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INSTITUTE  
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ANTWERP

# Reconstituting the genus *Mycobacterium*

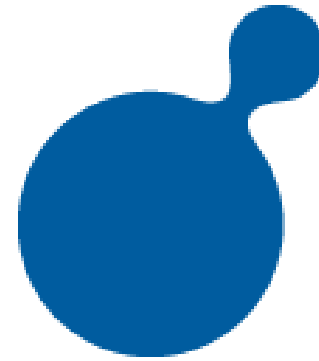
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# Authors and funding

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**BCCM**

BELGIAN  
CO-ORDINATED  
COLLECTIONS OF  
MICRO-ORGANISMS

# Reconstituting the genus *Mycobacterium*

Conor J. Meehan<sup>1,2,\*</sup>, Roman A. Barco<sup>3</sup>, Yong-Hwee E. Loh<sup>4</sup>, Sari Cogneau<sup>1,5</sup> and Leen Rigouts<sup>1,5,6</sup>

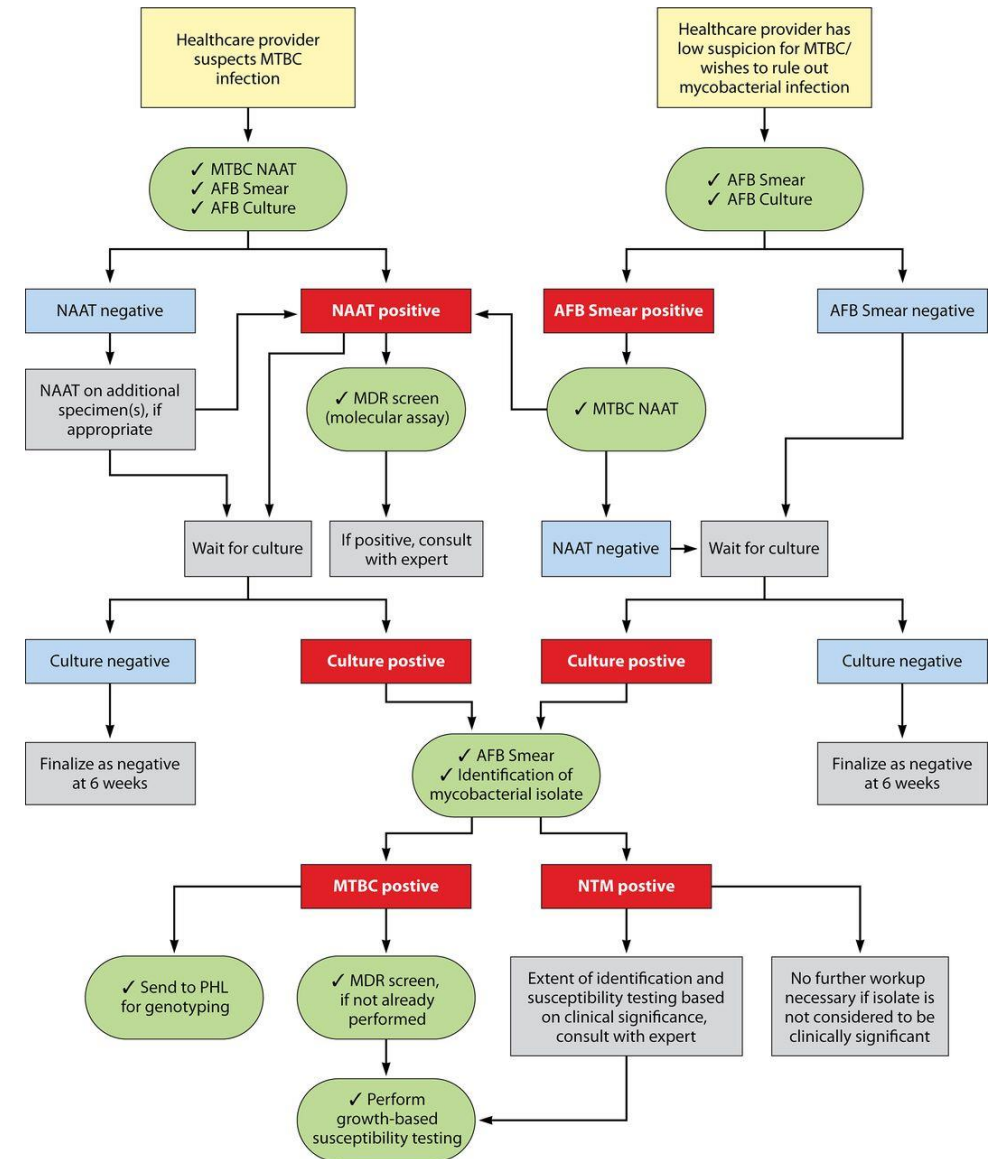
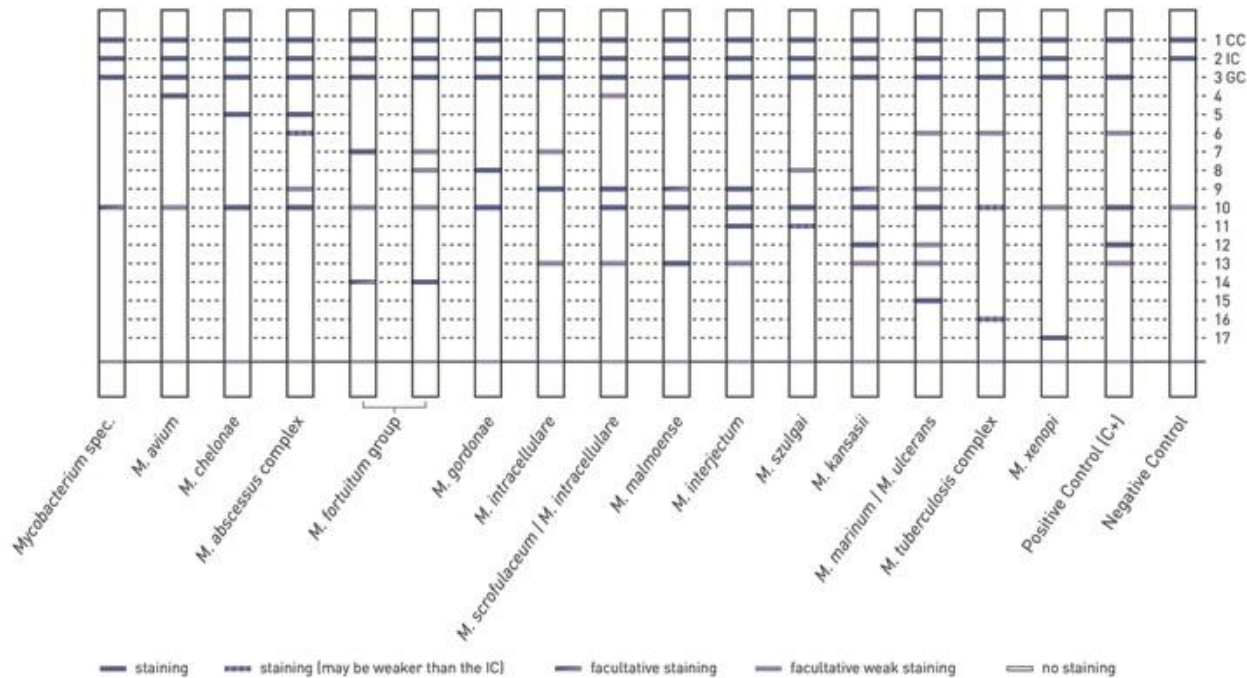
## Abstract

