Phylogenomic and Functional Reassessment of *Pseudogymnoascus destructans* Across Mitochondrial and Nuclear Scales



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Introduction

White-Nose Syndrome (caused by *P. destructans or* Pd) is the reason of 90% mortality among hibernating bats every year



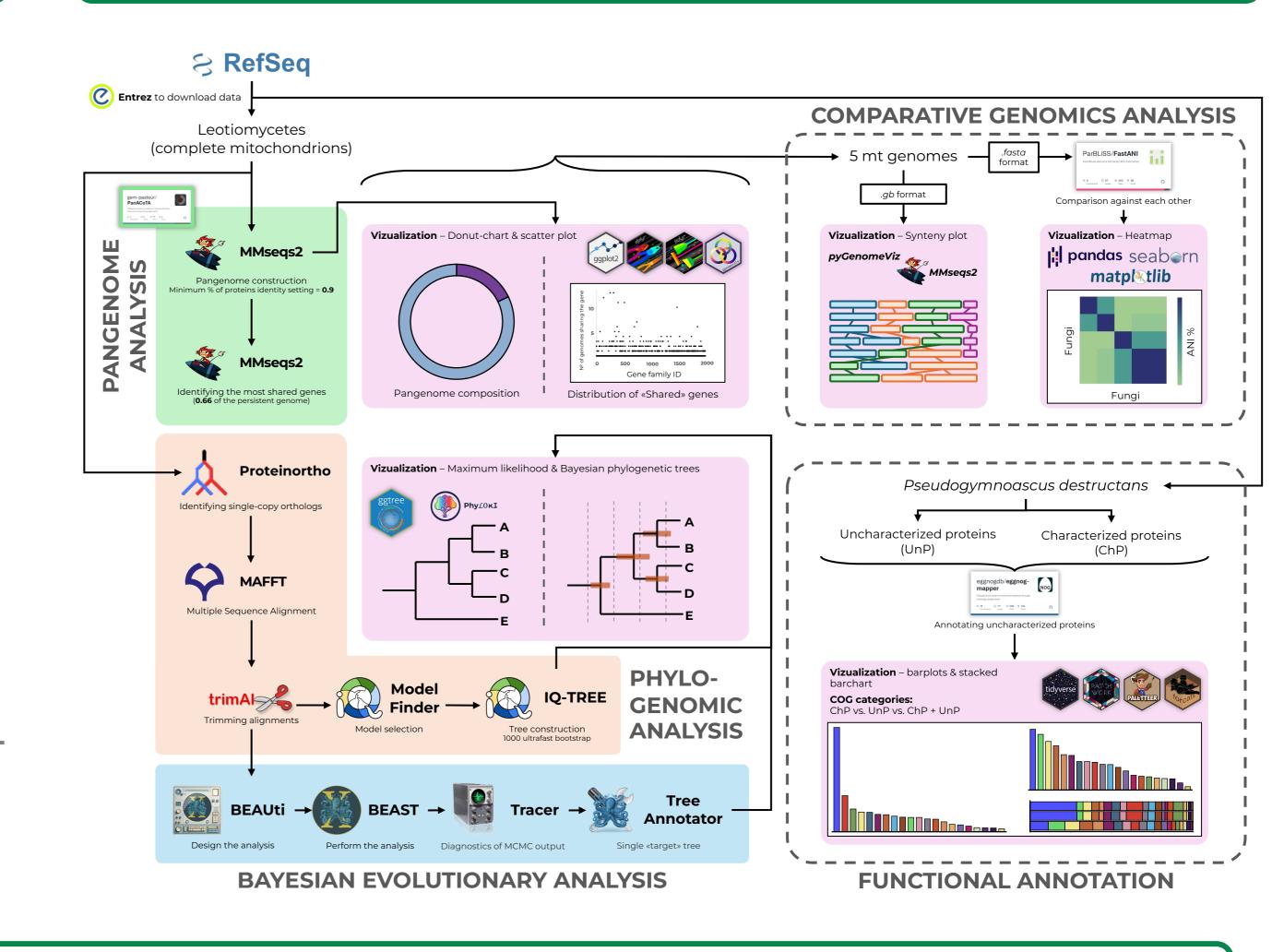
North America is the most affected by WNS region There are studies indicating that WNS came to America from Europe European strain of *Pd* is not pathogenic

