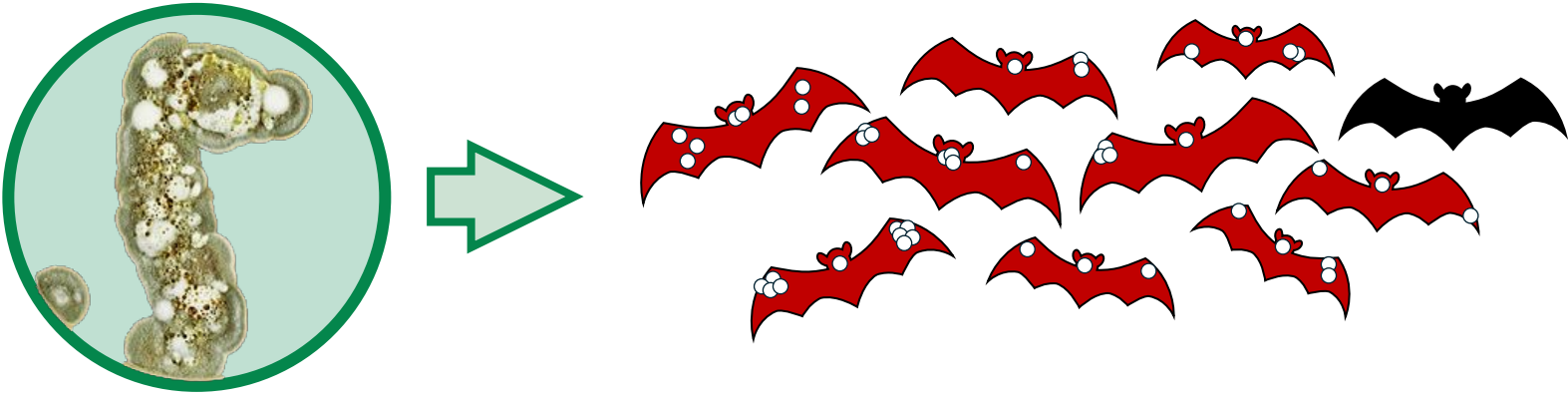


Introduction



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

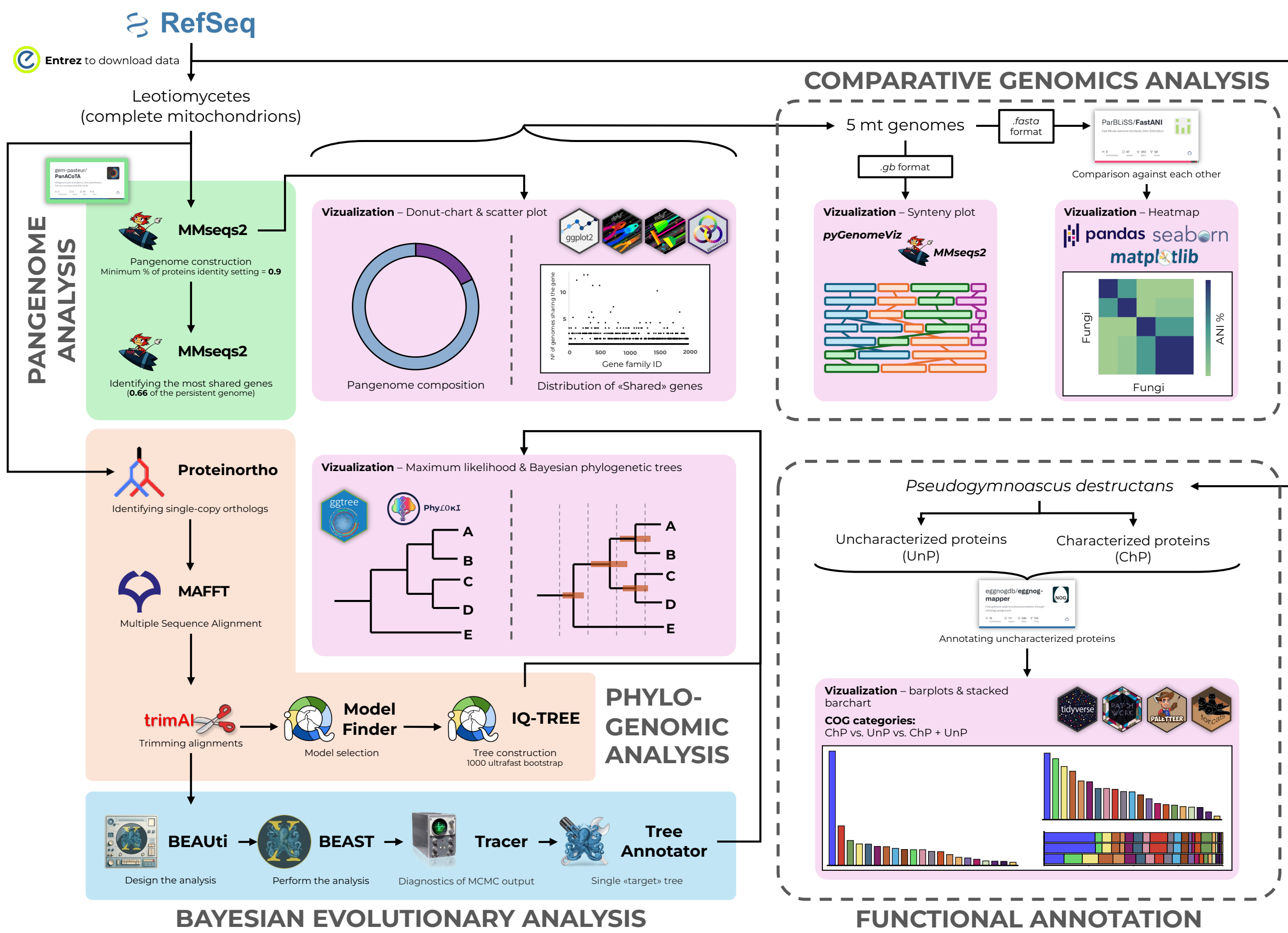


North America is the most affected by WNS region
There are studies indicating that WNS came to America from Europe
European strain of *Pd* is not pathogenic

