Corrigendum: phylogenomics and comparative genomic studies robustly support divis...

A Corrigendum on

[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.

References

Croce, O., Robert, C., Raoult, D., and Drancourt, M. (2014). Draft genome sequence of *Mycobacterium vulneris* DSM 45247T. *Genome Announc.* 2: e00370-14. doi: 10. 1128/genomeA. 00370-14

PubMed Abstract | CrossRef Full Text | Google Scholar

Gupta, R. S., Lo, B., and Son, J. (2018). Phylogenomics and comparative genomic studies robustly support division of the genus *Mycobacterium* into an emended genus *Mycobacterium* and four novel genera. *Front. Microbiol.* 9: 67. doi: 10. 3389/fmicb. 2018. 00067

PubMed Abstract | CrossRef Full Text | Google Scholar

Tortoli, E. (2018). Commentary: phylogenomics and comparative genomic studies robustly support division of the genus *Mycobacterium* into an emended genus *Mycobacterium* and four novel genera. *Front. Microbiol.* 9: 2065. doi: 10. 3389/fmicb. 2018. 02065

PubMed Abstract | CrossRef Full Text | Google Scholar

van Ingen, J., Boeree, M. J., Kosters, K., Wieland, A., Tortoli, E., Dekhuijzen, P. N., et al. (2009). Proposal to elevate *Mycobacterium avium* complex ITS sequevar MAC-Q to *Mycobacterium vulneris* sp. nov. *Int. J. Syst. Evol. Microbiol.* 59, 2277–2282. doi: 10. 1099/ijs. 0. 008854-0

PubMed Abstract | CrossRef Full Text | Google Scholar