



What's in a name?

Proposed update to MTBC Nomenclature

Al Bateman, PhD MPH D(ABMM)
Assistant Director, Communicable Diseases
Wisconsin State Laboratory of Hygiene
Allen.Bateman@slh.wisc.edu





Acknowledgement: Webinar by ATCC

Reclassification of the *Mycobacterium tuberculosis* Complex (MTBC) Species as *Mycobacterium tuberculosis*

Reclassification of the *Mycobacterium tuberculosis* Complex (MTBC) Species as *Mycobacterium tuberculosis*

4/26/2018



American Type Culture Collection (ATCC)

- Non-profit organization
- Manassas, VA and Gaithersburg, MN
- Premier biological materials resource and standards development organization
 - 5,000 cell lines
 - 80,000 microorganisms
 - Genomic and synthetic nucleic acids
 - Media/reagents
- Sales and distribution in 150 countries



What defines a species?

Each species:

- A “type strain” and description of that strain
- Type strain is basically the ‘definition’ of the species
- Type strain is reference point for identifying new strains

- New strain: compare to characteristics of existing species type strains
- If the new strain shares enough characteristics with an existing species, it’s said to be ‘within the circumscription’ of that species/type strain



Species A^T
Gram +
Aerobic
Motile
Nitrate +

Species B^T
Gram +
Anaerobic
Motile
Nitrate –

Species C^T
Gram –
Aerobic
Motile
Nitrate +

Species D^T
Gram –
Anaerobic
Non-motile
Nitrate –



Gram –
Aerobic
Motile
Nitrate +



What Characteristics?

- Historically phenotypic
- Now, more genotypic comparisons
- Single genes vulnerable to bias
 - 16S rRNA
 - rpoB
 - hsp65
- Best comparison: whole genomes



DNA-DNA hybridization (DDH)

(historical genomic comparison)

- Denature DNA for organisms A and B
- Mix the DNA together, allow to anneal
 - Results in hybrids
- Reassociation of genomic DNA ~ sequence similarity

- Gold standard species definition
- DDH similarity >70% = same species
- DDH similarity <70% = different species

- Digital DDH (dDDH) uses whole-genome sequences to compare in silico (bioinformatics)

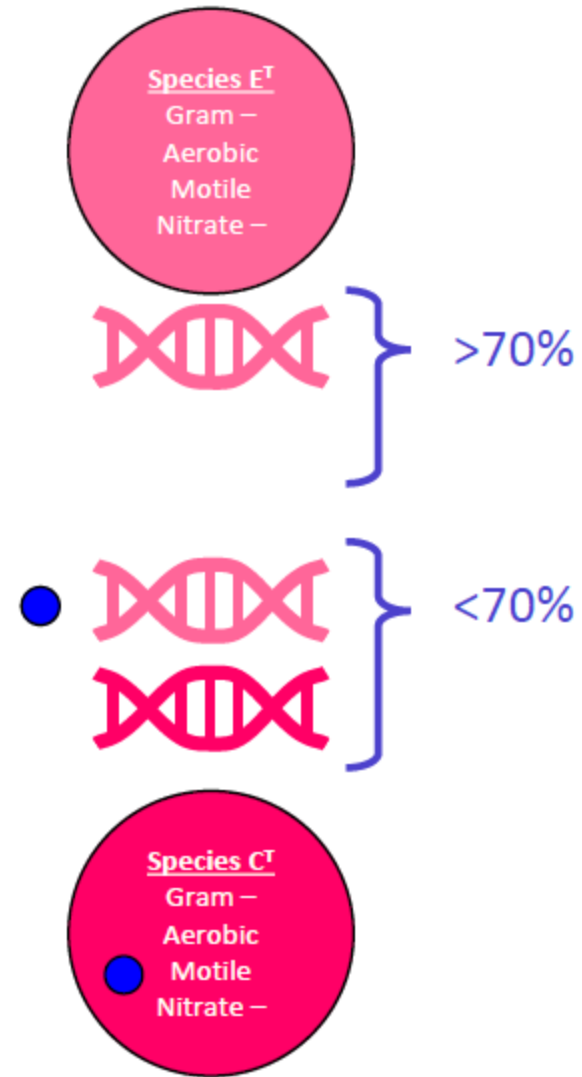
dDDH Range	Interpretation	
≥ 80%	Same species	Same subspecies
70 – 80%	Same species	Different subspecies
< 70%	Different species	



