



Draft Genome Sequences of *Legionella taurinensis* Recovered from a Hot Water System in Austria, 2018

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ABSTRACT Members of the genus *Legionella* are widespread in natural water sources. This is the first report on the draft genome sequences of *Legionella taurinensis* in Austria. The isolates were recovered from a hot water system associated with a case of Legionnaires' disease caused by *Legionella pneumophila* in 2018.

The Gram-negative *Legionella* species are intracellular bacteria living in natural and man-made aquatic environments. The genus *Legionella* consists of 59 species and 70 serogroups (sg). Even though *L. pneumophila* sg1 causes more than 90% of reported Legionnaires' disease cases (1, 2), infections with other *Legionella* species have been reported (3, 4).

Water samples from a hot water system of an apartment belonging to an Austrian patient infected with *L. pneumophila* were examined for *Legionella* as described (5). From each water sample, two portions were directly plated on buffered charcoal yeast extract (BCYE) and glycine vancomycin polymyxin cycloheximide (GVPC) agar (Oxoid, Hampshire, UK), another portion was membrane filtered (0.2- μ m-pore polyamide filter; Millipore, Billerica, MA) with subsequent filter placement on GVPC agar, and a fourth portion was heat treated (50°C for 30 min in a water bath) and subsequently spread on a GVPC agar plate. The plates were incubated at 36°C in a humidified environment with 2.5% CO₂ for 10 days and repeatedly inspected during the incubation. Colonies morphologically suspected to be *Legionella* were subcultured for species identification using a latex agglutination test (Oxoid, Hampshire, UK). The test did not reveal any of the species that were tested for, including *L. pneumophila*, *L. longbeachae*, *L. bozemanii*, *L. dumoffii*, *L. gormanii*, *L. jordanii*, *L. micdadei*, or *L. anisa*. For extraction of high-quality genomic DNA, five colonies from each water sample were subcultivated on GVPC and incubated for 48 h. Genomic DNA was extracted using the MagAttract high-molecular-weight (HMW) DNA kit (Qiagen, Hilden, Germany). A whole-genome sequencing library was prepared using an Illumina Nextera XT kit (Illumina, Inc., San Diego, CA), and paired-end sequencing (2 × 300 bp) was performed on a MiSeq system (Illumina, Inc.), generating 1,336,720 reads from 358,146,152 unassembled nucleotides and 1,182,150 reads from 311,991,780 unassembled nucleotides for isolate identification no. 4570-18-6 and 4567-18-4, respectively. Raw reads were *de novo* assembled using SPAdes version 3.11.1 (6) into a draft genome of 3,324,207 bp with 97 contigs, an *N*₅₀ value of 164,180 bp, and a 47.9% GC content (4570-18-6) and a draft genome of 3,212,147 bp with 118 contigs, an *N*₅₀ value of 213,110 bp, and a 45.9% GC content (4567-18-4). Contigs were filtered for a minimum coverage of 5× and a minimum length of 200 bp using SeqSphere+ (Ridom GmbH, Münster, Germany).

We used the NCBI Prokaryotic Genome Annotation Pipeline (7) for gene annotation and identified 3,026 total genes, 2,909 coding genes, 41 tRNAs, 4 noncoding RNAs

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(ncRNAs), and 62 pseudogenes (4570-18-6) and 3,110 total genes, 2,991 coding genes, 41 tRNAs, 4 ncRNAs, and 64 pseudogenes (4567-18-4).

Species identification was done via an NCBI 16S rRNA database BLAST search (8), and ribosomal multilocus sequencing typing (rMLST) was done via the PubMLST database (9). Both methods revealed 100% identity to *L. taurinensis* reference strain ATCC 700508. For phylogenetic analysis we generated an *ad hoc* core genome MLST scheme with 2,478 targets using the core genome MLST (cgMLST) target definer tool implemented in SeqSphere+ (10) and compared the Austrian strains with each other and with *L. taurinensis* reference strain ATCC 700508. We found the Austrian strains to differ from each other by 11 alleles and from the reference isolate ATCC 700508 by at least 53 alleles.

Data availability. The *Legionella taurinensis* whole-genome shotgun (WGS) projects have been deposited in DDBJ/ENA/GenBank under the accession no. [QZWB00000000](https://doi.org/10.1128/CMR.15.3.506-526.2002) (4570-18-6) and [QZWC00000000](https://doi.org/10.1128/CMR.15.3.506-526.2002) (4567-18-4). The versions described in this paper are the first versions, [QZWB01000000](https://doi.org/10.1128/CMR.15.3.506-526.2002) (4570-18-6) and [QZWC01000000](https://doi.org/10.1128/CMR.15.3.506-526.2002) (4567-18-4), and consist of sequences deposited under accession no. [QZWB01000001](https://doi.org/10.1128/CMR.15.3.506-526.2002) to [QZWB01000118](https://doi.org/10.1128/CMR.15.3.506-526.2002) (4570-18-6) and [QZWC01000001](https://doi.org/10.1128/CMR.15.3.506-526.2002) to [QZWC01000097](https://doi.org/10.1128/CMR.15.3.506-526.2002) (4567-18-4). SRA records are accessible under the accession no. [PRJNA492387](https://doi.org/10.1128/CMR.15.3.506-526.2002).

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