



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

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A Corrigendum on

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Gupta RS, Lo B and Son J (2019) Corrigendum: Phylogenomics and Comparative Genomic Studies Robustly Support Division of the Genus Mycobacterium into an Emended Genus Mycobacterium and Four Novel Genera. Front. Microbiol. 10:714. doi: 10.3389/fmicb.2019.00714 Phylogenomics and Comparative Genomic Studies Robustly Support Division of the Genus *Mycobacterium* into an Emended Genus *Mycobacterium* and Four Novel Genera *by Gupta, R. S., Lo, B., and Son, J. (2018). Front. Microbiol.* 9:67. doi: 10.3389/fmicb.2018.00067

In the original article, there was an error. Based on the branching position of *Mycobacterium vulneris* (van Ingen et al., 2009) in different phylogenomic trees and on multiple identified molecular signatures that this species shared with a clade of rapid growing mycobacteria, we proposed a reclassification of *M. vulneris*, into a new genus, *Mycolicibacterium*, corresponding to a clade of rapid-growing mycobacteria. However, it was noted in our article that the branching of *M. vulneris*, which is a slow-growing species with rapid-growing mycobacteria, was anomalous.

In a Frontiers commentary, Tortoli (2018) indicated that the genome sequence of M. vulneris, originally available in the NCBI genome database (accession CCBG00000000; Croce et al., 2014), was mislabeled and very likely corresponded to *Mycobacterium porcinum* (a rapid grower). Tortoli (2018) also reported the sequencing of the type strain of M. vulneris, DSM 45247^T and this genome sequence (accession NCXM01000000) showed the branching of M. vulneris within the slow-growing group of mycobacteria, belonging to the genus *Mycobacterium*.

Our own analysis with this new genome sequence also confirms the branching of *M. vulneris* within the delimited genus *Mycobacterium*, encompassing different slow-growing mycobacteria. As a result, the transfer of *M. vulneris* into the genus *Mycolicibacterium* as proposed in Table 11 of our article was incorrect as a direct result of the mislabeling of the available genome sequence for this species. To correct this error, we propose that the species *Mycolicibacterium vulneris* (Gupta et al., 2018) should be reinstated to its previous basonym *Mycobacterium vulneris* (van Ingen et al., 2009) and as part of the genus *Mycobacterium* (Gupta et al., 2018).

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way.

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