Genomic information can lead to updated taxonomy

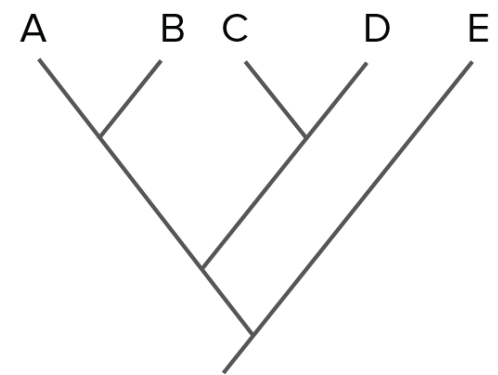
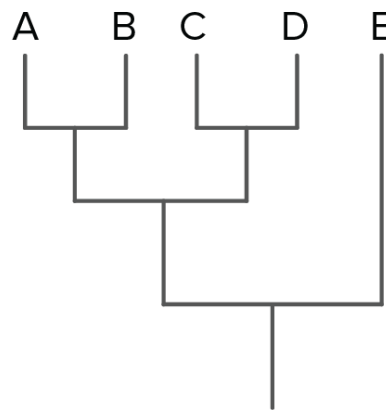
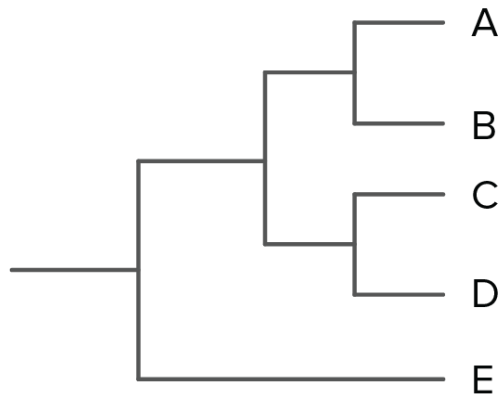


“Ay, there’s the rub”





Thanks for the taxonomy lesson,
but this is a TB conference!





Mycobacterium tuberculosis complex (MTBC)

- *Mycobacterium tuberculosis*
- *Mycobacterium africanum*
- *Mycobacterium bovis*
- *Mycobacterium caprae*
- *Mycobacterium microti*
- *Mycobacterium pinnipedii*
- Not validly published
 - “*Mycobacterium canettii*”
 - “*Mycobacterium mungi*”
 - “*Mycobacterium orygis*”



Maybe MTBC aren't separate species?

[Infect Genet Evol.](#) 2012 Jun;12(4):819-26. doi: 10.1016/j.meegid.2011.09.024. Epub 2011 Oct 8.

Alignment of multiple complete genomes suggests that gene rearrangements may contribute towards the speciation of Mycobacteria.

[Garcia-Betancur JC](#)¹, [Menendez MC](#), [Del Portillo P](#), [Garcia MJ](#).

- DNA-DNA hybridization
 - “...individual components of the Mycobacterium tuberculosis complex (MTBC) did not show sufficient diversity to classify them as a separate species.”
 - “...the absence of rearrangements amongst MTBC supports their consideration as a single genospecies.”



Phylogenomic analysis of the species of the *Mycobacterium tuberculosis* complex demonstrates that *Mycobacterium africanum*, *Mycobacterium bovis*, *Mycobacterium caprae*, *Mycobacterium microti* and *Mycobacterium pinnipedii* are later heterotypic synonyms of *Mycobacterium tuberculosis*

Marco A. Riojas,^{1,*} Katya J. McGough,^{1,2} Cristin J. Rider-Riojas,³ Nalin Rastogi⁴ and Manzour Hernando Hazbón¹



IJSEM paper by ATCC

- Performed whole-genome sequencing on the type strains of all species without sequence yet
- Compared WGS of the strains
 - dDDH
 - Average nucleotide identity (ANI)

Table 1. Genomes of type (or treated as type) strains of the MTBC

Current organism name	Strain
<i>M. tuberculosis</i>	H37Rv ^T
<i>M. africanum</i>	ATCC 25420 ^T
<i>M. bovis</i>	ATCC 19210 ^T
<i>M. caprae</i>	ATCC BAA-824 ^T
<i>M. microti</i>	ATCC 19422 ^T
<i>M. pinnipedii</i>	ATCC BAA-688 ^T
' <i>M. canettii</i> '	CIPT 140010059
' <i>M. mungi</i> '	BM22813
' <i>M. orygis</i> '	112400015
<i>M. pseudoshottsii</i>	L15 ^T
<i>Nocardia asteroides</i>	NBRC 15531 ^T



