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CORRECTION

Correction to: Analysis of resistance genes of clinical *Pannonibacter phragmitetus* strain 31801 by complete genome sequencing

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Correction to:
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Subsequent to publication it has been noticed that the below listed text parts, figures and tables of the above paper were taken from paper "Genomic insights of *Pannonibacter phragmitetus* strain 31801 isolated from a patient with a liver abscess", by Zhou Y et al., published in MicrobiologyOpen. 2017;6:e515; https://doi.org/10.1002/mbo3.515 without being referenced. The authors apologize for the mistake.

The correction reads as follows:

Tables

Table 1 Antimicrobial susceptibility of *Pannonibacter phragmitetus* 31801 (Table taken from Zhou et al. 2017)

Table 4 Resistance genes on the *Pannonibacter phragmitetus* 31801 chromosome genome extracted by CARD analysis (Table taken from Zhou et al. 2017)

Figures

Figure 1 Phyologenetic relationship between *Pannonibacter phragmitetus* P. phragmitetus 31801 and other closely related species (identity indicated by *) based on 16S rRNA nucleotide sequence data. The corresponding GenBank accession numbers are indicated in parentheses. Rhodobacteraceae bacterium SH22-2a was used as an outgroup (Figure taken from Zhou et al. 2017)

Figure 2 Circular representation of the genome of *Pannonibacter phragmitetus* 31801. Concentric rings, numbered from outer to inner rings, represent the following: coding sequences (CDS; light blue), rRNA genes (pink), tRNA genes (brown), GC content (percentage) as a peak to valley profile (black), GC-skew graph (purple and green). The scale starts at the center circle and runs in a clockwise direction (Figure taken from Zhou et al. 2017)

Figure 3 Subsystem distribution of *Pannonibacter phragmitetus* 31801 based on RAST annotation server data (Figure taken from Zhou et al. 2017)

Discussion

In the third paragraph: The genes associated with multidrug resistance efflux pumps could be classified into four groups based on the anti-biotics to which they confer resistance: (1) macrolides: *adeJ, cmeB, macAB-TolC, mdtF, mexB, mexD, mexY, smeE, cfrA*; (2) tetracycline: *acrB, adeA, adeB, adeG, adeJ, mexB, mexY, smeE*; (3) fluoroquinolones: *acrB, acrF, adeG, adeJ, ceoB, cmeB, mdtF, mexB, mexD, mexF, mexI, mexY, smeB, smeE*; (4) aminoglycosides: *acrD, amrB, ceoB, mexY, smeB*. All these genes encodes individual subunits of the efflux pumps (Zhou et al. 2017).

In the sixth paragraph: In *P. aeruginosa, mexY* promotes aminoglycoside resistance. The proximal binding pocket within MexY, which is jointed with a periplasm-linked cleft, confers the resistance (Lau et al. 2014). Interestingly, the AcrB drug efflux pathway shows a similar conformation. The genome of strain 31801 contained both *mexY* and *acrB*, but the isolate remained sensitive to amikacin, highlighting the inconsistencies between AST and CARD database analyses in the present study. Over-expression of *mexXY* in *P. aeruginosa* promoted resistance to aminoglycosides (Sobel et al. 2003), and *mexY* could be induced by chloramphenicol, tetracycline, macrolides, and aminoglycosides (Jeannot et al. 2005). *SmeB* and *mexB*, which showed 52% identity to each other, were also found in strain 31801 (Zhou et al. 2017).

The original article can be found online at https://doi.org/10.1007/s00203-018-1522-2.

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