

CORRECTION

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Correction to: Genomic analysis of *Leptospira interrogans* serovar Paidjan and Dadas isolates from carrier dogs and comparative genomic analysis to detect genes under positive selection

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Correction to: BMC Genomics (2019) 20:168
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Following the publication of this article [1], the authors noted an error in the caption of Fig. 4. The caption was published incorrectly as:

Figure 4 The distribution and conservation of 33 representative confirmed virulence genes in pathogenic, intermediate and non-pathogenic *Leptospira* species. Genes encoding for outer membrane protein (*loa22*), flagella motor switch protein (*fliY*), and hemolysins B and C (*tlyB* and *tlyC*) were conserved in all 24 *Leptospira* strains. Genes encoding was conserved only in pathogenic *Leptospira* strains. Strains CUDO5 and CUDO8 contained all of the 33 virulence genes

The correct figure and caption is reproduced in this Correction article:

The original article has been corrected.

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Reference

1. Kurilung A, et al. Genomic analysis of *Leptospira interrogans* serovar Paidjan and Dadas isolates from carrier dogs and comparative genomic analysis to detect genes under positive selection. *BMC Genomics*. 2019;20(168). <https://doi.org/10.1186/s12864-019-5562-z>.

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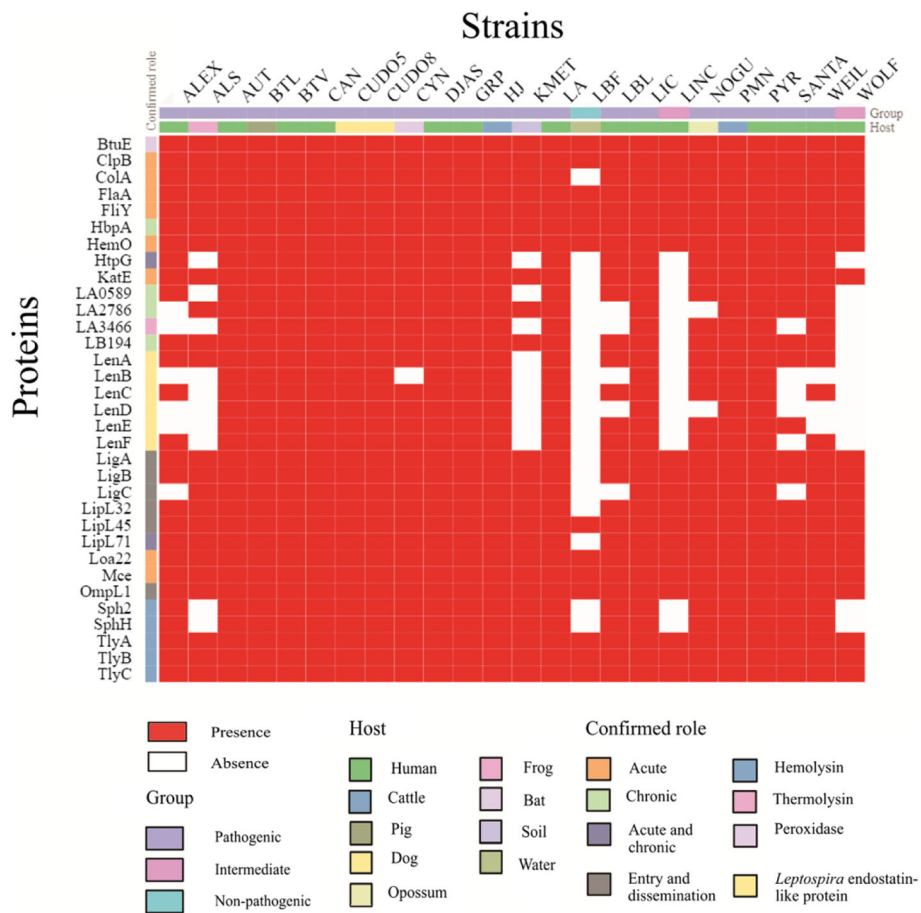


Fig. 4 The distribution and conservation of 33 representative confirmed virulence genes in pathogenic, intermediate and non-pathogenic *Leptospira* species. Genes encoding for outer membrane protein (*loa22*), flagella motor switch protein (*fliY*), and hemolysins B and C (*tlyB* and *tlyC*) were conserved in all 24 *Leptospira* strains. Gene involved with chronic infection (*lb194*) was conserved only in pathogenic *Leptospira* strains. Strains CUDO5 and CUDO8 contained all of the 33 virulence genes