The definition of a genus has wide-ranging implications both in terms of binomial species names and also evolutionary relationships. In recent years, the definition of the genus *Mycobacterium* has been debated due to the proposed split of this genus into five new genera (*Mycolicibacterium*, *Mycolicibacter*, *Mycolicibacillus*, *Mycobacteroides* and an emended *Mycobacterium*). Since this group of species contains many important obligate and opportunistic pathogens, it is important that any renaming of species does not cause confusion in clinical treatment as outlined by the *nomen periculosum* rule (56a) of the Prokaryotic Code. In this study, we evaluated the proposed and original genus boundaries for the mycobacteria, to determine if the split into five genera was warranted. By combining multiple approaches for defining genus boundaries (16S rRNA gene similarity, amino acid identity index, average nucleotide identity, alignment fraction and percentage of conserved proteins) we show that the original genus *Mycobacterium* is strongly supported over the proposed five-way split. Thus, we propose that the original genus label be reapplied to all species within this group, with the proposed five genera potentially used as sub-genus complex names.

# Relevance of taxonomic definitions

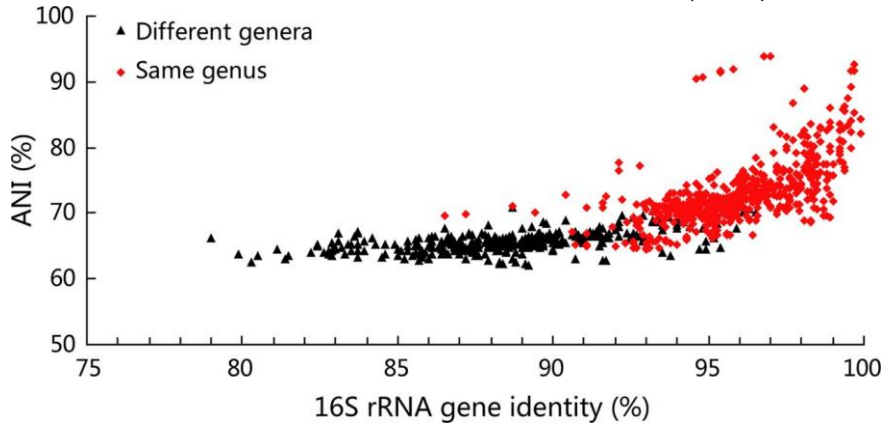


# Clinical relevance of taxonomic definitions

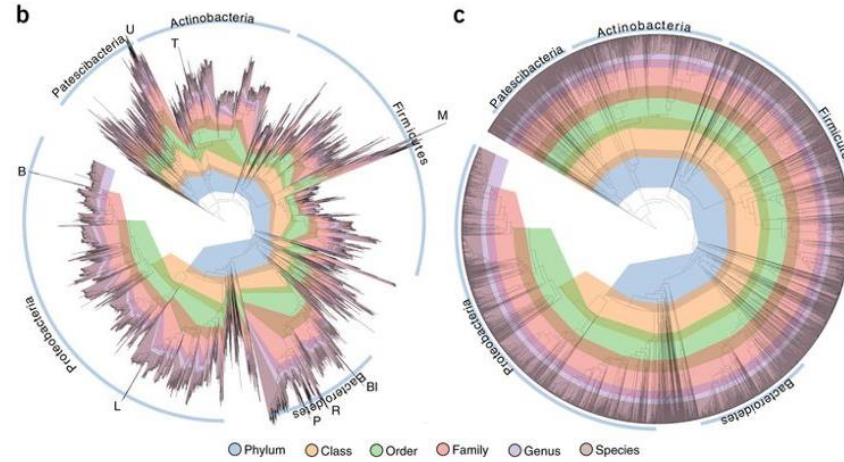


# Defining a genus

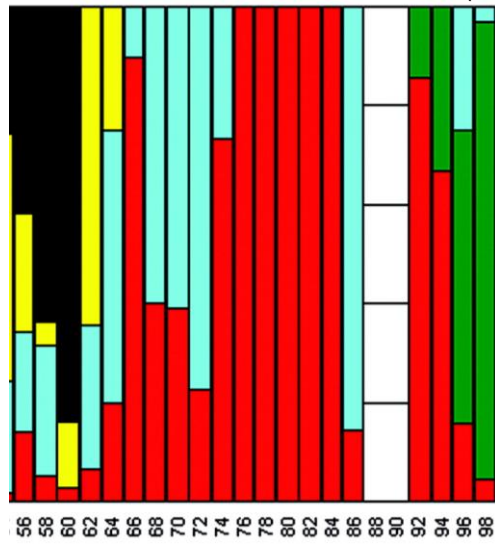
Qin et al (2014); J. Bact



Parks et al (2018); Nature Biotech

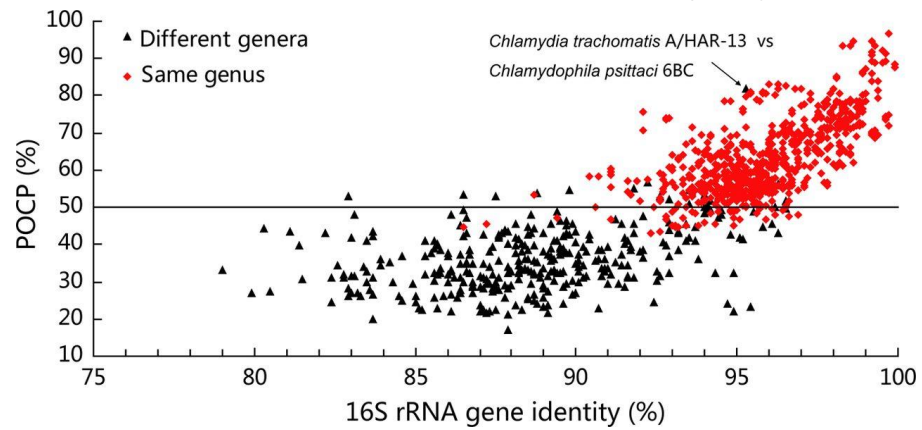


Konstantinidis et al (2005); J. Bact

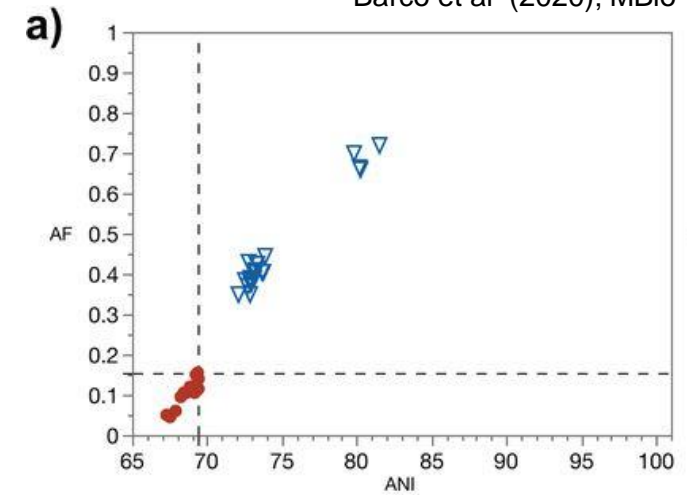


Average Amino-acid Identity (AAI) units.

Qin et al (2014); J. Bact



Barco et al (2020); MBio



# Mycobacterium genus

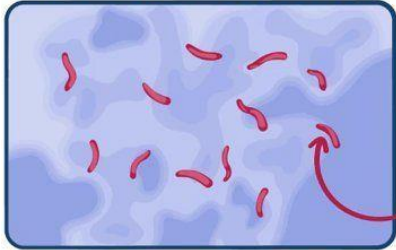


## MYCOBACTERIUM TUBERCULOSIS (TB)

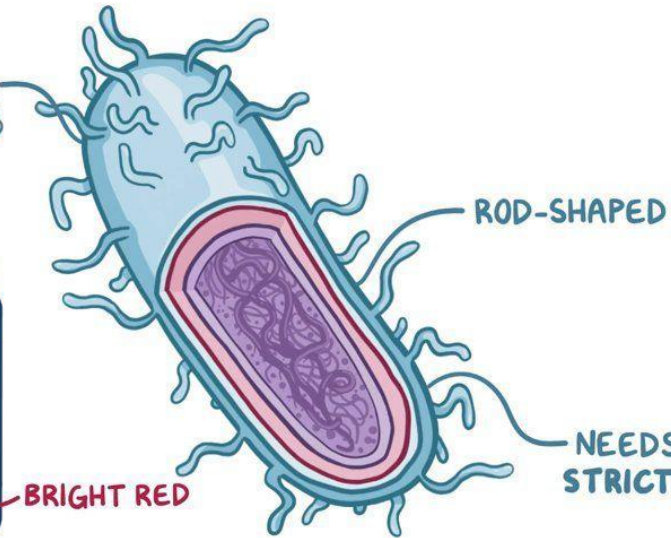
WAXY CELL WALL

- ↳ from MYCOLIC ACID
- ↳ "ACID-FAST"

