

HOSTED BY



ELSEVIER

Available at www.sciencedirect.com

ScienceDirect

journal homepage: www.elsevier.com/locate/IJMYCO

The new phylogenesis of the genus *Mycobacterium*

Enrico Tortoli ^{a,*}, Tarcisio Fedrizzi ^b, Monica Pecorari ^c, Elisabetta Giacobazzi ^b,
Veronica De Sanctis ^b, Roberto Bertorelli ^b, Antonella Grottola ^c, Anna Fabio ^c,
Pamela Ferretti ^b, Francesca Di Leva ^b, Giulia Fregni Serpini ^c, Sara Tagliacruzchi ^c,
Fabio Rumpianesi ^c, Olivier Jousson ^b, Nicola Segata ^b

^a Emerging Bacterial Pathogens Unit, San Raffaele Scientific Institute, Milano, Italy

^b NGS Facility, Laboratory of Biomolecular Sequence and Structure Analysis for Health, Centre for Integrative Biology, University of Trento, Italy

^c Microbiology and Virology Unit, Policlinico University Hospital, Modena, Italy

ARTICLE INFO

Article history:

Received 9 October 2014

Accepted 12 October 2014

Available online xxxx

Keywords:

Nontuberculos mycobacteria

Whole genome sequencing

Taxonomy

Phylogenesis

ABSTRACT

Phylogenetic knowledge of the genus *Mycobacterium* is based on comparative analysis of their genetic sequences. The 16S rRNA has remained for many years the only target of such analyses, but in the last few years, other housekeeping genes have been investigated and the phylogeny based on their concatenated sequences become a standard. It is now clear that the robustness of the phylogenetic analysis is strictly related to the size of the genomic target used. Whole genome sequencing (WGS) is nowadays becoming widely accessible and comparatively cheap. It was decided, therefore, to use this approach to reconstruct the ultimate phylogeny of the genus *Mycobacterium*. Over 50 types of strains of the same number of species of *Mycobacterium* were sequenced using the Illumina HiSeq platform. The majority of the strains of which the whole sequence was already available in GenBank were excluded from this panel with the aim of maximizing the number of the species with genome available. Following assembling and annotation with proper software, the phylogenetic analysis was conducted with PhyloPhlAn and the pan-genome analysis pipeline. The phylogenetic tree which emerged was characterized by a clear-cut distinction of slowly and rapidly growing species with the latter being more ancestral. The species of the *Mycobacterium terrae* complex occupied an intermediate position between rapid and slow growers. Most of the species revealed clearly related and occupied specific phylogenetic branches. Thanks to the WGS technology, the genus *Mycobacterium* is finally approaching its definitive location.

© 2014 Asian-African Society for Mycobacteriology. Published by Elsevier Ltd. All rights reserved.

* Corresponding author.

<http://dx.doi.org/10.1016/j.ijmyco.2014.10.017>

2212-5531/© 2014 Asian-African Society for Mycobacteriology. Published by Elsevier Ltd. All rights reserved.