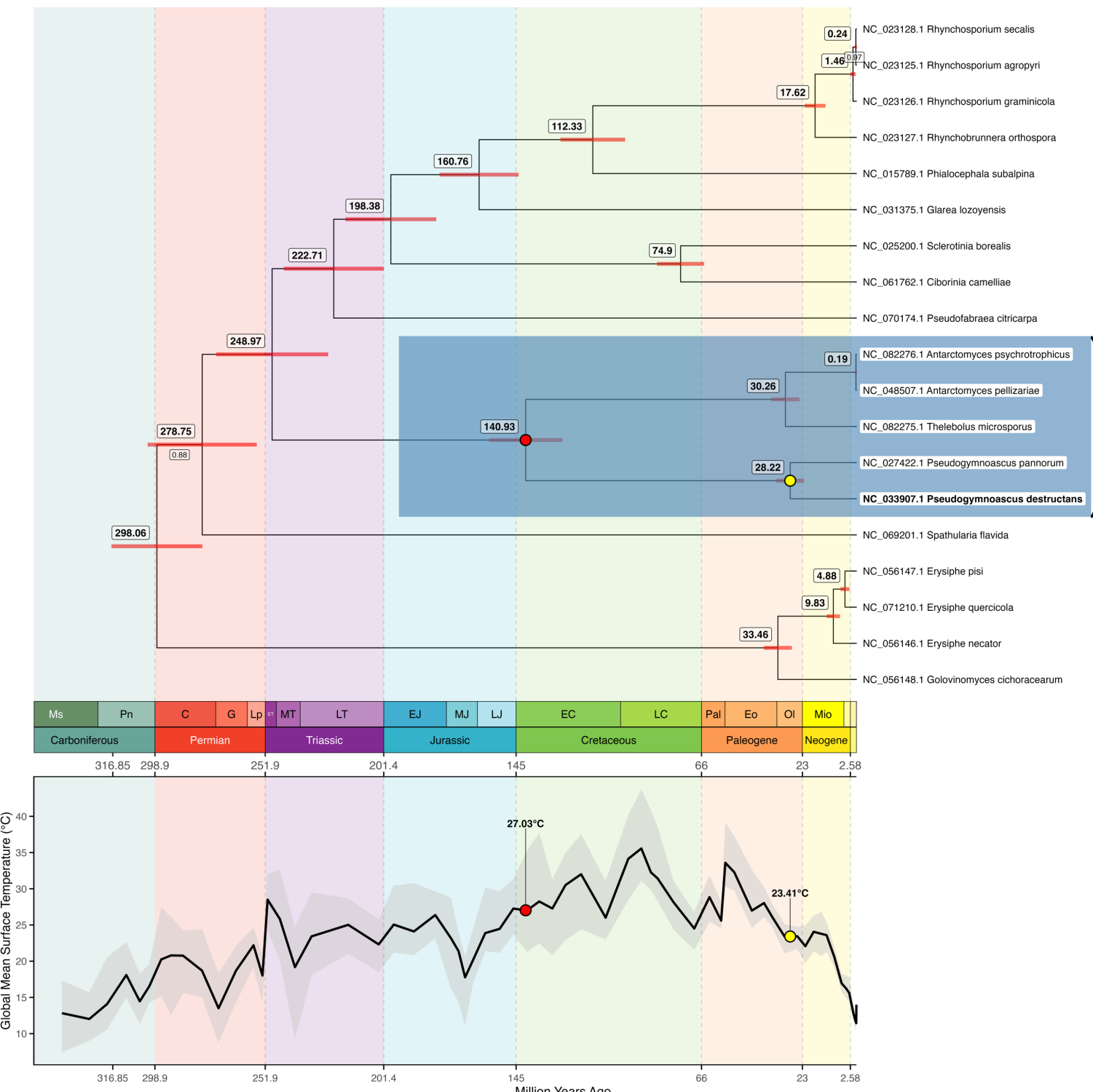
- But there were little studies on the genome of Pd
Its genome was a mystery:
- ~20k genes marked "uncharacterized" in RefSeq
 - There were no comparative genomic studies
 - What is Pd? Where does it come from?
 - Does it have non-pathogenic relatives (except for *P. pannorum*)?

