



Contents lists available at [ScienceDirect](#)

Journal of Global Antimicrobial Resistance

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



Corrigendum

Corrigendum to “Whole-genome sequencing reveals genetic signature of bedaquiline resistance in a clinical isolate of *Mycobacterium tuberculosis*” [J Glob Antimicrob Resist 15 (2018) 103–104]



Kiran Chawla^a, Elena Martinez^b, Ajay Kumar^a, Vishnu Prasad Shenoy^a, Vitali Sintchenko^{b,*}

^a Department of Microbiology, Kasturba Medical College, Manipal Academy of Higher Education, Manipal, India

^b Centre for Infectious Diseases and Microbiology, NSW Health Pathology, Level 3 ICPMR Building, Westmead Hospital, Wentworthville, NSW 2145, Australia

The authors regret there was an error in the mutation listed on page one, column two, line 9 of their article. The correct sentence should have read:

Unexpectedly, a mutation in Rv0678 (Ile64fs, G deletion at 193) was also observed, which has been associated with phenotypic bedaquiline resistance via increased expression of the MmpL5–MmpS5 efflux pump [2].

The incorrect sentence read:

Unexpectedly, a mutation in Rv0678 (Ile68fs, G deletion at 193) was also observed, which has been associated with phenotypic bedaquiline resistance via increased expression of the MmpL5–MmpS5 efflux pump [2].

The authors would like to apologise for any inconvenience caused.

DOI of original article: <http://dx.doi.org/10.1016/j.jgar.2018.09.006>

* Corresponding author.

E-mail address: vitali.sintchenko@sydney.edu.au (V. Sintchenko).

<http://dx.doi.org/10.1016/j.jgar.2019.05.011>

2213-7165/© 2019 International Society for Antimicrobial Chemotherapy. Published by Elsevier Ltd. All rights reserved.