ZIEHL-NEELEN STAIN

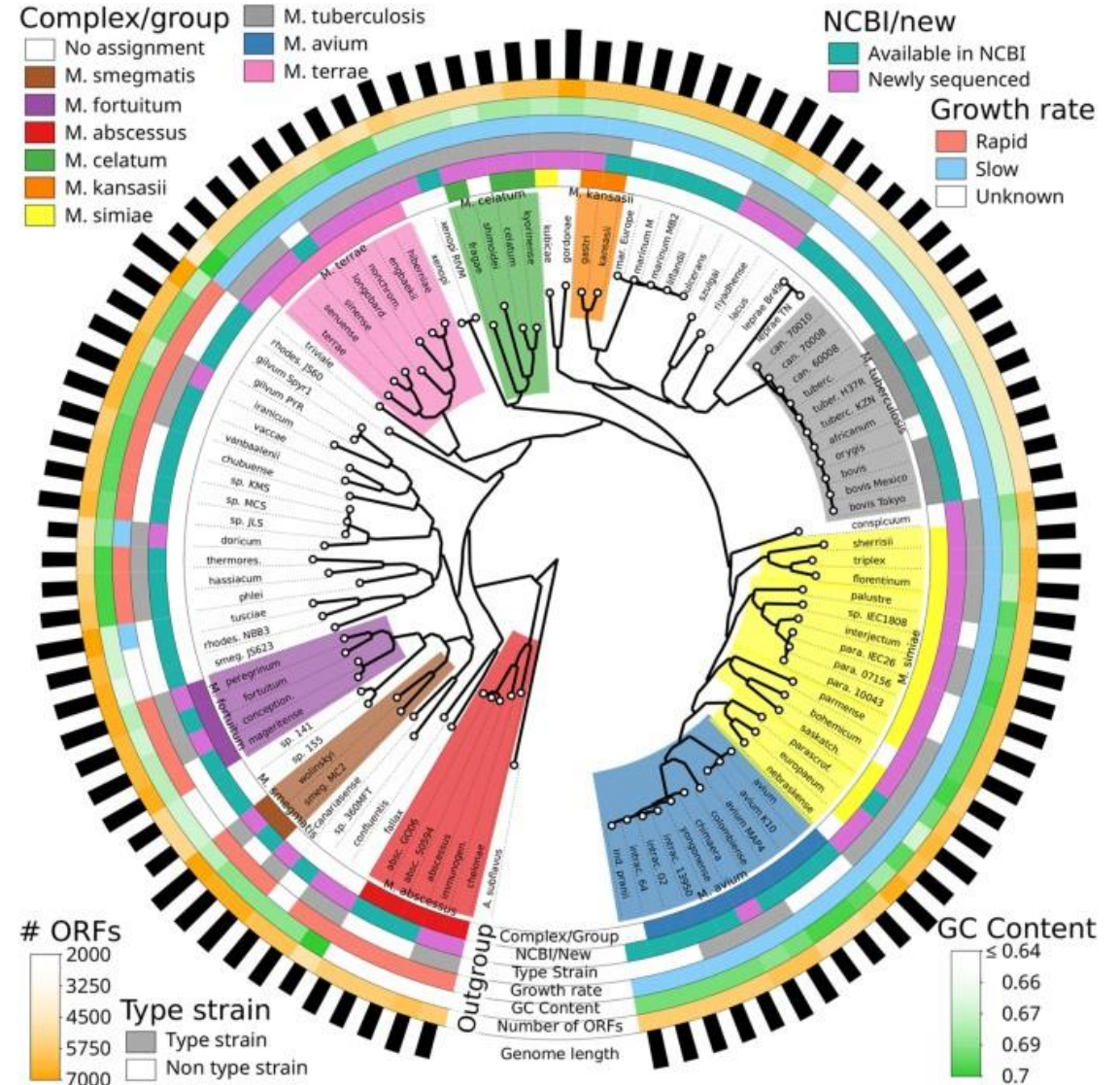


BRIGHT RED