IJSEM paper by ATCC

	Species/ Strain	dDDH ANI	MTBC1	MTBC2	MTBC3	MTBC4	MTBC5	MTBC6	MTBC7	MTBC8	MTBC9	OUT1	OUT2
MTBC1	<i>M. tuberculosis</i> H37Rv ^T		100	97.7	97.5	97.9	98.7	97.3	91.2	97.9	97.6	22.1	18.8
MTBC2	<i>M. africanum</i> ATCC® 25420 ^T		99.88	100	98	98.5	98.9	98.2	92.2	98.9	98.4	22.2	18.8
MTBC3	<i>M. bovis</i> ATCC® 19210 ^T		99.78	99.82	100	98.2	98.2	97.8	91.6	98.1	97.8	22.3	19
MTBC4	<i>M. caprae</i> ATCC® BAA-824 ^T		99.86	99.87	99.83	100	98.8	97.7	91.7	98.6	98.2	22.1	18.8
MTBC5	<i>M. microti</i> ATCC® 19422 ^T		99.89	99.89	99.79	99.91	100	99.2	93.3	99	98.9	22.3	18.9
MTBC6	<i>M. pinnipedii</i> ATCC® BAA-688 ^T		99.84	99.86	99.78	99.84	99.92	100	91.6	98.3	97.6	22.1	18.8
MTBC7	" <i>M. canettii</i> " CIPT 140010059		99.25	99.28	99.21	99.26	99.36	99.26	100	92.5	91.8	22.2	19
MTBC8	" <i>M. mungi</i> " BM22813		99.88	99.91	99.81	99.88	99.92	99.89	99.31	100	98.6	22.2	18.8
MTBC9	" <i>M. orygis</i> " 112400015		99.85	99.87	99.80	99.87	99.91	99.86	99.28	99.88	100	22.1	18.8
OUT1	<i>M. pseudoshottsii</i> L15 ^T		79.33	79.27	79.21	79.34	79.34	79.25	79.29	79.25	79.37	100	19.2
OUT2	<i>Nocardia asteroides</i> NBRC 15531 ^T		70.92	70.76	70.96	70.94	70.88	71.02	70.99	71.00	70.84	70.75	100

