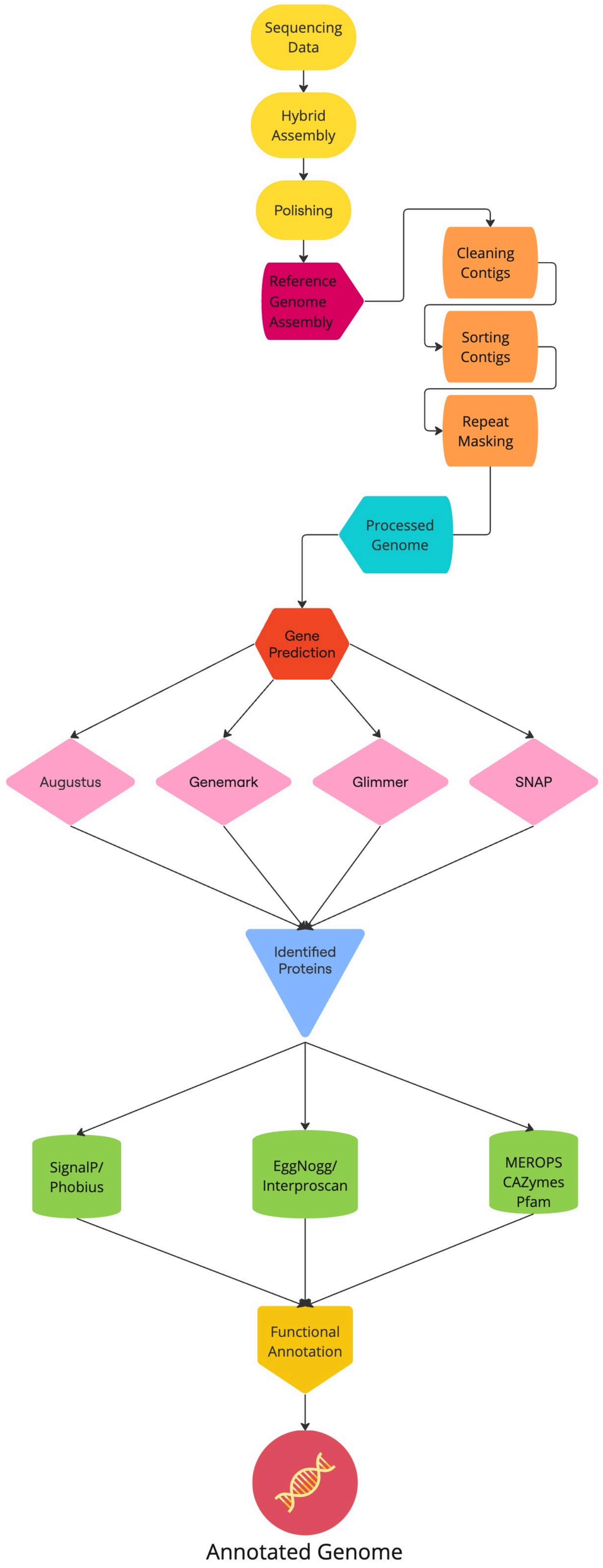
Maximum Likelihood phylogeny  
1000 bootstrap replicates  
# of Specimens



Busco Score Plot, genome assembly stats,  
comparison of GO Terms or something else



## Annotation flowchart



## Annotation stats

## Conclusions and Future Directions

Issac and Zack, what do you think should happen next

## Acknowledgements

Terry Henkel for providing material