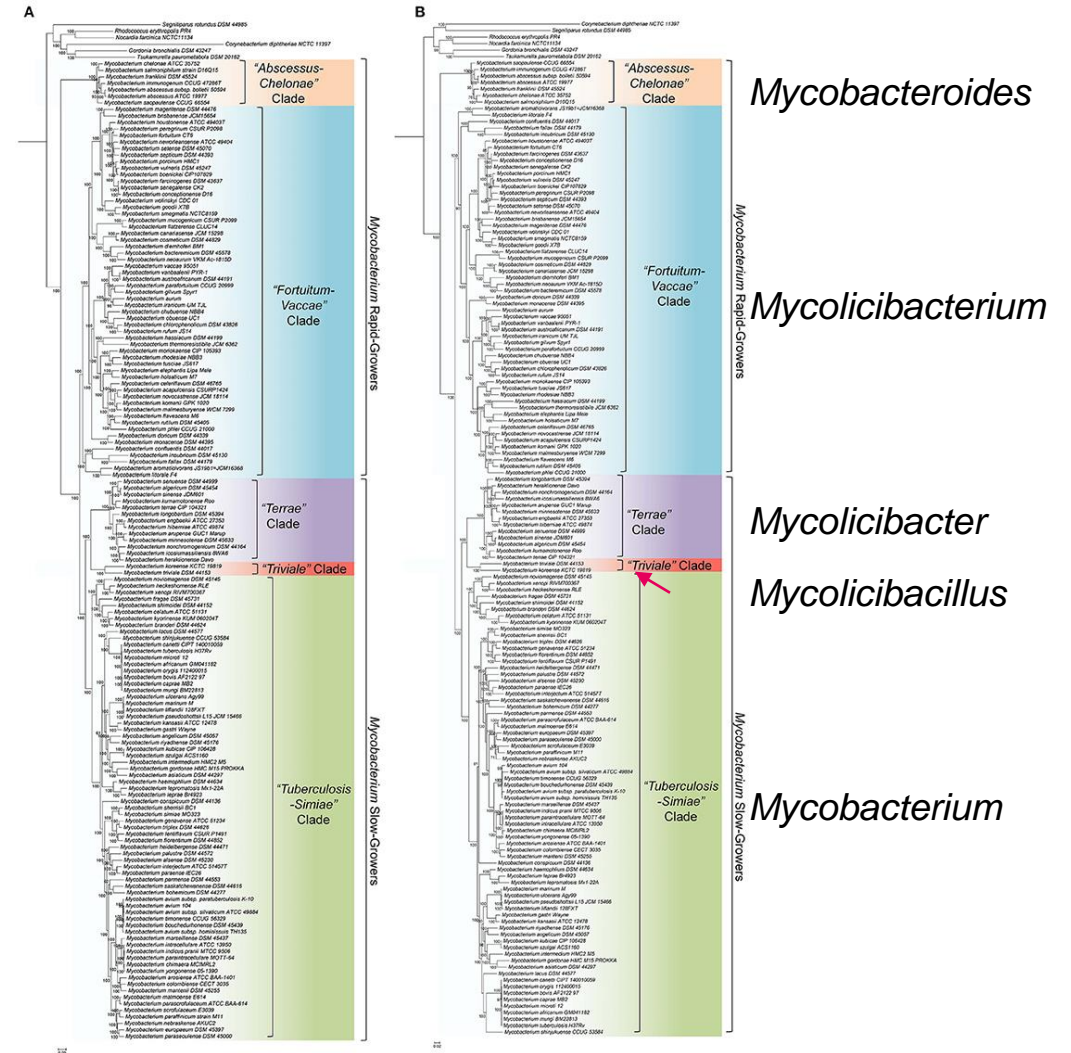
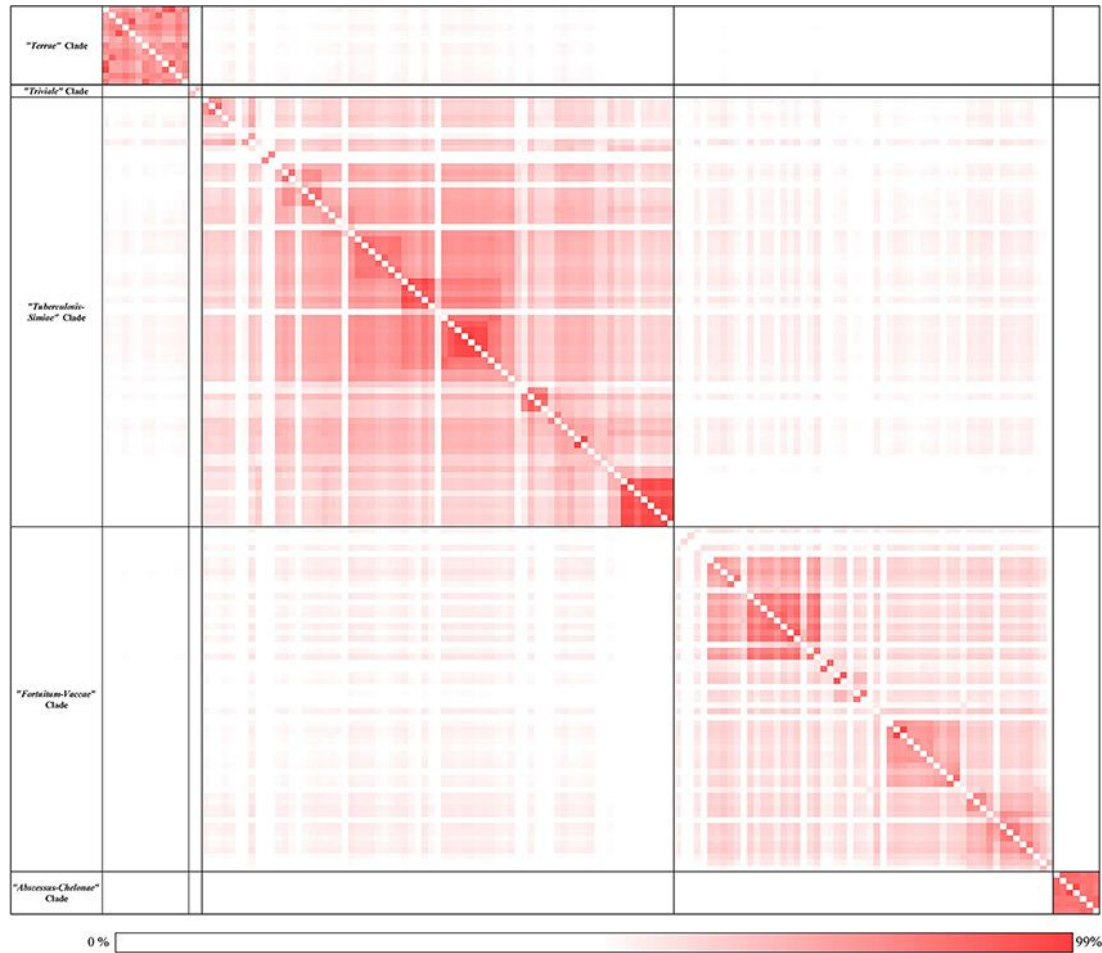