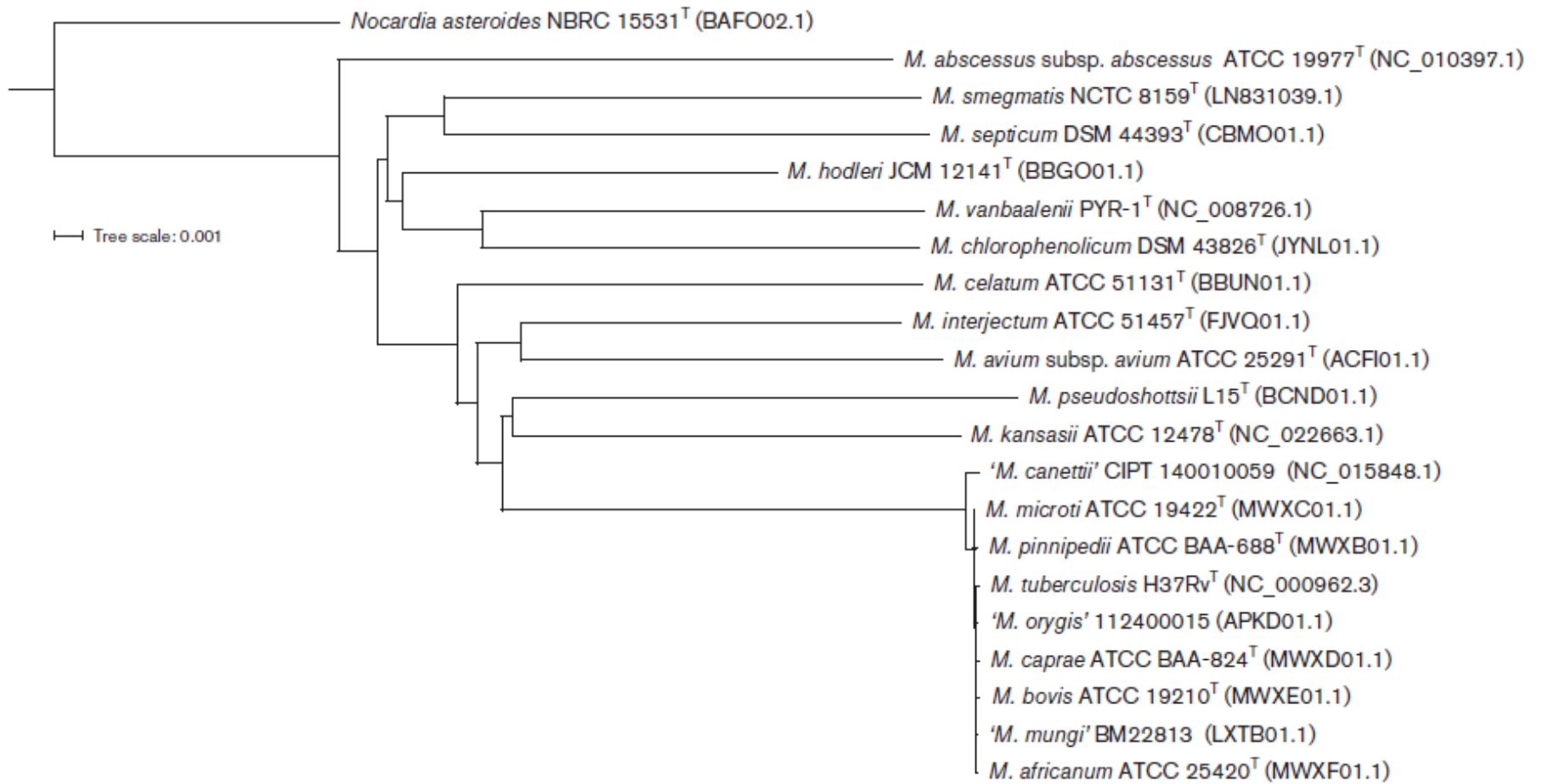


Fig. 1. Phylogenomic tree showing the relationship between the whole genomes of type strains of species of MTBC and the type strains of various other species of the genus *Mycobacterium* with *Nocardia asteroides* as an outgroup. Bar, 0.001 substitutions per site.



What about other (non-type strains) of each MTBC member?

Table 3. dDDH Analysis of type strains of members of the MTBC

dDDH GGD values are between the GenBank genomes identified as respective species and the type strain of *M. tuberculosis* (H37Rv^T).

GenBank organism identifier	<i>n</i>	dDDH GGD to <i>M. tuberculosis</i> , H37Rv ^T (%)		
		Minimum	Mean	Maximum
<i>M. africanum</i>	30	96.7	97.5	98.3
<i>M. bovis</i>	69	95.7	97.8	99.1
' <i>M. canettii</i> '	9	80.1	89.8	94.1
<i>M. caprae</i>	2	97.4	97.7	97.9
<i>M. microti</i>	1	97.1	97.1	97.1
<i>M. tuberculosis</i>	3631*	83.5	98.6	100.0



Proposed name changes

Table 4. Recommended infrasubspecific designations and reference strains

Current Name	Recommended Name
<i>M. tuberculosis</i>	<i>M. tuberculosis</i> var. <i>tuberculosis</i>
<i>M. africanum</i>	<i>M. tuberculosis</i> var. <i>africanum</i>
<i>M. bovis</i>	<i>M. tuberculosis</i> var. <i>bovis</i>
<i>M. bovis</i> BCG	<i>M. tuberculosis</i> var. BCG
<i>M. caprae</i>	<i>M. tuberculosis</i> var. <i>caprae</i>
<i>M. microti</i>	<i>M. tuberculosis</i> var. <i>microti</i>
<i>M. pinnipedii</i>	<i>M. tuberculosis</i> var. <i>pinnipedii</i>
' <i>M. canettii</i> '	<i>M. tuberculosis</i> var. <i>canettii</i>
' <i>M. mungi</i> '	<i>M. tuberculosis</i> var. <i>mungi</i>
' <i>M. orygis</i> '	<i>M. tuberculosis</i> var. <i>orygis</i>

