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GENOME ANNOUNCEMENT

Draft Genome Sequences of Two *Legionella dumoffii* Strains, TEX-KL and NY-23

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***Legionella* (*Fluoribacter*) *dumoffii* is one of the agents causing Legionnaires' disease. Here, we used Illumina second-generation sequencing technology to decipher for the first time the whole-genome sequences of two strains of this species, TEX-KL and NY-23. The assembly results for both strains consist of one chromosome and two plasmids.**

Legionella dumoffii, a pathogen that is a less common cause of Legionnaires' disease than *Legionella pneumophila* (6), was first isolated in 1979 as atypical *Legionella*-like organisms (ALLO) (4, 9), and it was designated as a new species in 1980 (1). *L. dumoffii* lives in soil and freshwater environments, and it is capable of surviving in human alveolar macrophages and epithelial cells as well (10). Infection by *L. dumoffii* can cause human pneumonia and accidentally induce other diseases, such as prosthetic-valve endocarditis and septic arthritis (7, 15). Based on its phenotypic differences from other species of the *Legionella* genus and the experimental results of DNA hybridization, Brown et al. suggested that *L. dumoffii* be transferred to the genus *Fluoribacter* as *F. dumoffii*, which is not yet widely accepted (2).

According to the Genomes Online Database (http://www.genomesonline.org), there is no genome sequence for *L. dumoffii* reported so far, and only one plasmid sequence from this species was described by us (11). Here, we present the whole-genome sequences of two *L. dumoffii* strains, TEX-KL (ATCC 33343) and NY-23 (ATCC 33279). TEX-KL was initially isolated from a postmortem lung specimen of a patient with fatal atypical pneumonia in Houston, TX (9), and NY-23 was isolated from a cooling tower in New York (4).

The strains were cultured on buffered charcoal-yeast extract (BCYE) agar, and DNAs were extracted as previously described (12). Whole-genome sequencing was performed using Illumina HiSeq 2000 (Illumina, Inc., United States) by generating paired-end libraries (500 bp and 6 kb) following the manufacturer's instructions. The read lengths were 90 bp and 49 bp for each library, from which 400 Mb and 210 Mb, respectively, of high-quality data were generated. The paired-end reads were first *de novo* assembled using SOAPdenovo version 1.06 (13), and then the scaffolds were manually connected according to 6-kb paired-end relationships. The coding sequences (CDS) were predicted by using Glimmer version 3.02 (5), and homologous comparison to the NCBI nonredundant public database for function annotations was performed by BLAST. The rRNA and tRNA were identified using RNAmmer (8) and tRNAscan-SE 1.21 (14), respectively, and the insertion sequence (IS) elements were annotated with ISsaga (16).

We obtained three scaffolds for each strain, which were identified as one circular chromosome and two plasmid sequences for each of them. The G+C contents of the chromosome are 39.7%, and the G+C contents of the plasmids are slightly lower (37.5 to 39.5%). The average nucleotide identity (ANI) between the chromosomes of the two strains is 99.4%. For strain TEX-KL, the smaller plasmid (pLD-TEX-KL, 66.5 kb) is identical to the one published previously (11). The smaller plasmid in strain NY-23 (pLDNY1, 81.8 kb) is similar to pLD-TEX-KL, with 51.3-kb common sequences identified between them (identity, >80%). The larger plasmids, the 126.5-kb pLDTK for TEX-KL and the 138.3-kb pLDNY2 for NY-23, were found to be homologous with pLPP, a previously reported plasmid of *L. pneumophila* strain Paris (132 kb) (3). There are 3,562 predicted CDS in TEX-KL (3,370 in chromosome and 192 in the plasmids), while there are 3,637 CDS in NY-23 (3,409 in the chromosome and 228 in the plasmids).

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under accession numbers AGVT00000000 (Tex-KL) and AGVU00000000 (NY 23). The versions described in this paper are the first versions, AGVT01000000 and AGVU01000000.

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