ROD-SHAPED

NEEDS OXYGEN  
STRICT AEROBES



# Splitting into 5 genera



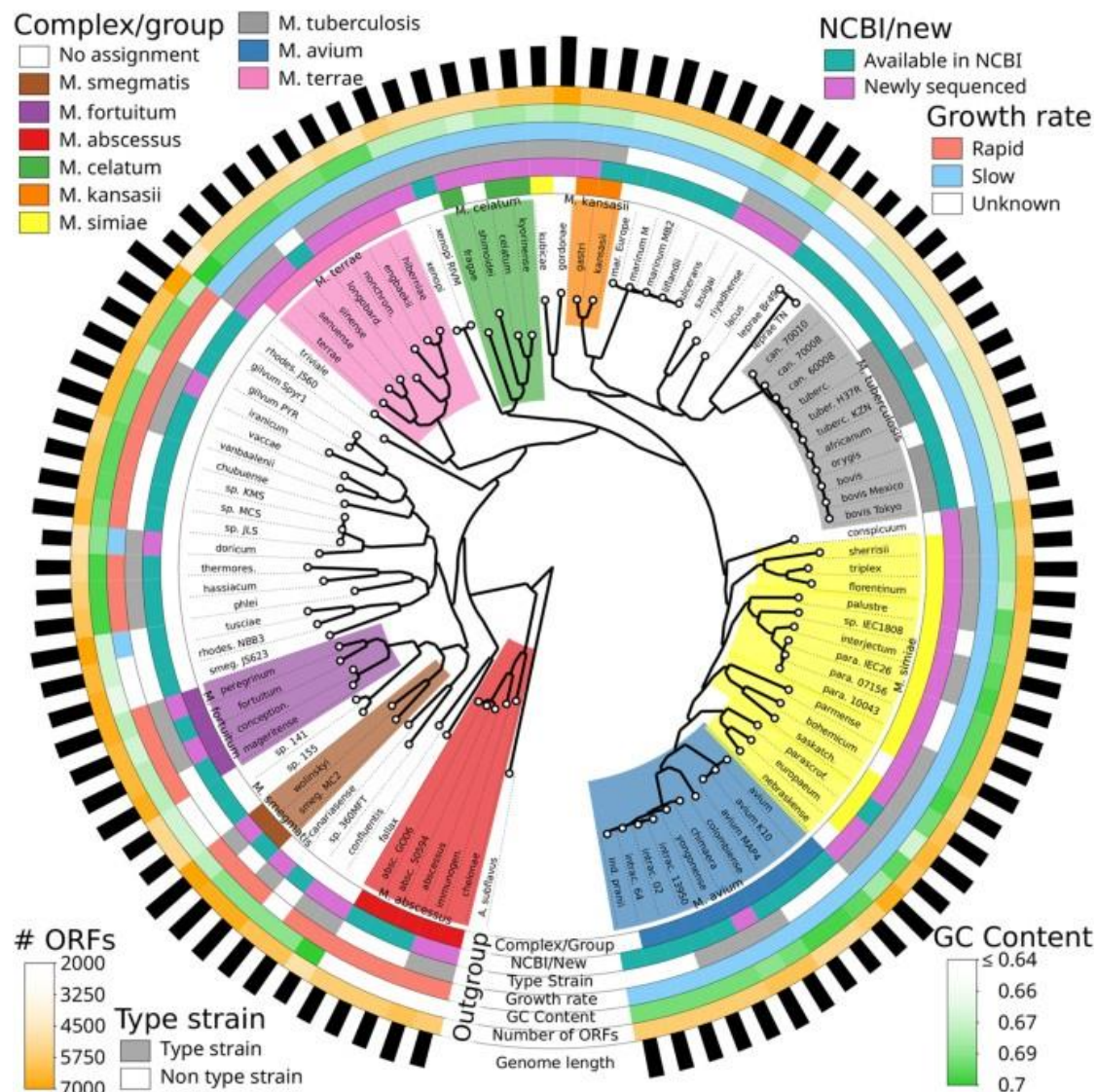
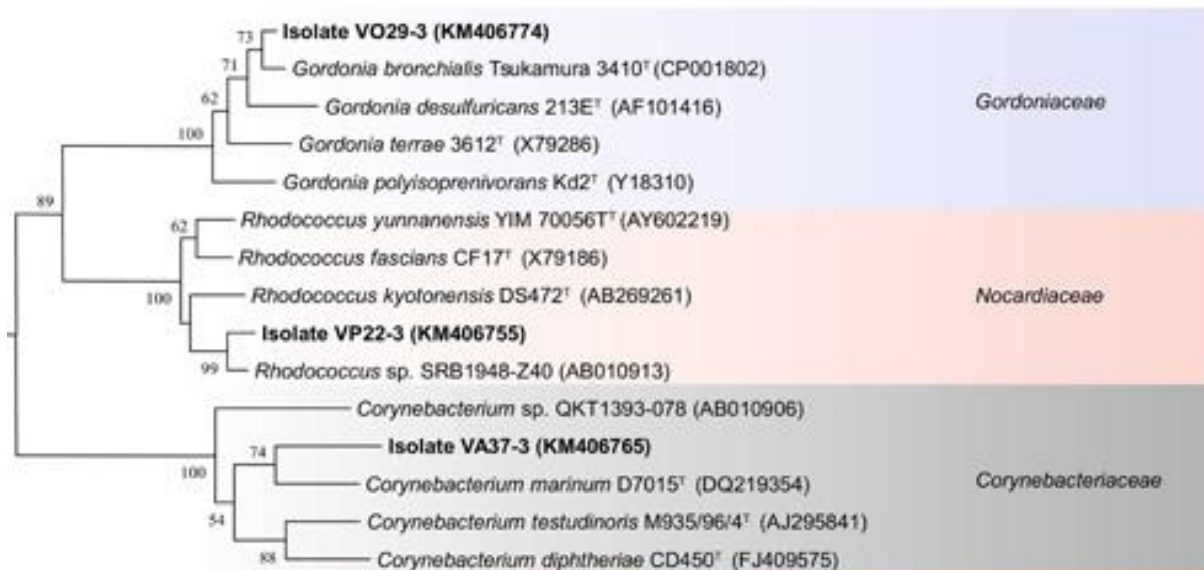
AAI

