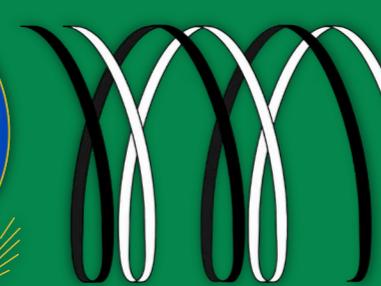


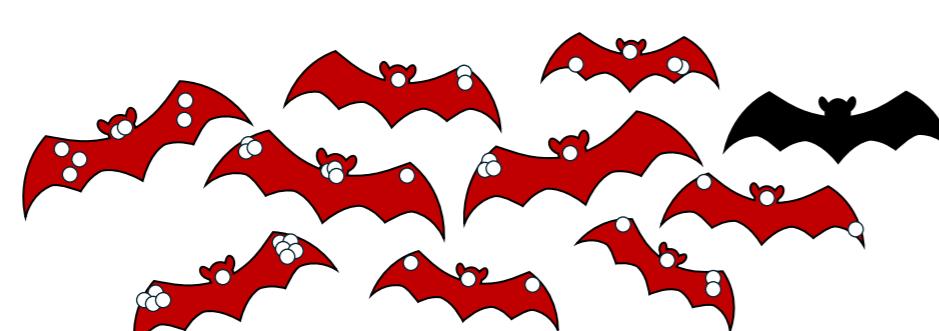
Phylogenomic and Functional Reassessment of *Pseudogymnoascus destructans* Across Mitochondrial and Nuclear Scales



MCCMB 2025

Ilia Popov, Alexey Ermakov, Igor Popov
Don State Technical University, Rostov-on-Don, Russia

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;

Aguileta et al. 2014;

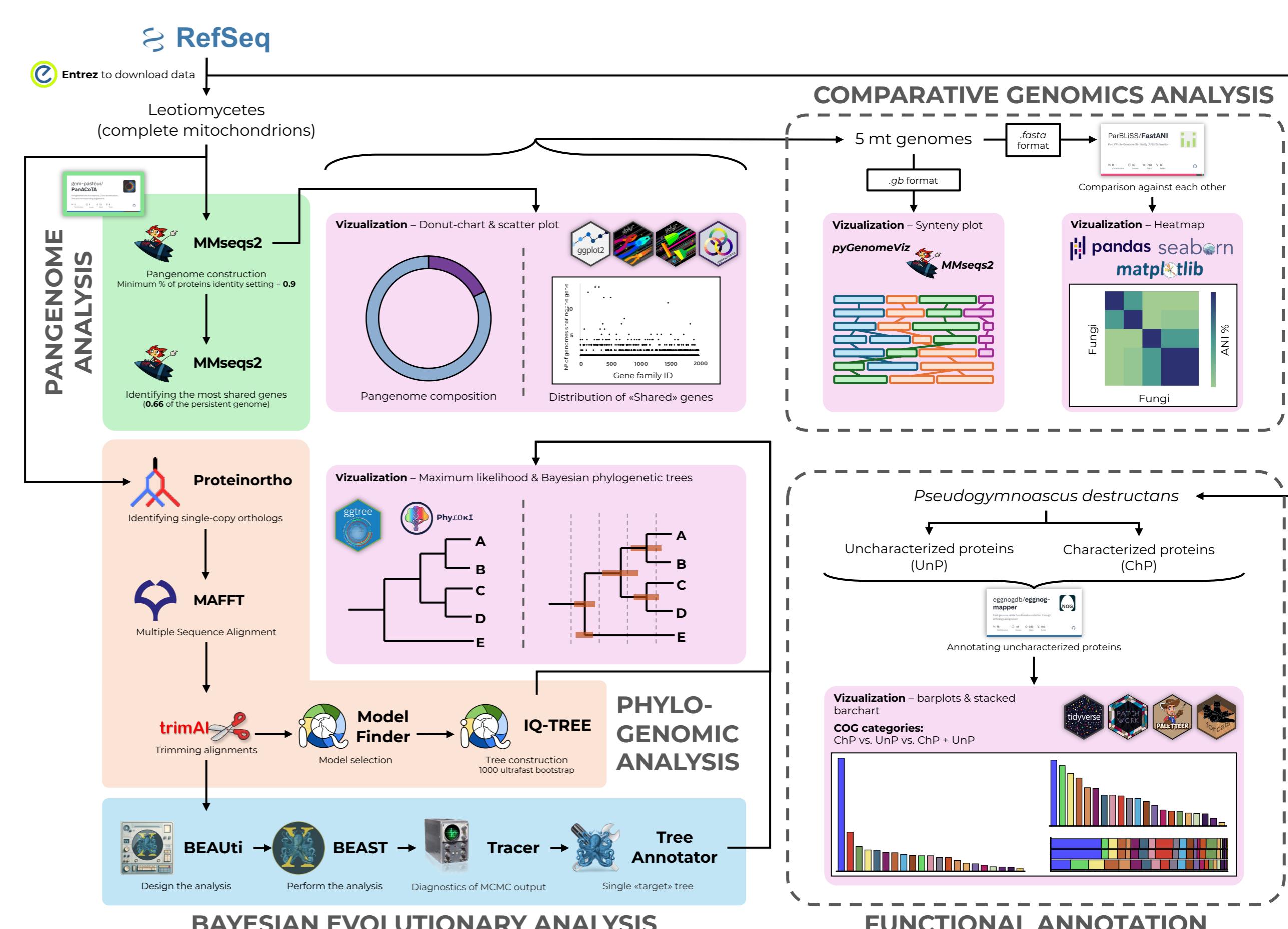
Judd et al. 2024:

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

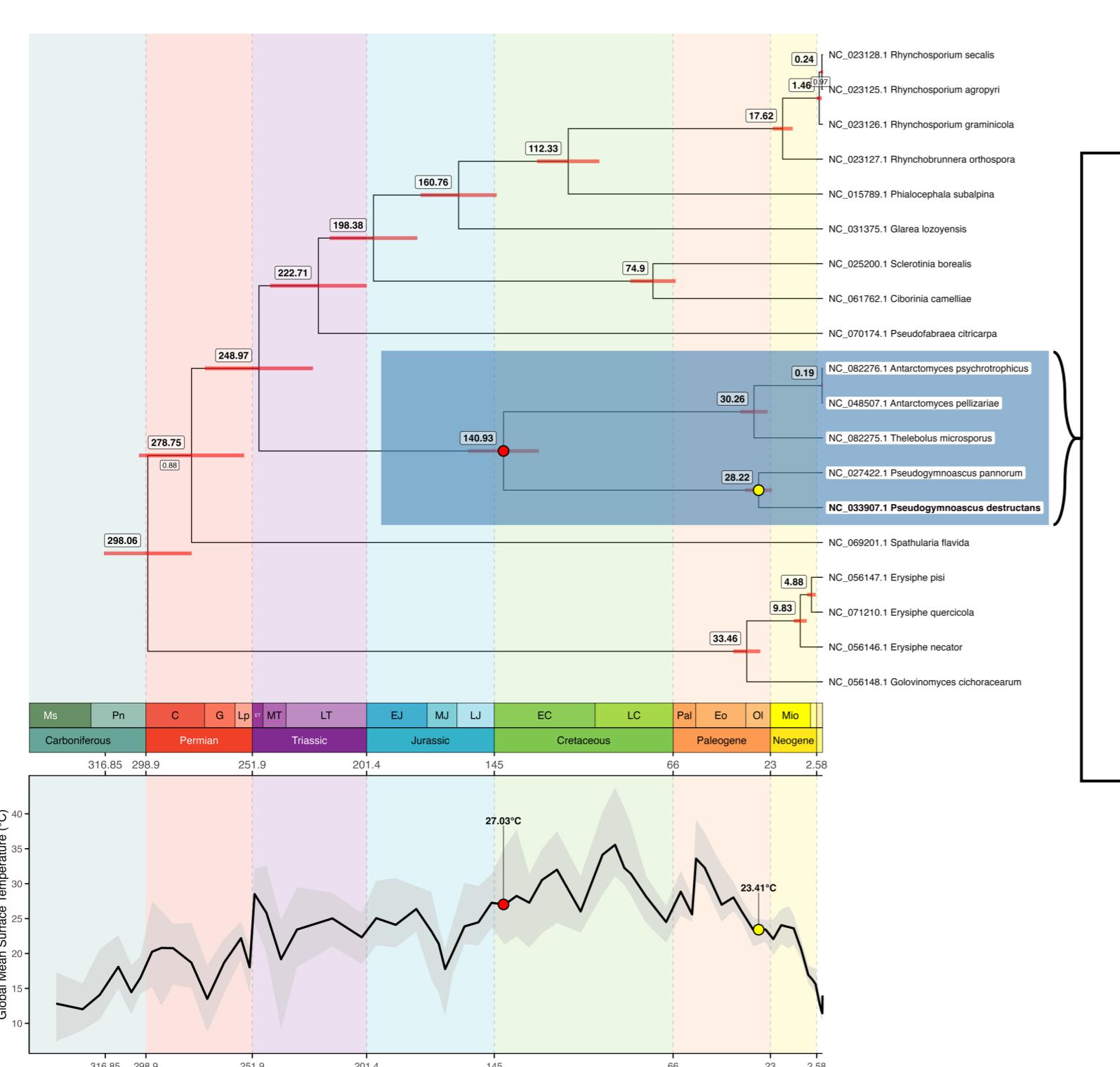
Sordariomycetes have 0.01 substitutions per site per million years!

