Streptomyces albidoflavus SM254: Genomic markers for counteracting White-Nose Syndrome in bats

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Introduction

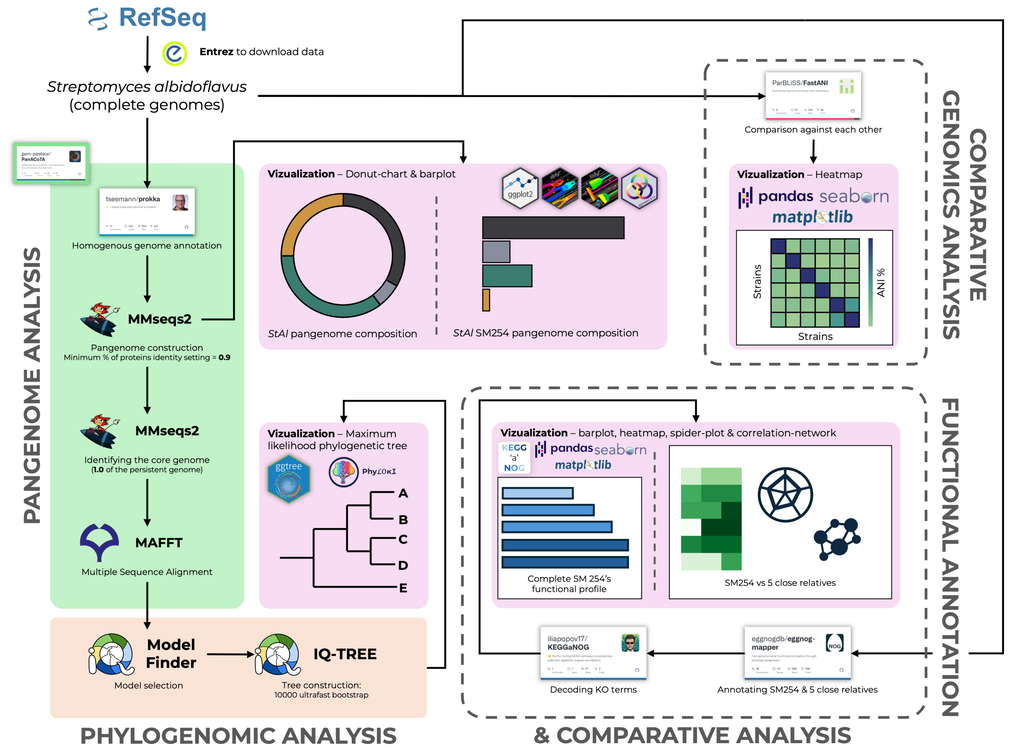
White-Nose Syndrome (WNS; caused by *P. destructans*) is the reason of 90% mortality among hibernating bats every year

- **North America** is the region most affected by **WNS**.
- **Bats** are major nocturnal insectivores.
- Their **population collapse** disrupts natural pest control.
- **Farmers** compensate by using more **synthetic insecticides**.
- A recent study (Frank, 2024, *Science*) quantified these effects:
  - In counties with severe bat die-offs, **insecticide use rose by ~31%**.
  - In the same areas, [human] **infant mortality increased by ~7.9%** relative to unaffected regions.

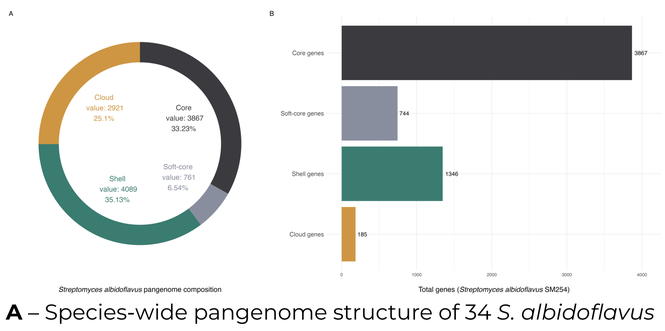
WHAT TO DO?

- Badalamenti et al. (2016) isolated a ***Streptomyces albidoflavus* SM254** from copper-rich subsurface fluids in the Soudan Iron Mine (Minnesota, USA)
- Researchers claimed – the strain shows **antagonistic activity** against ***P. destructans***!
- The original study **does not provide detailed mechanistic data** on how SM254 interacts with or inhibit *P. destructans*, leaving room for experimental validation and functional assays.

