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Draft Genome Sequence of *Providencia heimbachae*, Isolated from a Diabetic Foot Ulcer

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***Providencia* spp. are ubiquitous Gram-negative bacteria of the family Enterobacteriaceae that are common opportunistic pathogens. In the present work, we have sequenced, annotated, and compared the draft genome of *Providencia heimbachae*, which was recovered from a diabetic foot ulcer. It is composed of 4.22 Mb and encodes 3,843 protein-coding genes and 79 RNA genes, including 11 rRNA genes.**

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Providencia spp. are ubiquitous Gram-negative bacteria in the Enterobacteriaceae family that are often opportunistic pathogens. Members of this genus have been identified as part of the normal human gut flora (1) and have been associated with numerous animals worldwide (2, 3). In 1986, Muller et al. (4) characterized a new group of *Providencia* and described *Providencia heimbachae* on the basis of biochemical and DNA hybridization tests. The first isolate was obtained from the stool of a 23-year-old woman in Seattle–King County, Washington, USA, who suffered from unexplained diarrhea (5).

In the present work, we have sequenced, annotated, and compared the draft genome of *P. heimbachae*, isolated from a diabetic foot ulcer in 2014 and deposited in our collection CSUR under number P2169. The genomic DNA was sequenced using a combination of paired-end libraries (average insert size of 250 bp) and mate-pair (2.5-kb) libraries on the Illumina MiSeq. The generated reads were assembled using the SPAdes genome assembler (6). The assembled genome counts eight contigs regrouped in seven scaffolds. The estimated genome size was 4,220,813 bp with a G+C content of 40.31%, which is identical to *Providencia rettgeri* strain H1736 (GenBank: NZ_CVLT01000017). Both the estimated genome size and the G+C content are in the range of the species of the *Providencia* genus.

A total of 3,843 protein-coding sequences were predicted, forming the sequence coding and representing 85.71% of the genome size. We identified 79 structural RNAs (8 genes are 5S rRNA, 1 gene is 16S rRNA, 2 genes are 23S rRNA, and 68 genes are tRNA genes) using tRNAscan-SE version 1.3 (7) and RNAmmer (8). A homology search against the public protein database from NCBI using the BLASTp program identified 455 hypothetical proteins; 1,094 proteins associated to virulence were found, representing 28.46% of the total genes.

Nucleotide sequence accession numbers. This whole-genome project has been deposited at DDBJ/EMBL under the accession numbers [FIZD01000001](https://ncbi.nlm.nih.gov/nucl/FIZD01000001) to [FIZD01000008](https://ncbi.nlm.nih.gov/nucl/FIZD01000008).

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