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

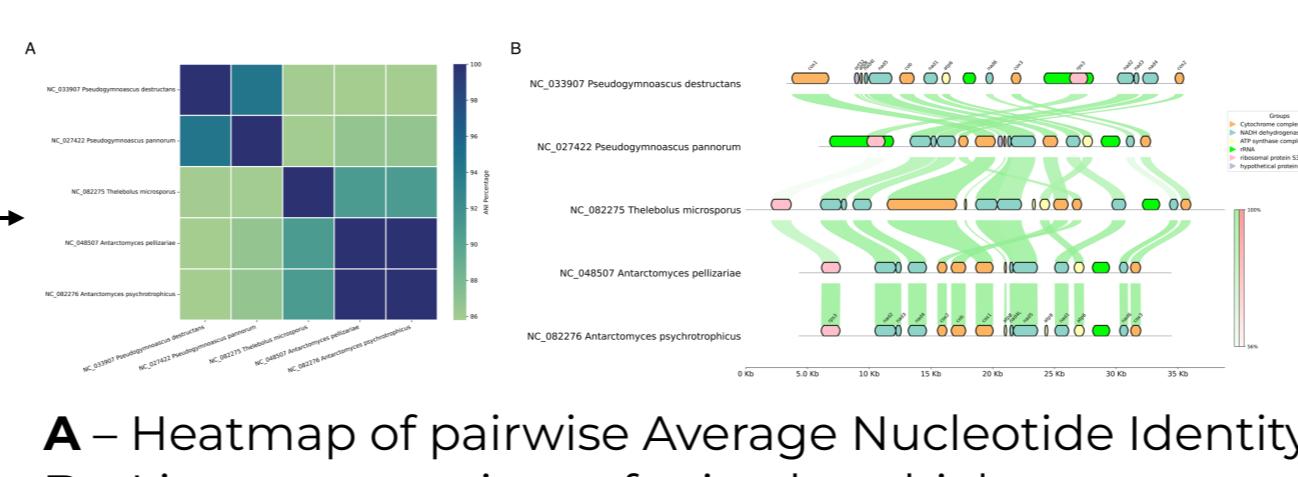
Materials & Methods



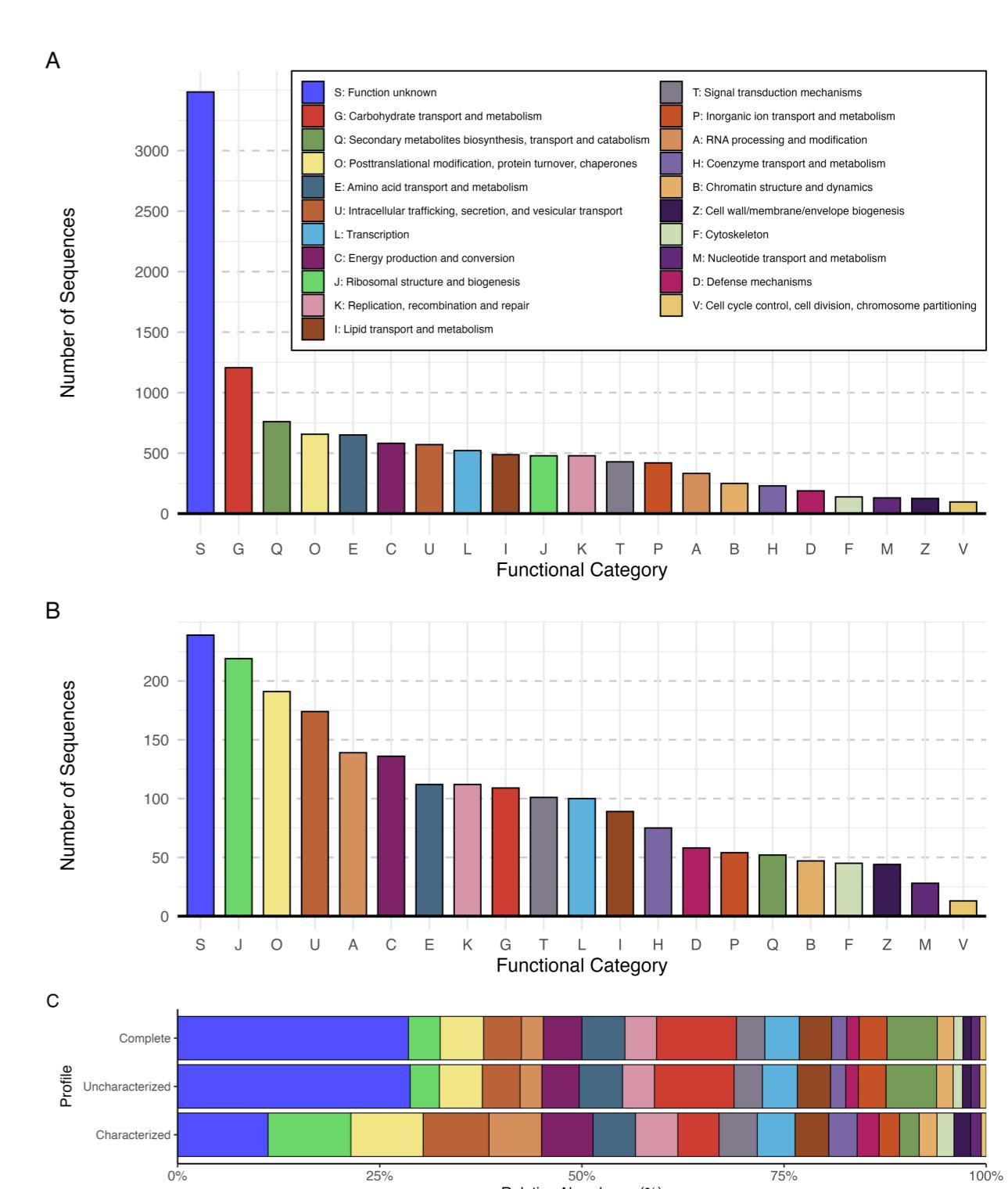
Main Results



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, 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).

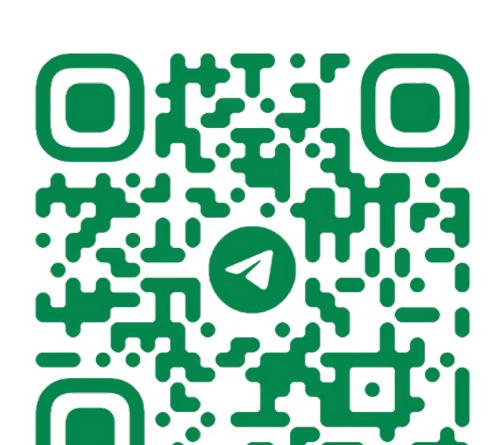
Funding: The study was supported by the Russian Science Foundation (project 25-24-00351)

Supplementary



GitHub

Lab journal



Contacts

Telegram

@ILYA_POPOV