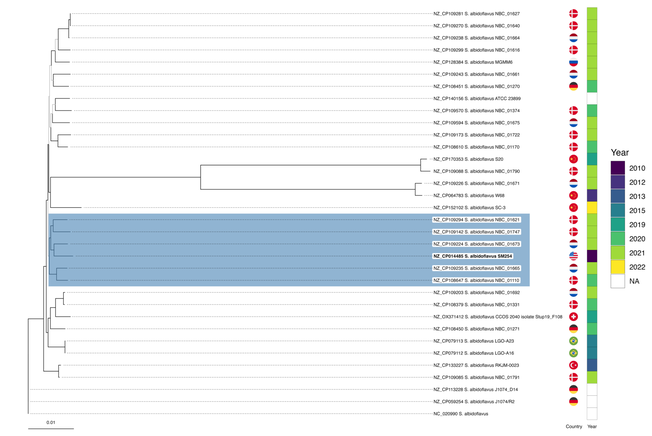
Materials & Methods



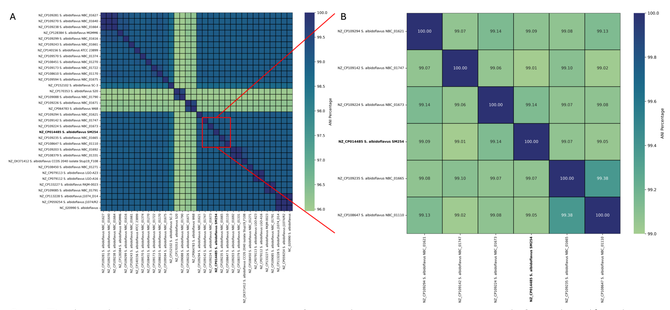
Main Results



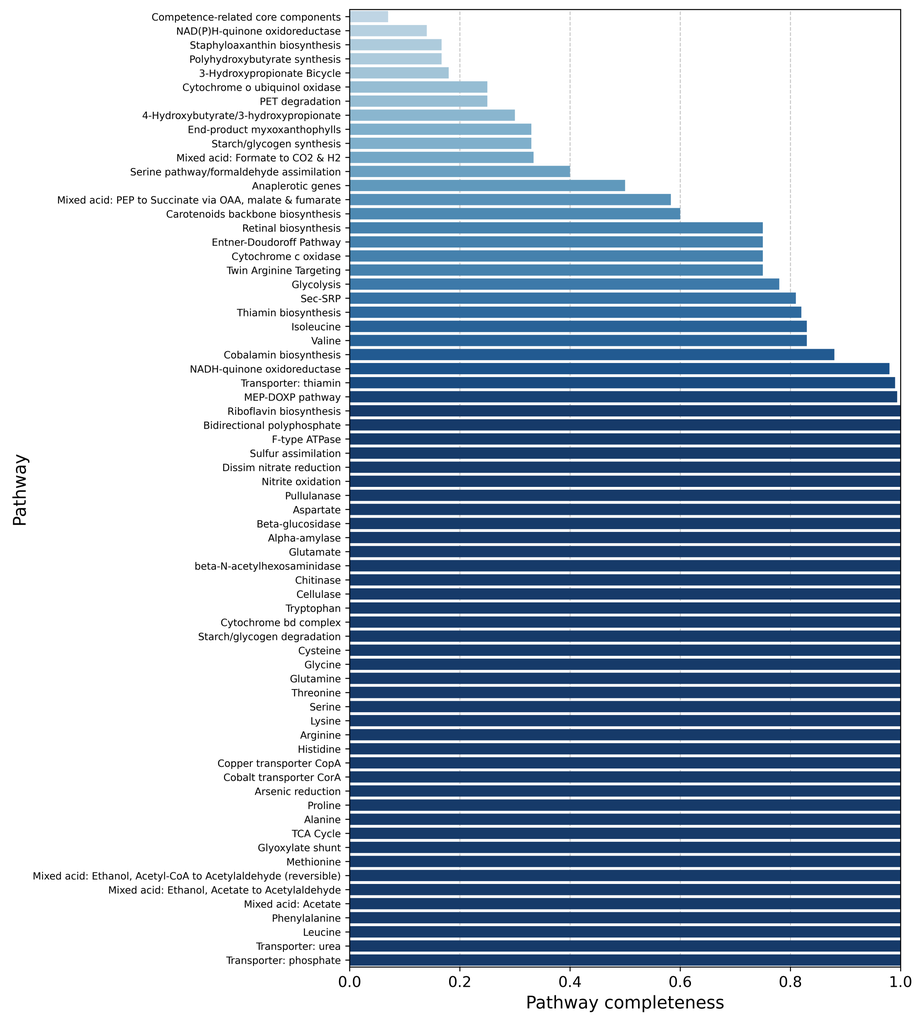
A – Species-wide pangenome structure of 34 *S. albidoflavus* genomes
B – Gene family distribution in the SM254 strain genome