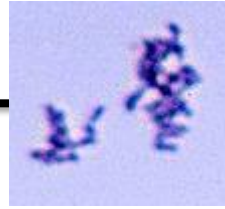
Reminiscent of *Salmonella*:

S. Enterica subsp. *enterica* serovar Typhi



Other recent name changes

Propionibacterium acnes
(*P. acnes*)



→ *Cutibacterium acnes*

Clostridium difficile



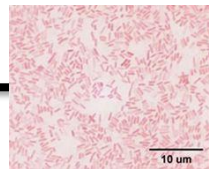
→ *Clostridioides difficile*

Scedosporium prolificans



→ *Lomentosporium prolificans*

Enterobacter aerogenes



→ *Klebsiella aerogenes*



Other recent name changes

Chlamydia pneumoniae

Chlamydia psittaci

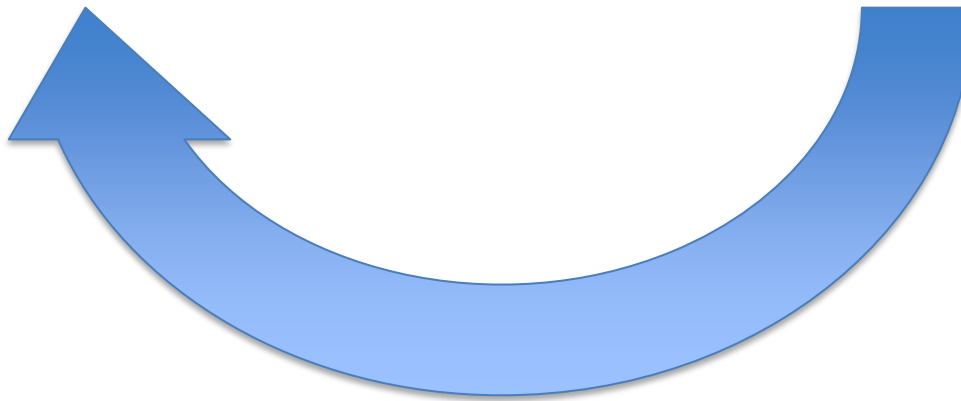
Chlamydia pecorum



Chlamydophila pneumoniae

Chlamydophila psittaci

Chlamydophila pecorum



“new genera was objected to by experts in the field”

“the scientific chlamydia community rejected the use of *Chlamydophila*”

“its use has been abandoned”

List of new names and new combinations previously effectively, but not validly, published

Aharon Oren^{1,*} and George Garrity^{2,*}

[Front Microbiol.](#) 2018 Feb 13;9:67. doi: 10.3389/fmicb.2018.00067. eCollection 2018.

Phylogenomics and Comparative Genomic Studies Robustly Support Division of the Genus *Mycobacterium* into an Emended Genus *Mycobacterium* and Four Novel Genera.

[Gupta RS](#)¹, [Lo B](#)¹, [Son J](#)¹.

five distinct groups within the genus *Mycobacterium*:

<u>Group</u>	<u>New Genus name</u>
• <i>Tuberculosis-Simiae</i>	(<i>Mycobacterium</i>)
• <i>Terrae</i>	(<i>Mycolicibacter</i>)
• <i>Triviale</i>	(<i>Mycolicibacillus</i>)
• <i>Fortuitum-Vaccaae</i>	(<i>Mycolicibacterium</i>)
• <i>Abscessus-Chelonae</i>	(<i>Mycobacteroides</i>)



Old Name	New name
<i>Mycobacterium tuberculosis</i>	No change
<i>Mycobacterium avium</i> complex	No change
<i>Mycobacterium kansasii</i>	No change
<i>Mycobacterium abscessus</i>	<u><i>Mycobacteriodes abscessus</i></u>
<i>Mycobacterium arupense</i>	<u><i>Mycolicibacter arupensis</i></u>
<i>Mycobacterium agri</i>	<u><i>Mycolicibacterium agri</i></u>
<i>Mycobacterium fortuitum</i>	<u><i>Mycolicibacterium fortuitum</i></u>
<i>Mycobacterium mucogenicum</i>	<u><i>Mycolicibacterium mucogenicum</i></u>
<i>Mycobacterium senegalense</i>	<u><i>Mycolicibacterium senegalense</i></u>