But there were little studies on the genome of Pd Its genome was a mystery:

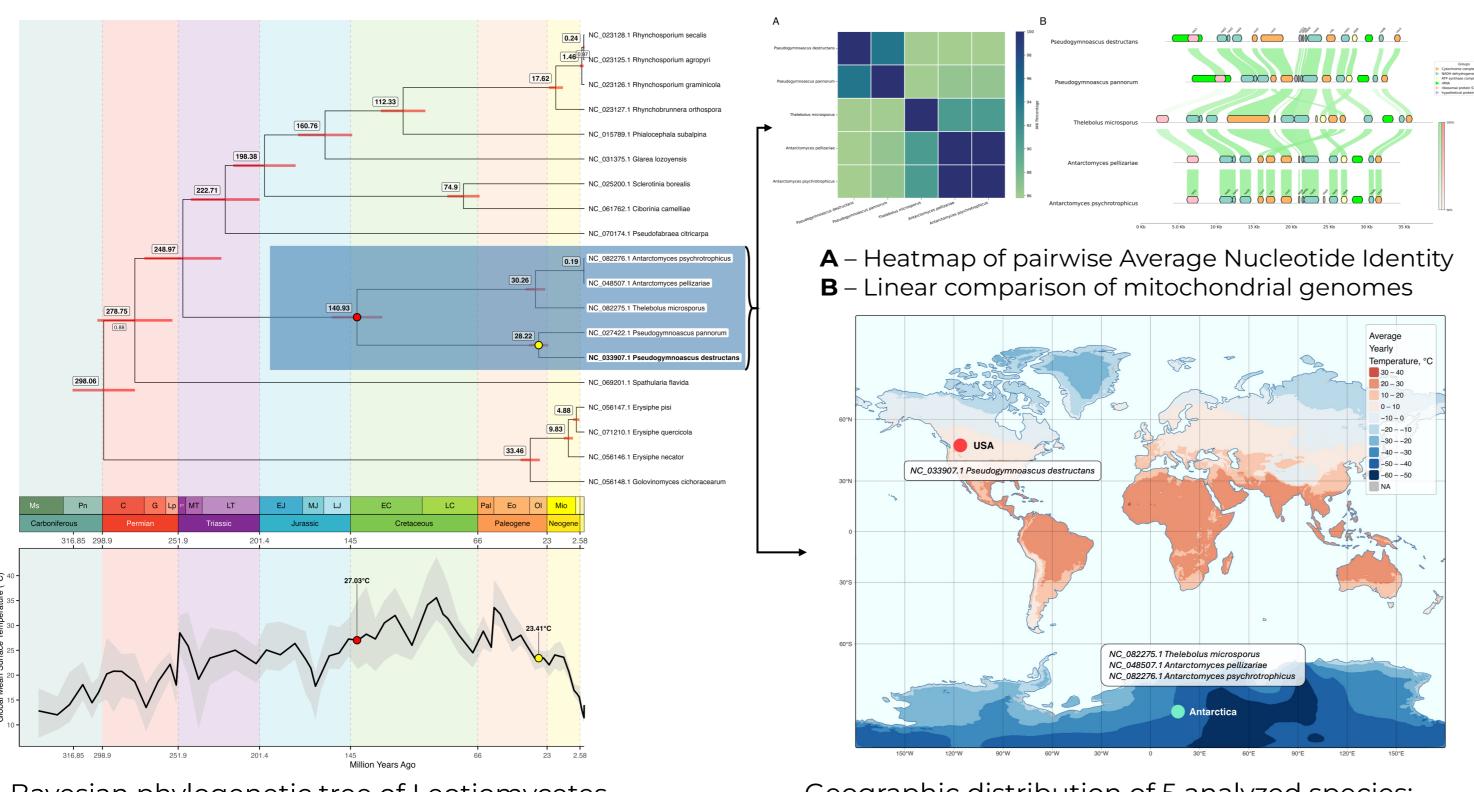
- ~ 20k genes marked "uncharacterized" in RefSeq
- There were no comparative genomic studies
- What is Pd? Where does it come from?
- Does it have non-pathogenic relatives (except for P. pannorum)?

