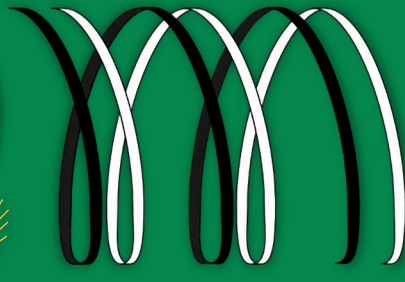


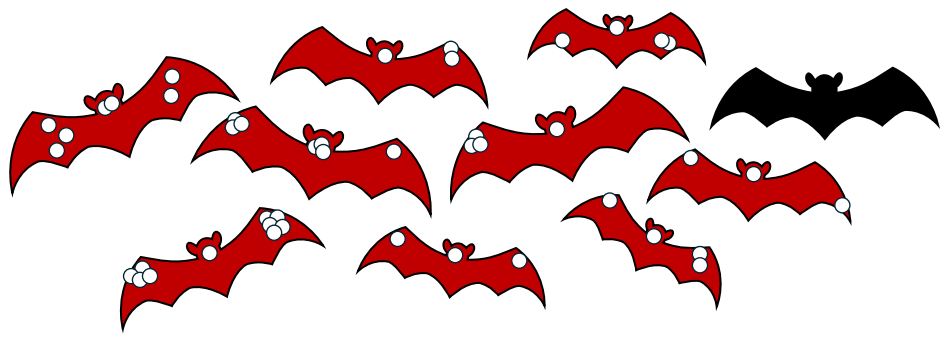
# Phylogenomic and Functional Reassessment of *Pseudogymnoascus destructans* Across Mitochondrial and Nuclear Scales



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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 contagious

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

- 10k genes marked "uncharacterized" in RefSeq
- There were no comparative genomic studies
- What is *Pd*? Where does it come from?
- Does it have non-contagious relatives (except for *P. pannorum*)?

Beimforde et al. 2014:

Leotiomycetes and Sordariomycetes are brothers! They are coupled with equivalent fossil-calibrated divergence times!

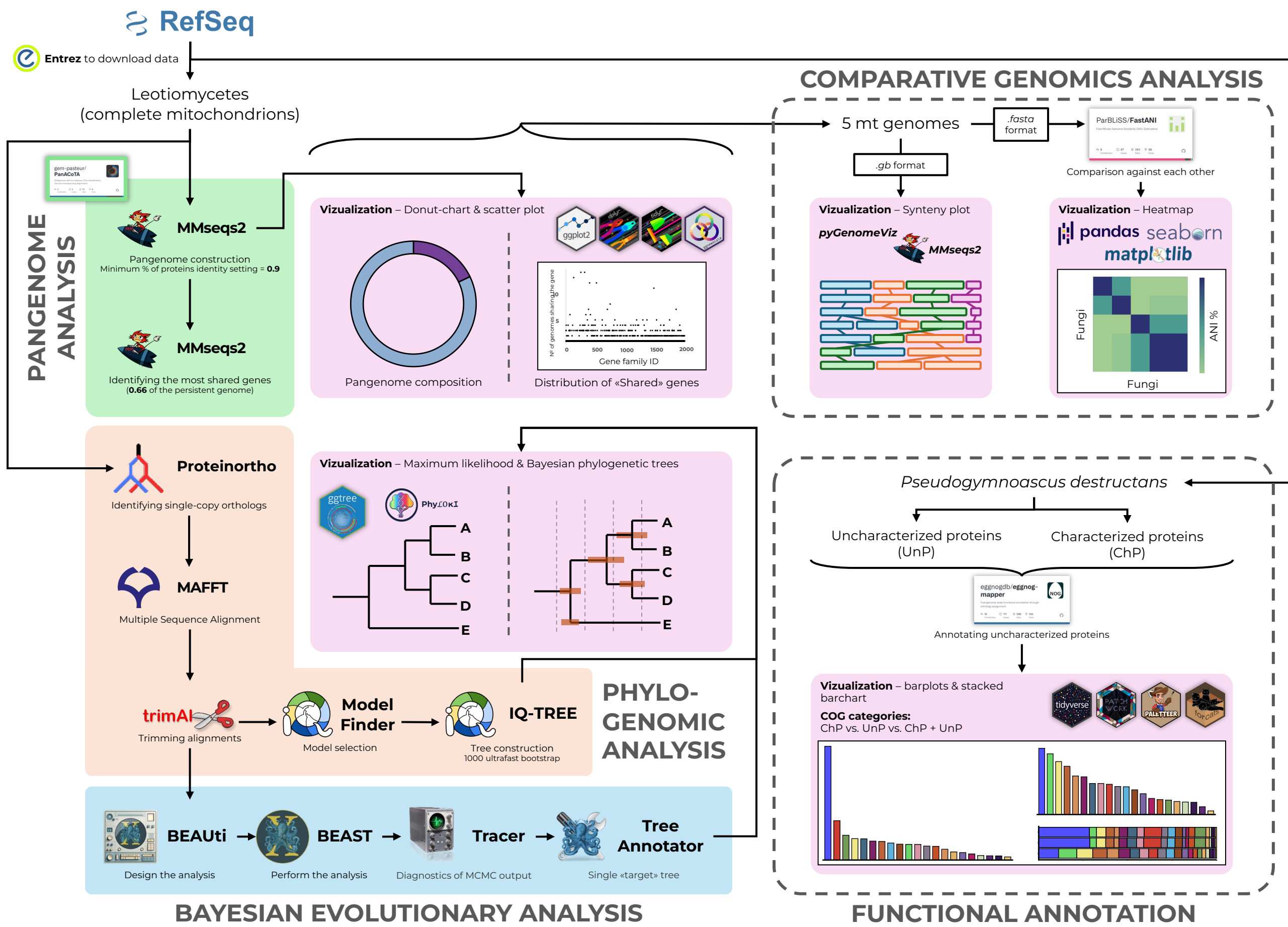
Aguileta et al. 2014:

