



JOBIM 2006



Analysis of horizontal transfers in the *Mycobacterium tuberculosis* complex in relation with pathogenicity emergence

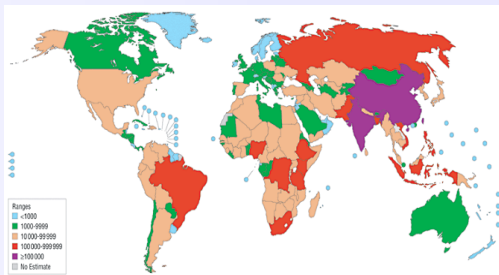
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The *Mycobacterium tuberculosis* complex agents of tuberculosis in mammals

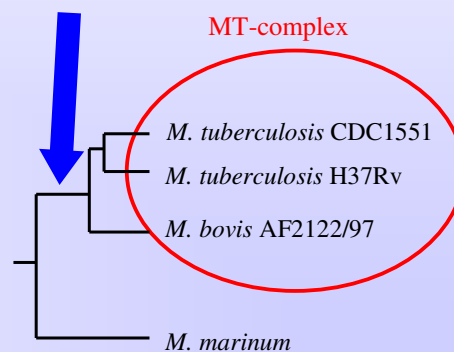
Estimated numbers of tuberculosis cases by country in 2000



Corbett, E. L. et al. Arch Intern Med 2003;163:1009-1021.

Acquisition of new genomic sequences by horizontal transfer ? (Pathogenicity, host specificity, drug resistance...)

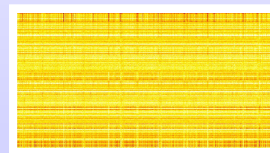
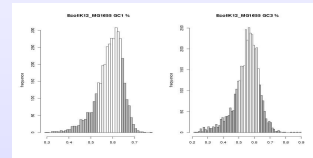
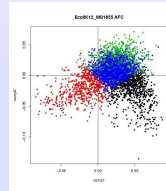
Horizontal transfers ?



Methods

- Detection of horizontal transfers (HT),
consensus method (2/3)

- GC1% & GC3%
- Codon usage analysis
- Signature

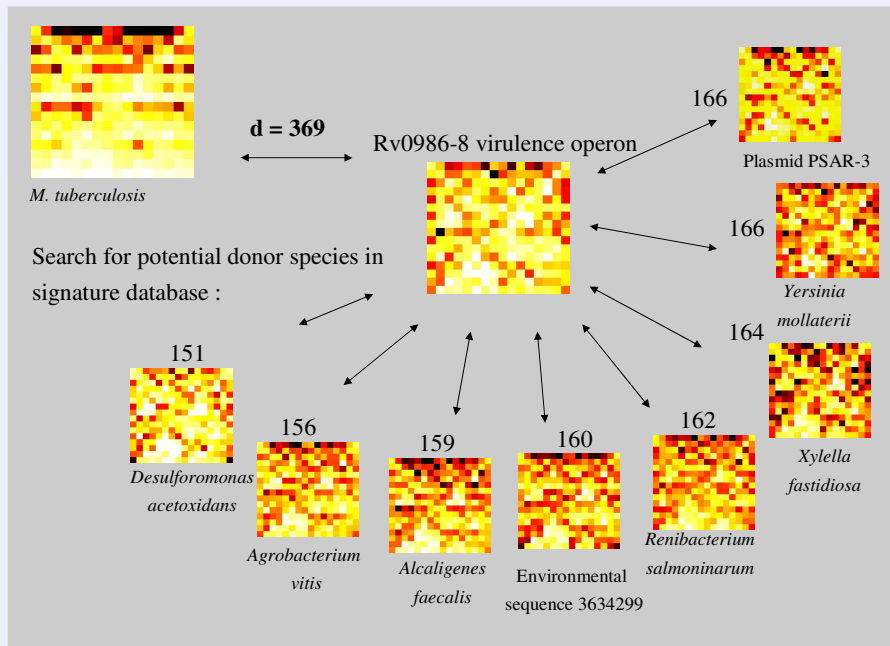


- Attribution of potential source species for HT
using sequence signature

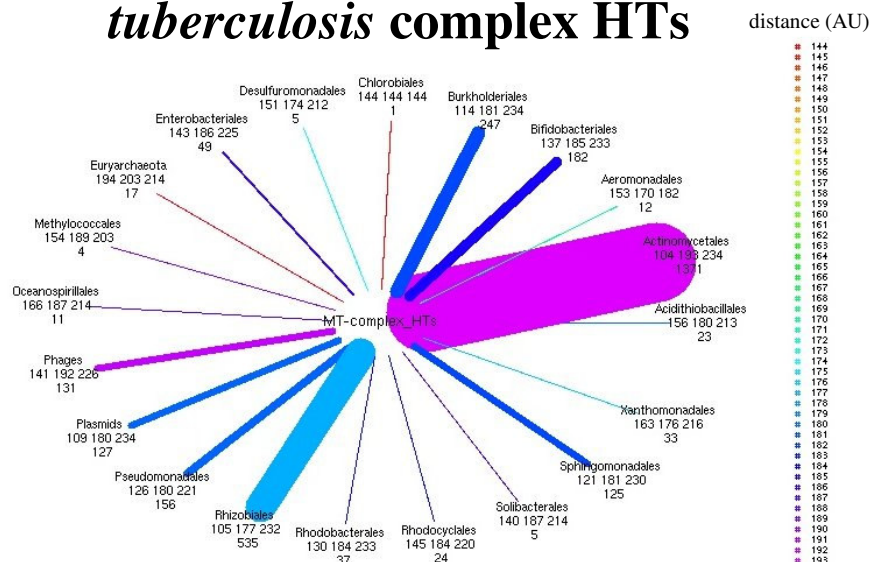
Atypical regions detected

atypical regions (complete genome)	Number	Total size (kb)	Mean size (kb)	Number of genes	G+C %
<i>M. bovis</i>	187	306 (4.35 Mb)	1.6	309 (3953)	63.7 (65.6)
<i>M. tub.</i> CDC1551	226	327 (4.4 Mb)	1.5	374 (4189)	64.2 (65.6)
<i>M. tub.</i> H37Rv	180	298 (4.41 Mb)	1.7	288 (3999)	63.3 (65.6)

The Rv0986-8 virulence operon



Potential donors of *Mycobacterium tuberculosis* complex HTs



top row numbers : distance minimum, mean and maximum
bottom row : number of potential donor species in each taxonomic group
the color corresponds to the mean distance (see scale on the right)
the width is correlated to the number of potential donor species

For further explanations

Poster 39

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Mycobacteria

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