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Draft Genome Sequence of *Enterobacter cloacae* Strain JD6301

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***Enterobacter cloacae* strain JD6301 was isolated from a mixed culture with wastewater collected from a municipal treatment facility and oleaginous microorganisms. A draft genome sequence of this organism indicates that it has a genome size of 4,772,910 bp, an average G+C content of 53%, and 4,509 protein-coding genes.**

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Enterobacter is a genus in the family *Enterobacteriaceae*. This family is composed of Gram-negative rods, which can be found in many different environments, ranging from soil to humans. Many strains of *Enterobacter* are known to be resistant to an array of antibiotics, and some are considered nosocomial pathogens (1). Here, we report the genome sequence of the novel *Enterobacter cloacae* strain JD6301. This novel strain was isolated from a coculture of wastewater collected from a municipal treatment facility and oleaginous bacteria. The bacterial strain was isolated by subsequent dilutions into fresh medium and finally by culturing onto nutrient agar under aerobic conditions at 30°C. The bacteria were found to grow under a wide variety of conditions, including temperatures ranging from 28 to 39°C, and they were also found to tolerate slightly acidic conditions (pH 4.5). On blood agar, JD6301 exhibits alpha-hemolysis. MacConkey and eosin methylene blue agar confirm that it is capable of utilizing lactose. It is oxidase negative and produces gas in triple sugar iron agar. The most unique feature of JD6301 is its ability to form inclusion bodies, which has not been characterized for this species. The lipid weight of this strain was found to constitute approximately 50% of the total cellular weight, suggesting that these inclusion bodies may contain lipids.

A draft of the genome of *E. cloacae* JD6301 was generated at the DOE Joint Genome Institute (JGI) using Illumina HiSeq 2000 technology. To remove any artifacts following Illumina sequencing, raw data were passed through DUK, a program developed by JGI. The Illumina reads were assembled using Velvet version 1.104 (2), and 1- to 3-kb simulated paired ends were created from Velvet contigs using wgsim (<https://github.com/lh3/wgsim>); the Illumina reads were then assembled with simulated pairs using Allpaths-LG versus r42328 (3). The assembly yielded 53 contigs in 49 scaffolds. For genome annotation, Prodigal was used to identify genes (4). This was followed by manual curation using GeneP-RIMP (5). tRNAscanSE (6) was used to find tRNA genes, while rRNA genes were identified using SILVA (7). INFERNAL (<http://infernal.janelia.org>) was used to identify noncoding RNAs. Other gene predictions and manual function annotation were per-

formed using the Integrated Microbial Genomes (IMG) platform (<http://img.jgi.doe.gov>) developed by JGI (8).

The completed genome of strain JD6301 is 4,772,910 bp in length. There are an estimated 4,288,696 coding bases, and the G+C content is near 53%. There are a total of 4,509 protein-coding genes, with 84.91% having predicted functions. Of the genes identified, 4,246 match those of *E. cloacae*. Multiple multi-drug efflux pumps were identified, which is common among *E. cloacae* strains (1). Genes associated with a type IV secretion system were also identified, another common feature of *E. cloacae* (9). Proteins associated with pilus production were also identified, which may have contributed to the inclusion bodies observed in this novel strain. The novel aspect of an *Enterobacter* sp. strain producing large quantities of lipids warrants further investigation.

Nucleotide sequence accession numbers. This draft genome sequence has been deposited in the IMG system under accession no. 20133 and GenBank under accession no. [JDWH00000000](https://www.ncbi.nlm.nih.gov/nuccore/JDWH00000000).

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For strain and DNA requests, please contact J.R.D.

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