Sordariomycetes have 0.01 substitutions per site per million years!

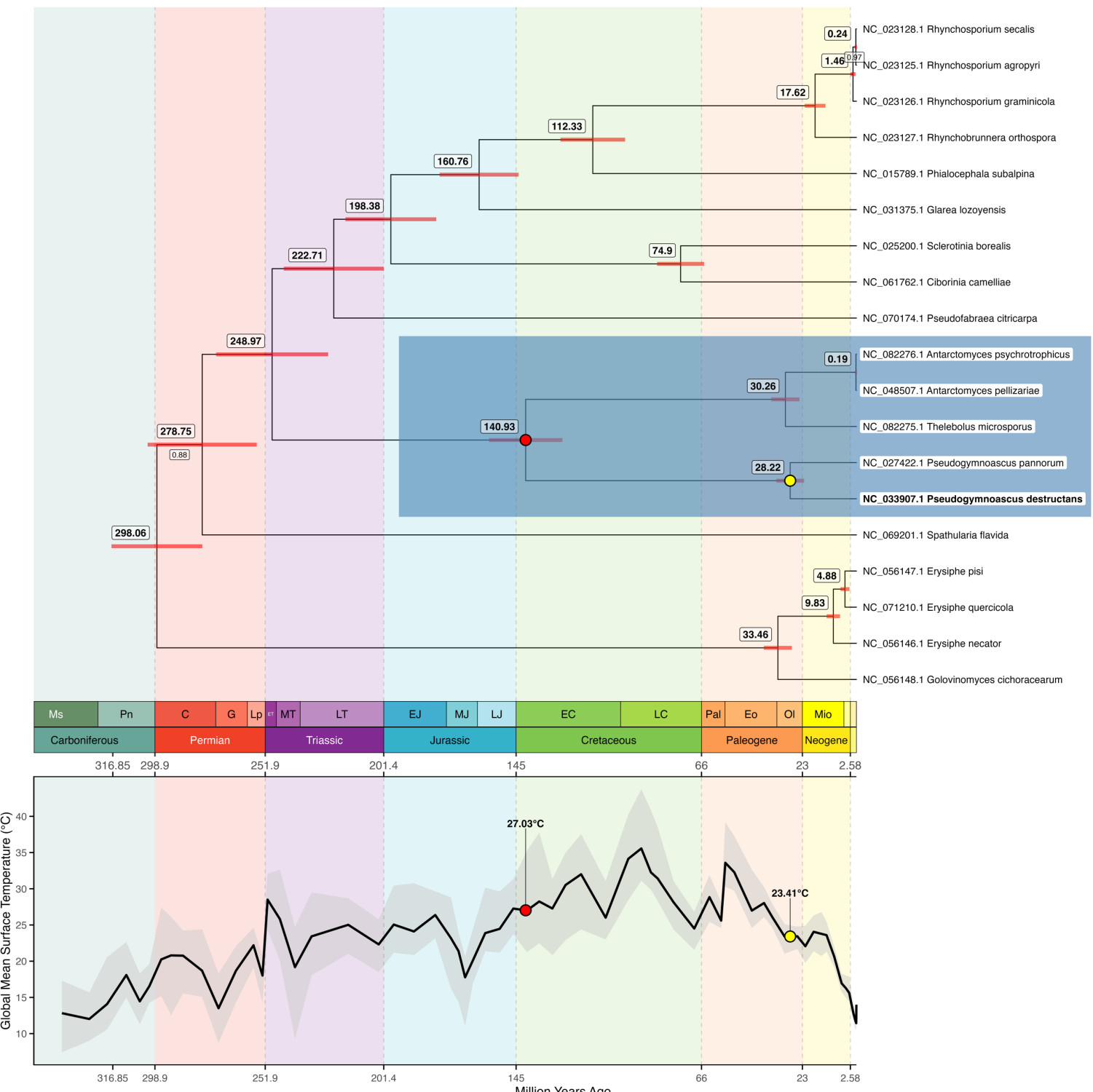
Judd et al. 2024:

