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Draft Genome Sequence of a Diarrheagenic *Morganella morganii* Isolate

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This is a report of the whole-genome draft sequence of a diarrheagenic *Morganella morganii* isolate from a patient in Michigan, USA. This genome represents an important addition to the limited number of pathogenic *M. morganii* genomes available.

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Morganella morganii was originally identified as a cause of diarrheal disease (1) and is now recognized as an important opportunistic pathogen. It has been linked to catheter-based urinary tract infections, sepsis, and wound infections and has also been reported among immunocompromised, postoperative, and intensive care unit patients (2, 3). *M. morganii* was found to produce β-lactamases, which results in resistance to a set of clinically relevant antibiotics, while the *in vivo* transfer of an *M. morganii*-derived plasmid ($bla_{OXA-181}$) encoding carbapenem resistance was recently observed in *Escherichia coli* cultured from a wound infection (4). To date, only a subset of *M. morganii* genomes have been sequenced (5–7); hence, additional genomes are needed to facilitate comparative genomic analyses and the identification of virulence and resistance genes.

The *M. morganii* isolate TW17014 was recovered in 2011 from the stool of an adult male who had been hospitalized after suffering from abdominal pains, diarrhea, and bloody diarrhea. Genomic DNA was extracted and purified using the Qiagen DNA extraction kit (Qiagen Sciences, MD). Whole-genome sequencing was performed with the Illumina MiSeq platform using 500 cycles with 250-bp paired-end reads following library preparation with the Nextera XT kit (Illumina, Inc., San Diego, CA). The draft genome (3,982,639 bp) with 32× coverage was assembled using Velvet 1.2.07 (8), and ambiguous sequences and adapters were trimmed using Trimmomatic (9), followed by quality checking using FastQC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/). The genome was annotated using the Prokaryotic Genomes Annotation Pipeline (10), which identified 3,873 genes with 3,724 coding sequences (CDSs), 9 rRNAs, 52 tRNAs, and 3 noncoding RNAs (ncRNAs). Functional annotation was carried out using the Rapid Annotations using Subsystems Technology (RAST) server (11), and 3,810 coding sequences with 59 RNAs were identified. Among the annotated subsystem features, 361 genes were identified as amino acids and derivatives, 307 genes were linked to carbohydrate metabolism, 299 genes encode cofactors or vitamins, and 237 genes were associated with protein metabolism. A total of 78 genes were found to be associated with virulence, disease, and defense, along with 21 phage-related genes. Use of the Resistance Gene Identifier (RGI) version 2 via the Comprehensive Antibiotic Resistance Database (12) identified 571 genes associated with antibiotic resistance, multidrug efflux transporter systems, macrolide efflux proteins, resistance-nodulation-cell division, and two-component regulatory systems. Antibiotic resistance genes targeting β-lactams (n = 2), chloramphenicol (n = 1), polymyxin (n = 4), lincosamide (n = 1), fosfomycin (n = 1) and mac/lin/phe/str/lin (n = 1) were found, as well as 16 genes associated with antibiotic efflux pumps. This *M. morganii* genome was most closely related to *Providencia rustigianii* DSM 4541 (score, 530), *Providencia alcalifaciens* DmeI2 (score, 306), and *Proteus mirabilis* WGLW4 and WGLW6 (scores, 280 and 272, respectively) genomes.

Nucleotide sequence accession numbers. The annotated draft genome has been deposited at DDBJ/EMBL/GenBank under the accession no. LFWB00000000. The version described in this paper is LFWB01000000.

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