

# [Corrigendum: phylogenomics and comparative genomic studies robustly support divis...](https://assignbuster.com/corrigendum-phylogenomics-and-comparative-genomic-studies-robustly-support-division-of-the-genus-mycobacterium-into-an-emended-genus-mycobacterium-and-four-novel-genera/)

[Health & Medicine](https://assignbuster.com/essay-subjects/health-n-medicine/)

A Corrigendum on
[Phylogenomics and Comparative Genomic Studies Robustly Support Division of the Genus *Mycobacterium* into an Emended Genus *Mycobacterium* and Four Novel Genera](https://doi.org/10.3389/fmicb.2018.00067)

*by Gupta, R. S., Lo, B., and Son, J. (2018). Front. Microbiol. 9: 67. doi:* [*10. 3389/fmicb. 2018. 00067*](https://doi.org/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](#B4) ) 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)](#B3) indicated that the genome sequence of *M. vulneris* , originally available in the NCBI genome database (accession CCBG00000000; [Croce et al., 2014](#B1) ), was mislabeled and very likely corresponded to *Mycobacterium porcinum* (a rapid grower). [Tortoli (2018)](#B3) 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](#B2) ) should be reinstated to its previous basonym *Mycobacterium vulneris* ( [van Ingen et al., 2009](#B4) ) and as part of the genus *Mycobacterium* ( [Gupta et al., 2018](#B2) ).

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](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=ShowDetailView&TermToSearch=24812218) | [CrossRef Full Text](https://doi.org/10.1128/genomeA.00370-14) | [Google Scholar](http://scholar.google.com/scholar_lookup?author=O.+Croce&author=C.+Robert&author=D.+Raoult&author=M.+Drancourt+&publication_year=2014&title=Draft+genome+sequence+of+Mycobacterium+vulneris+DSM+45247T&journal=Genome+Announc.&volume=2&pages=e00370)

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](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=ShowDetailView&TermToSearch=29497402) | [CrossRef Full Text](https://doi.org/10.3389/fmicb.2018.00067) | [Google Scholar](http://scholar.google.com/scholar_lookup?author=R.+S.+Gupta&author=B.+Lo&author=J.+Son+&publication_year=2018&title=Phylogenomics+and+comparative+genomic+studies+robustly+support+division+of+the+genus+Mycobacterium+into+an+emended+genus+Mycobacterium+and+four+novel+genera&journal=Front.+Microbiol.&volume=9&pages=67)

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](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=ShowDetailView&TermToSearch=30237789) | [CrossRef Full Text](https://doi.org/10.3389/fmicb.2018.02065) | [Google Scholar](http://scholar.google.com/scholar_lookup?author=E.+Tortoli+&publication_year=2018&title=Commentary%3A+phylogenomics+and+comparative+genomic+studies+robustly+support+division+of+the+genus+Mycobacterium+into+an+emended+genus+Mycobacterium+and+four+novel+genera&journal=Front.+Microbiol.&volume=9&pages=2065)

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](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=ShowDetailView&TermToSearch=19620376) | [CrossRef Full Text](https://doi.org/10.1099/ijs.0.008854-0) | [Google Scholar](http://scholar.google.com/scholar_lookup?author=J.+van+Ingen&author=M.+J.+Boeree&author=K.+Kosters&author=A.+Wieland&author=E.+Tortoli&author=P.+N.+Dekhuijzen+&publication_year=2009&title=Proposal+to+elevate+Mycobacterium+avium+complex+ITS+sequevar+MAC-Q+to+Mycobacterium+vulneris+sp.+nov&journal=Int.+J.+Syst.+Evol.+Microbiol.&volume=59&pages=2277-2282)