



HAL
open science

Correction: Genus-wide *Leptospira* core genome multilocus sequence typing for strain taxonomy and global surveillance

Julien Guglielmini, Pascale Bourhy, Olivier Schiettekatte, Farida Zinini, Sylvain Brisse, Mathieu Picardeau

► To cite this version:

Julien Guglielmini, Pascale Bourhy, Olivier Schiettekatte, Farida Zinini, Sylvain Brisse, et al.. Correction: Genus-wide *Leptospira* core genome multilocus sequence typing for strain taxonomy and global surveillance. PLoS Neglected Tropical Diseases, 2020, 14 (8), pp.e0008673. 10.1371/journal.pntd.0008673 . pasteur-02938924

HAL Id: pasteur-02938924

<https://pasteur.hal.science/pasteur-02938924>

Submitted on 15 Sep 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License

CORRECTION

Correction: Genus-wide *Leptospira* core genome multilocus sequence typing for strain taxonomy and global surveillance

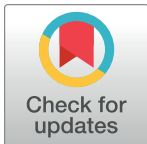
Julien Guglielmini, Pascale Bourhy, Olivier Schiettekatte, Farida Zinini, Sylvain Brisse, Mathieu Picardeau

The Funding section listed in the article [1] is incomplete and the contribution of the Pasteur International Joint Research Unit "Integrative Microbiology of Zoonotic Agents" (IMiZA) was mistakenly omitted. The updated Funding section reads:

“This work was supported in part by a donation from Foundation MSD to the ‘PIBnet’ programme of Institut Pasteur, by Public Health France (SPF), by Institut Pasteur through grant PTR 30–2017, and the Pasteur International Joint Research Unit "Integrative Microbiology of Zoonotic Agents" (IMiZA). This work was part of the PhD thesis of O. S. who received financial support from “Université Paris Diderot” and “Sorbonne Paris Cité”. The funders had no role in the design, conduct or conclusions of the study.”

In the Acknowledgments section the sharing of *Leptospira* genomes by contributors was mistakenly omitted. The updated Acknowledgments section reads:

“We thank the technicians of the National Reference Center for Leptospirosis, in particular Céline Lorigoux, for cultures and typing of *Leptospira* strains, and Evelyne Bégaud and Chantal Bizet from Collection de l’Institut Pasteur (CIP) for providing type and reference strains. We thank Cyrille Goarant (Institut Pasteur de Nouméa, New Caledonia), Anissa Amara Korba (Institut Pasteur d’Alger, Algeria), Fairuz Amran (Institute for Medical Research, Malaysia), Toshiyuki Masuzawa (Chiba Institute of Science, Japan), Vasantha Kumari Neela (Universiti Putra Malaysia, Malaysia) and Alejandro Buschiazzi, Leticia Zarantonelli and the consortium “Grupo de Trabajo Interinstitucional de Leptospirosis” (Institut Pasteur Montevideo/UdelaR/INIA/MGAP, Uruguay) for sharing *Leptospira* genomes or isolates. We also thank Vincent Enouf and the team of core facility P2M (Institut Pasteur, Mutualized Platform for Microbiology) for genomic sequencing.”



OPEN ACCESS

Citation: Guglielmini J, Bourhy P, Schiettekatte O, Zinini F, Brisse S, Picardeau M (2020) Correction: Genus-wide *Leptospira* core genome multilocus sequence typing for strain taxonomy and global surveillance. PLoS Negl Trop Dis 14(8): e0008673. <https://doi.org/10.1371/journal.pntd.0008673>

Published: August 21, 2020

Copyright: © 2020 Guglielmini et al. This is an open access article distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Reference

1. Guglielmini J, Bourhy P, Schiettekatte O, Zinini F, Brisse S, Picardeau M (2019) Genus-wide *Leptospira* core genome multilocus sequence typing for strain taxonomy and global surveillance. PLoS Negl Trop Dis 13(4): e0007374. <https://doi.org/10.1371/journal.pntd.0007374> PMID: 31026256