Take the retrospective open data on Global Mean Surface Temperature to complement your study!

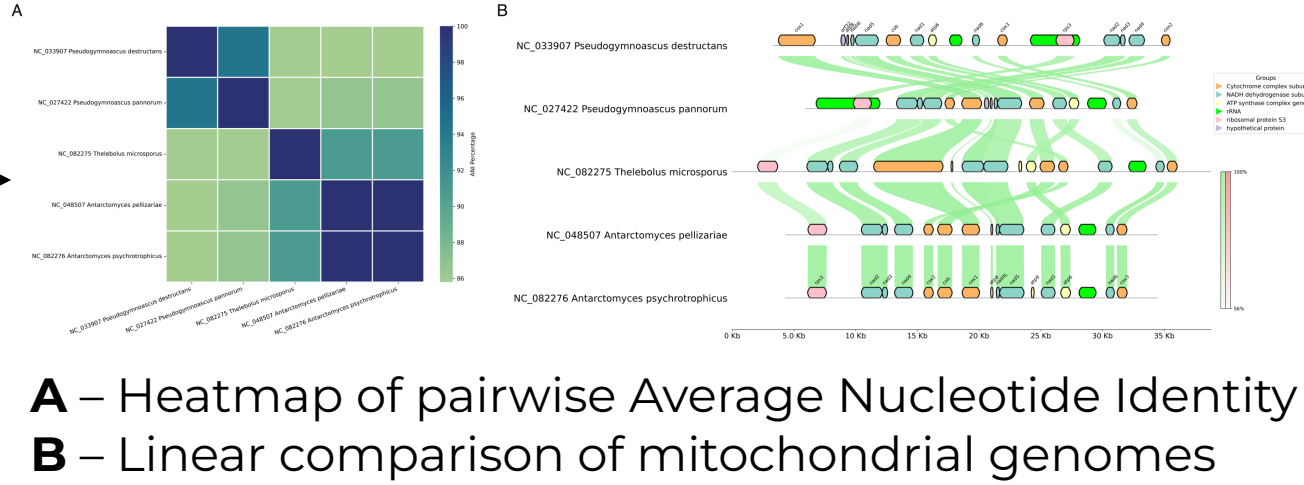
## Materials & Methods



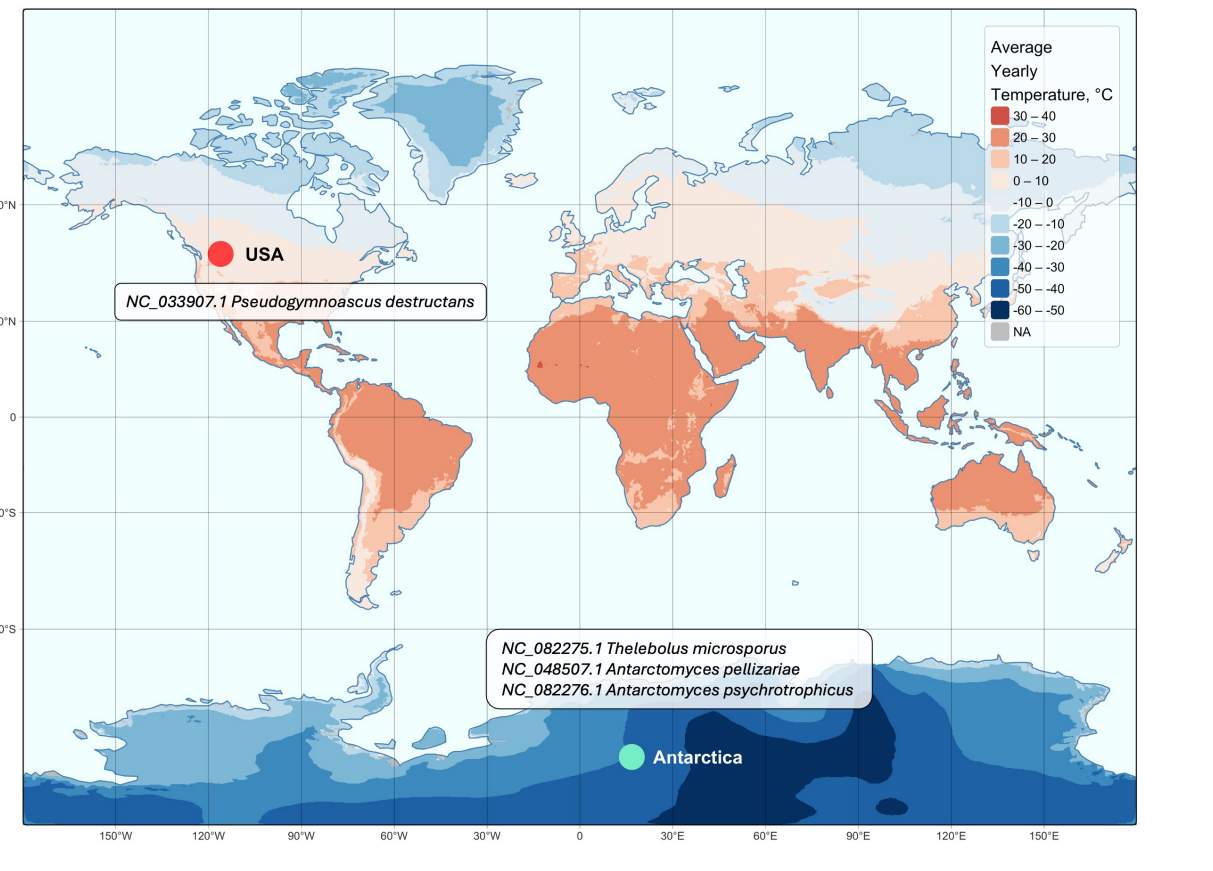
## Main Results



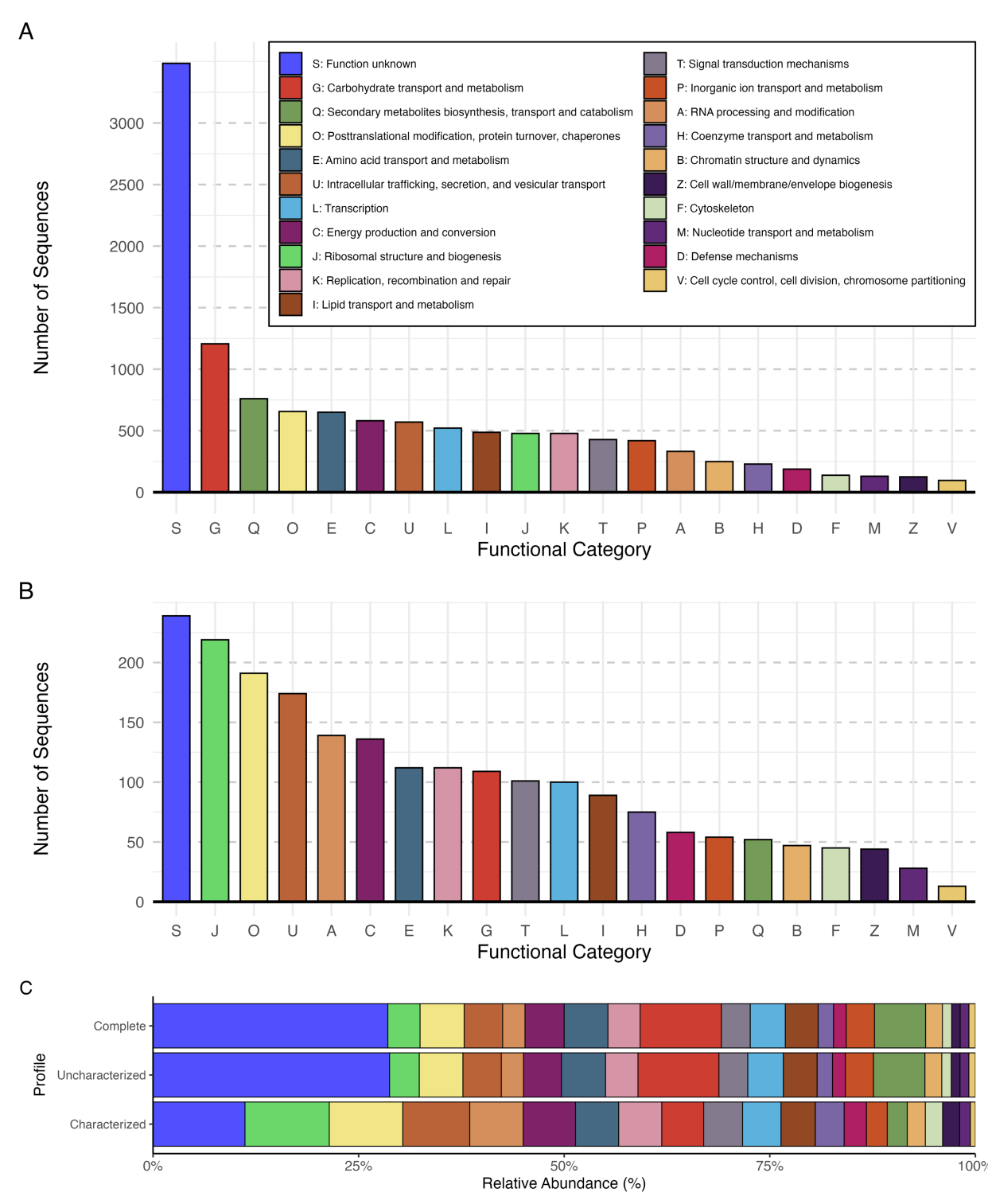
Bayesian phylogenetic tree of Leotiomycetes mitochondrial genomes with estimated divergence times



A – Heatmap of pairwise Average Nucleotide Identity  
B – Linear comparison of mitochondrial genomes



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*, but **shows complete gene-order reshuffling**; 3 Antarctic relatives retain collinearity.
- **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).

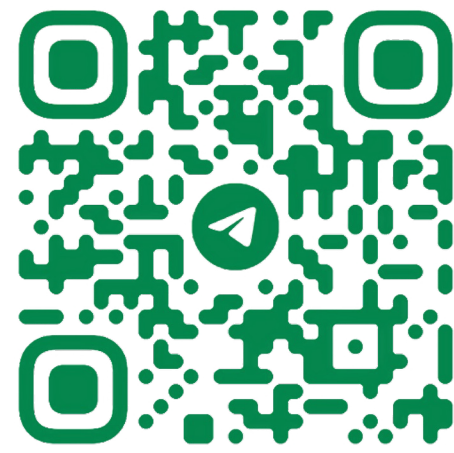
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## Supplementary



GitHub

Lab journal



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Contacts

Telegram