

CORRECTION

Correction: Within-host whole genome analysis of an antibiotic resistant *Pseudomonas aeruginosa* strain sub-type in cystic fibrosis

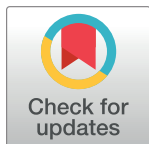
Laura J. Sherrard, Anna S. Tai, Bryan A. Wee, Kay A. Ramsay, Timothy J. Kidd, Nouri L. Ben Zakour, David M. Whiley, Scott A. Beatson, Scott C. Bell

PoxB (PA5297) has not been associated with antibiotic resistance (specifically beta-lactamase activity) as indicated in the original article's Supplementary Tables. The authors have provided updated and corrected [S1](#) and [S2](#) Tables here.

There is an error in the seventh sentence of the abstract. The correct sentence is: Small genetic variations, shared by all 11 isolates, were found in 48 genes associated with antibiotic resistance including frame-shift mutations (*mexA*, *mexT*), premature stop codons (*oprD*, *mexB*) and mutations in quinolone-resistance determining regions (*gyrA*, *parE*).

In the Materials and methods, there is an error in the first sentence of the second paragraph in the Identification of genes associated with antibiotic resistance, hypermutation and pathoadaptation section. The correct sentence is: Single or multiple nucleotide substitutions, insertions or deletions in chromosomally encoded genes (n = 135) associated with antibiotic resistance, hypermutation and pathoadaptive genes (identified based on a literature search; [S2 Table](#)), and intergenic regions were determined using both read mapping and sequence alignment of assembled contigs.

In the Results and discussion, there is an error in the second sentence of the second paragraph in the Variation in chromosomally encoded genes was observed section. The correct sentence is: In total, mutations, shared by all 11 isolates, were identified in 48 chromosomal genes previously implicated in conferring *P. aeruginosa* antibiotic resistance ([S1 Table](#)).



Supporting information

S1 Table. Ternary plot of amino acid sequence variation.
(XLSX)

S2 Table. Literature search.
(DOCX)

Reference

1. Sherrard LJ, Tai AS, Wee BA, Ramsay KA, Kidd TJ, Ben Zakour NL, et al. (2017) Within-host whole genome analysis of an antibiotic resistant *Pseudomonas aeruginosa* strain sub-type in cystic fibrosis. *PLoS ONE* 12(3): e0172179. <https://doi.org/10.1371/journal.pone.0172179> PMID: 28273168

OPEN ACCESS

Citation: Sherrard LJ, Tai AS, Wee BA, Ramsay KA, Kidd TJ, Ben Zakour NL, et al. (2019) Correction: Within-host whole genome analysis of an antibiotic resistant *Pseudomonas aeruginosa* strain sub-type in cystic fibrosis. *PLoS ONE* 14(1): e0210929. <https://doi.org/10.1371/journal.pone.0210929>

Published: January 14, 2019

Copyright: © 2019 Sherrard 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.