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!

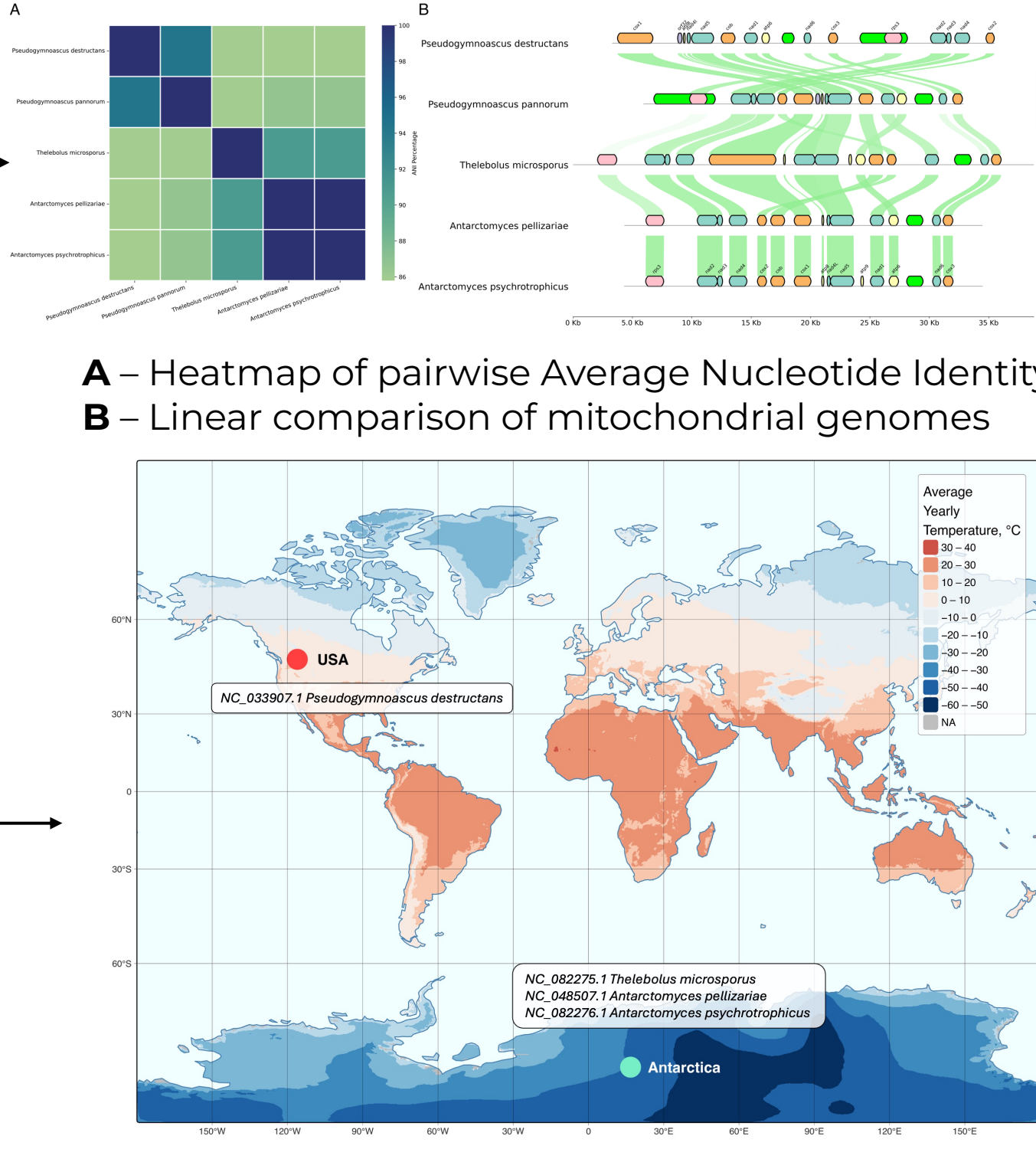
Materials & Methods



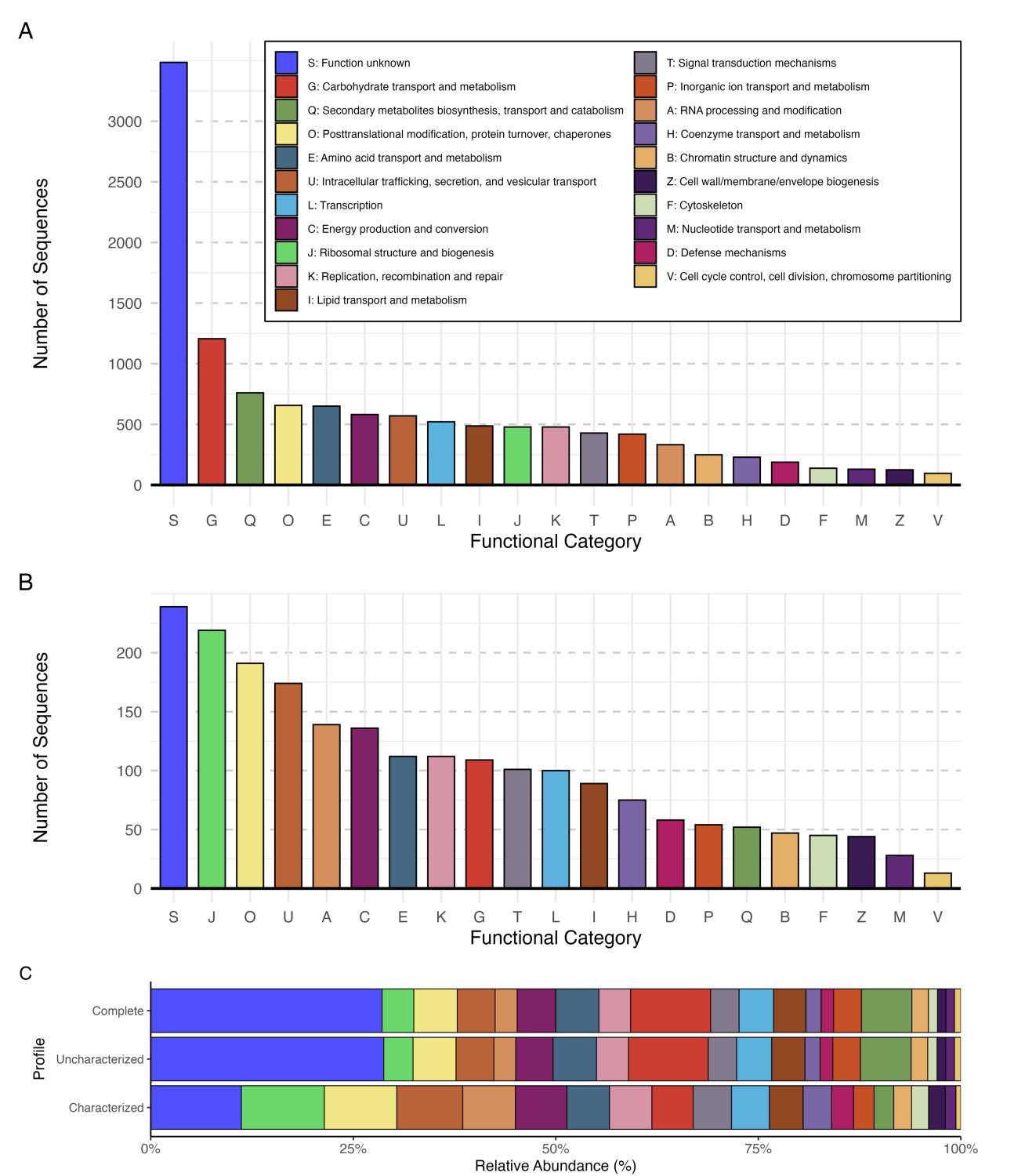
Main Results



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, 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



Full text
Journal of Fungi



GitHub
Lab journal



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