ML trees

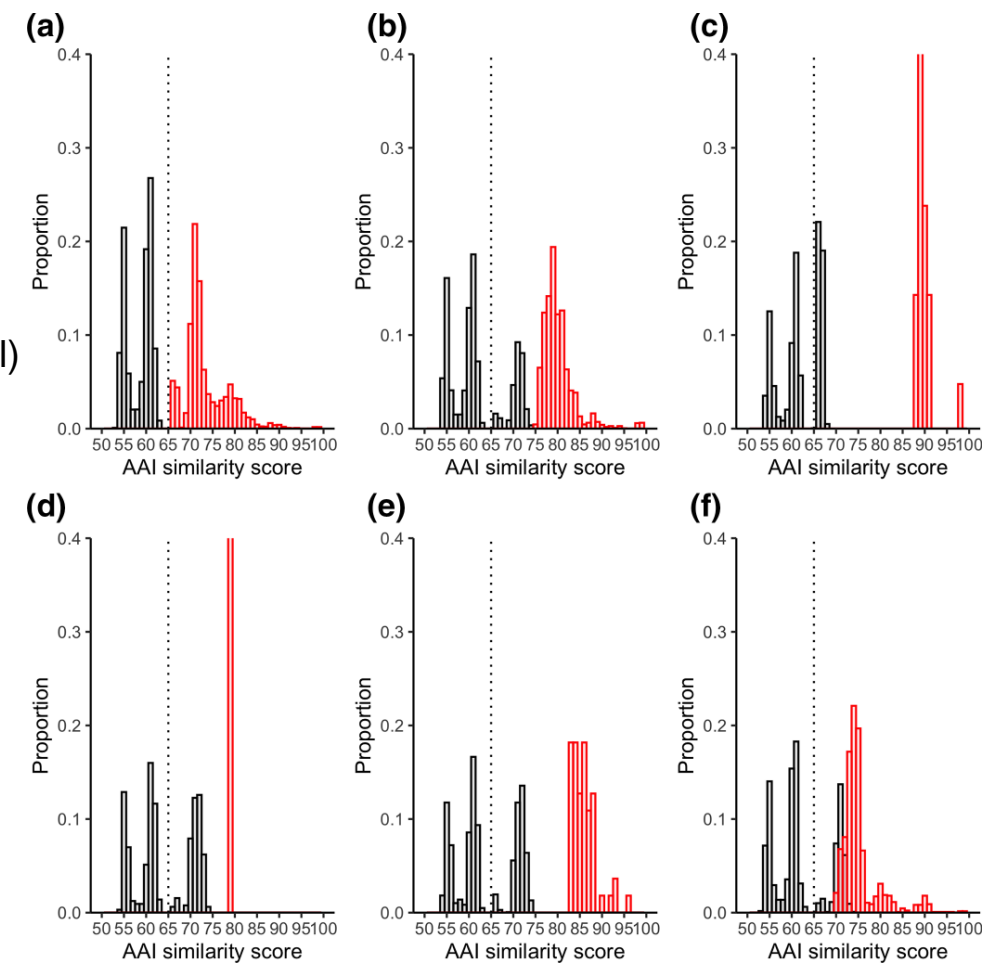
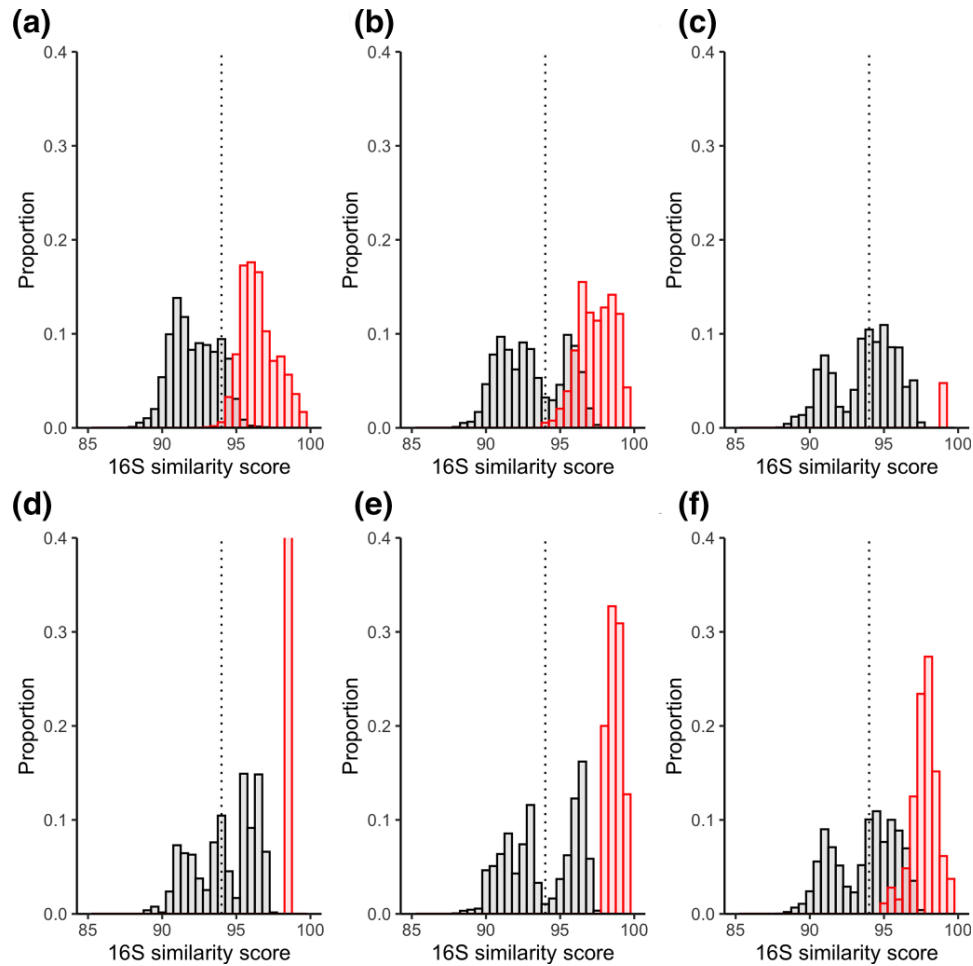