Beimforde et al. ²⁰¹⁴ :	Aguileta et al. ²⁰¹⁴ :	Judd et al. ²⁰²⁴ :
Leotiomycetes and Sordariomycetes are brothers! They are coupled with equivalent fossil- calibrated divergence times!	Sordariomycetes have 0.01 substitutions per site per million years!	Take the retrospective open data on Global Mean Surface Temperature to complement your study!

Materials & Methods

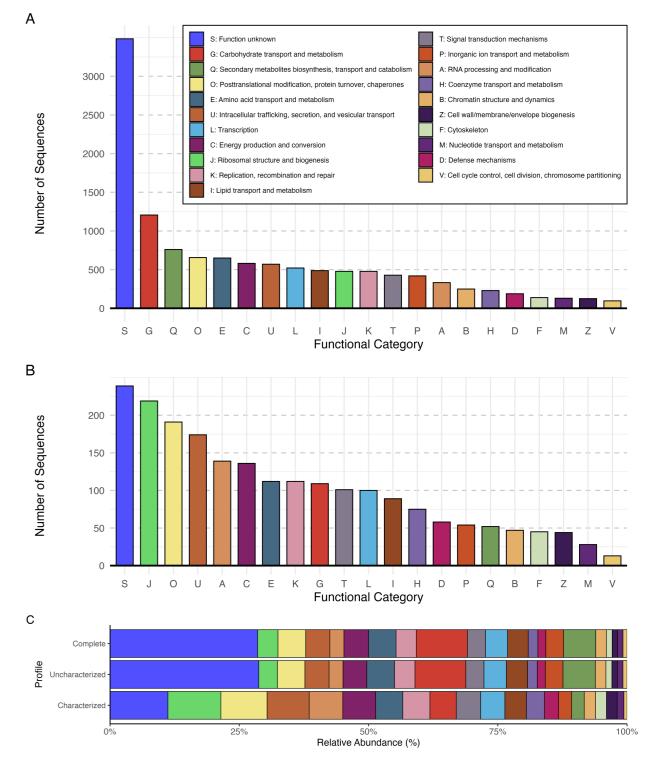


Main Results



Bayesian phylogenetic tree of Leotiomycetes mitochondrial genomes with estimated divergence times

Geographic distribution of 5 analyzed species: locations of fungi in relation to global mean annual temperature



A – complete Pd profile (UnP + ChP)

B – "characterized" Pd profile (ChP)

C – comparison: Complete vs. UnP vs. ChP

Outcomes

- Bayesian dating: Pd-P. pannorum split = 28.2 Million years ago (MYA);
 5-species MRCA = 140.9 MYA; Leotiomycetes crown = 298 MYA.
 Comparative genomics: Pd mito genome 32.2 kb, 94.4 % ANI to Pp, gene content and order largely conserved; Antarctic relatives retain full collinearity, indicating evolutionary stability in psychrophilic lineages.
- Geographical signal: Pd isolates = North America; closest relatives = Antarctic
- Functional expansion: Re-annotation boosts known Pd protein functions from 2 137 to 12 206; carbohydrate-metabolism genes now 1 206 (+1 097); secondary-metabolite genes 760 (+708).

Supplementary



Full textJournal of Fungi



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