Erratum

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Description of *Vagococcus coleopterorum* sp. nov., isolated from the intestine of the diving beetle, *Cybister lewisianus*, and *Vagococcus hydrophili* sp. nov., isolated from the intestine of the dark diving beetle, *Hydrophilus acuminatus*, and emended description of the genus *Vagococcus*

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In the article by Hyun *et al.* published in Journal of Microbiology 2021; 59, 132–141,

The figure on line 11 in the Abstract should be corrected to 98.8%.

The sentence 'We propose the name *Vagococcus coleopterorum* sp. nov. for strain HDW17A^T (= KACC 21348^T = KCTC 49324^T = JCM 33674^T) and the name *Vagococcus hydrophili* sp. nov. for strain HDW17B^T (= KACC 21349^T = KCTC 49325^T = JCM 33675^T).' should be corrected to 'We propose the name *Vagococcus coleopterorum* sp. nov. for strain HDW17A^T (= KACC 21344^T = KCTC 43112^T = JCM 33682^T) and the name *Vagococcus hydrophili* sp. nov. for strain HDW17B^T (= KACC 21345^T = KCTC 43113^T = JCM 33683^T).' in the Abstract.

The Abstract should have read:

A polyphasic taxonomic approach was used to characterize two novel bacterial strains, HDW17A^T and HDW17B^T, isolated from the intestine of the diving beetle *Cybister lewisianus*, and the dark diving beetle *Hydrophilus acuminatus*, respectively. Both strains were Gram-positive and facultative anaerobic cocci forming cream-colored colonies. The isolates grew optimally at 25°C, pH 7, in the presence of 0.3% (wt/vol) NaCl. Phylogenetic analysis based on 16S rRNA gene sequences and genome sequences showed that the isolates were members of the genus *Vagococcus*, and strain HDW17A^T was closely related to *Vagococcus fessus* CCUG 41755^T (98.8% of 16S rRNA gene sequence similarity and 74.3% of average nucleotide identity [ANI]), whereas strain HDW17B^T was closely related to *Vagococcus fluvialis* NCFB 2497^T (98.9% of 16S rRNA gene sequence similarity and 76.6% of ANI). Both strains contained C16:0, and C18:1 ω 9c as the major cellular fatty acids, but C16:1 ω 9c was also observed only in strain HDW17B^T as the major cellular fatty acid. The respi-

ratory quinone of the isolates was MK-7. The major polar lipid components were phosphatidylglycerol, phosphatidylethanolamine, and diphosphatidylglycerol. The genomic DNA G + C content of strains HDW17A^T and HDW17B^T were 36.6 and 34.4%, respectively. Both strains had cell wall peptidoglycan composed of the amino acids L-alanine, glycine, D-glutamic acid, L-tryptophan, L-lysine, and L-aspartic acid, and the sugars ribose, glucose, and galactose. Based on phylogenetic, phenotypic, chemotaxonomic, and genotypic analyses, strains HDW17A^T and HDW17B^T represent two novel species in the genus *Vagococcus*. We propose the name *Vagococcus coleopterorum* sp. nov. for strain HDW17A^T (= KACC 21344^T = KCTC 43112^T = JCM 33682^T) and the name *Vagococcus hydrophili* sp. nov. for strain HDW17B^T (= KACC 21345^T = KCTC 43113^T = JCM 33683^T).

Authors apologize for any inconvenience that this may have caused.