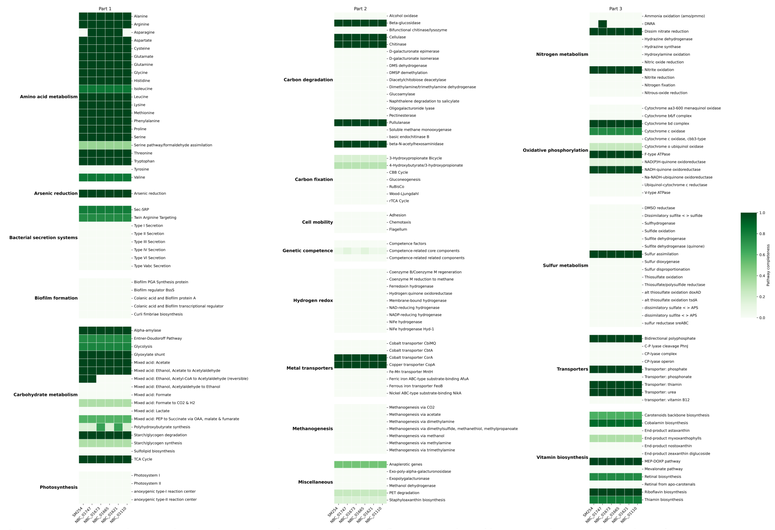
Phylogenomic structure of *S. albidoflavus*.
Maximum-likelihood tree (TVM+F+R5 model); SM254 clade in blue, branch tip bolded.
Branches with bootstrap <70 gray, ≥70 black.



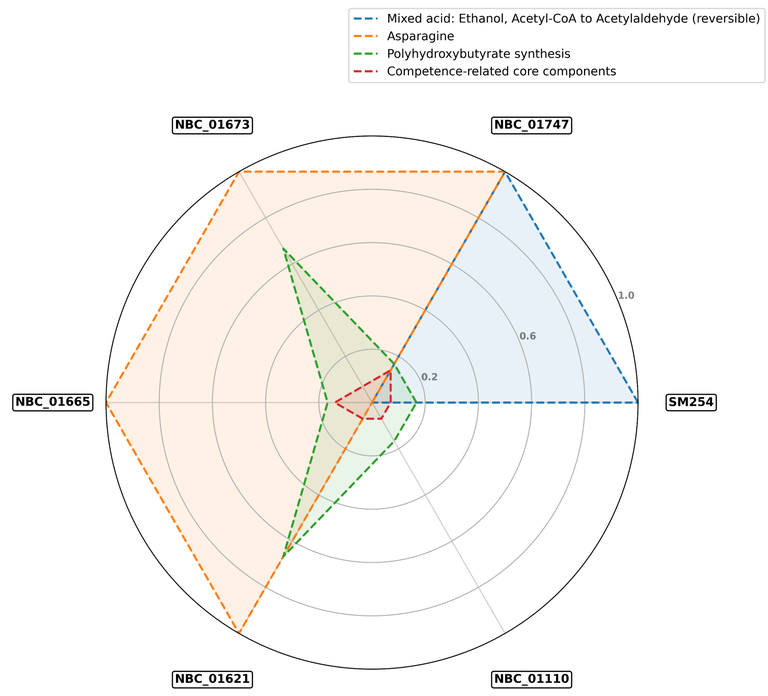
A – Pairwise ANI heatmap showing genome-wide similarity among 34 *S. albidoflavus* strains.
B – Subset highlighting ANI values for SM254 and its six closest relatives.



Functional pathway completeness in *S. albidoflavus* SM254. Barplot showing the KEGG-based completeness of 74 annotated metabolic pathways with non-zero completeness values, ranging from partial to fully complete (0 < completeness ≤ 1)



Heatmap showing completeness of metabolic and ecological pathways across SM254 and its five closest *S. albidoflavus* relatives.



Functional divergence within the SM254 clade of *S. albidoflavus*. Radar plot comparing completeness values of four KEGG pathways across SM254 and its five closest relatives.

Outcomes

- **SM254** shares > 99 % ANI with five closest *S. albidoflavus* strains but **exhibits distinct metabolic traits**.
- **Unique to SM254**: **complete** ethanol fermentation pathway & **deficiency** in asparagine biosynthesis.
  - Ethanol is known to inhibit fungal growth and mycotoxin production.
  - By depleting available asparagine in the environment, SM254 could potentially inhibit *P. destructans*.
- Does **SM254**'s unique metabolic profile make it a **specialized antagonist of *P. destructans*?** Maybe – specific inhibition mechanisms remain unknown; ***in vitro* experiments are required** for confirmation.
- **The *S. albidoflavus* species is broadly antifungal.** Multiple studies document potent activity against diverse fungal pathogens (Bautista-Crescencio et al. 2023, Giordano et al. 2024, Ma et al. 2025 etc.).
- **This study highlights SM254's genomic signatures**, revealing key biosynthetic pathways and metabolic traits. We aim to **draw the scientific community's attention** to its potential for WNS biocontrol and functional characterization.

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Supplementary

GitHub Lab Journal

Full Text Brazilian Journal of Microbiology

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