# Genomic dataset

- 137 *Mycobacterium*
- 210 *Corynebacteriaceae*



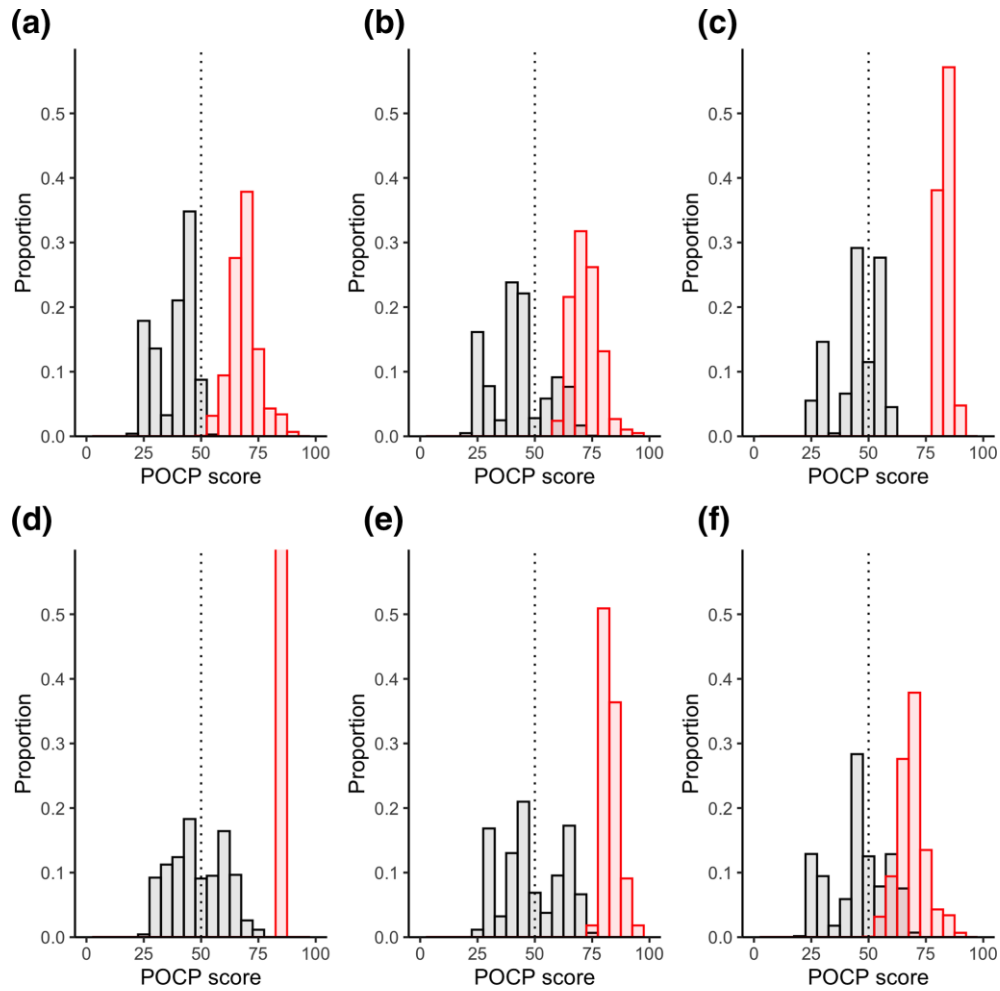
# 16S and AAI



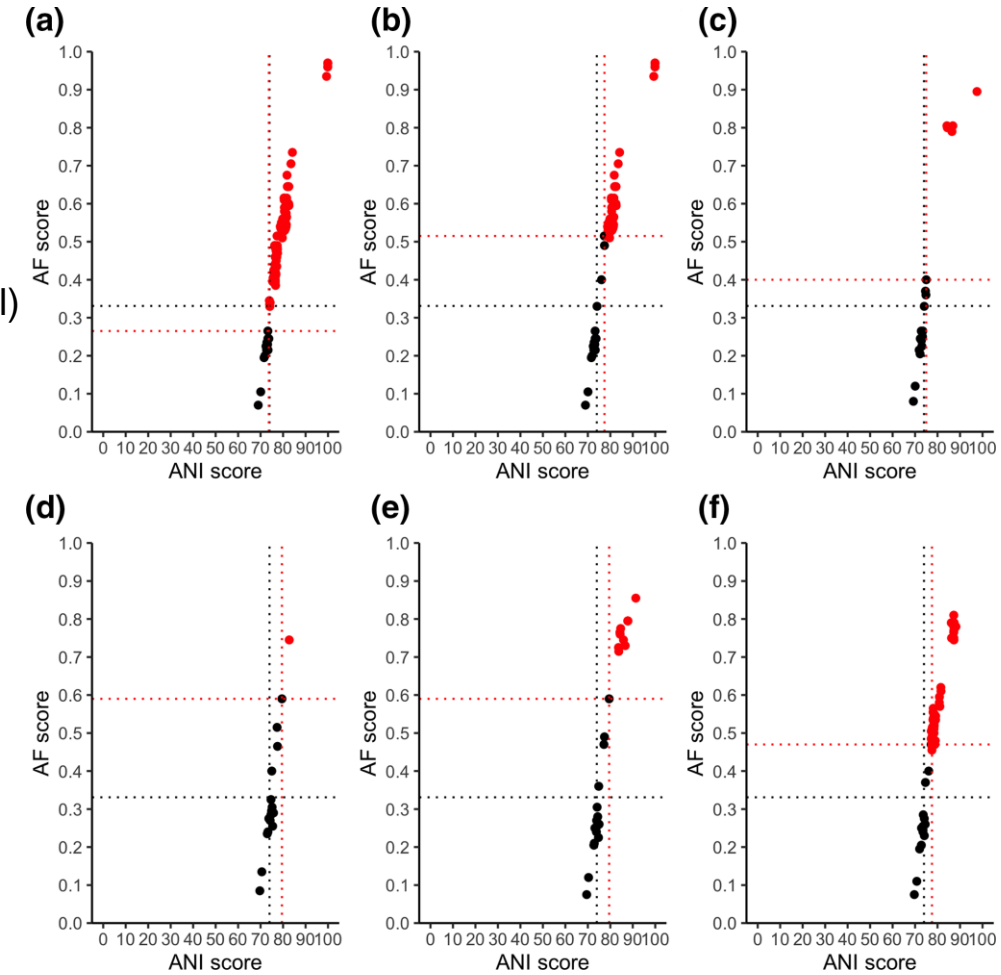
- (a) *Mycobacterium* (original)
- (b) *Mycobacterium* (Gupta)
- (c) *Mycobacteroides*
- (d) *Mycolicibacillus*
- (e) *Mycolicibacter*
- (f) *Mycolicibacterium*

- *Red: intra-genus comparison*
- *Black: inter-genus comparison*

# POCP and AF/ANI



(a) *Mycobacterium* (original)  
 (b) *Mycobacterium* (Gupta)  
 (c) *Mycobacteroides*  
 (d) *Mycolicibacillus*  
 (e) *Mycolicibacter*  
 (f) *Mycolicibacterium*



- Red: intra-genus comparison
- Black: inter-genus comparison

# Mycobacterium: single genus

