

Genome Sequence of the Lactate-Utilizing *Pseudomonas aeruginosa* Strain XMG

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***Pseudomonas aeruginosa* XMG, isolated from soil, utilizes lactate. Here we present a 6.45-Mb assembly of its genome sequence. Besides the lactate utilization mechanism of the strain, the genome sequence may also provide other useful information related to *P. aeruginosa*, such as identifying genes involved in virulence, drug resistance, and aromatic catabolism.**

Certain *Pseudomonas* species, such as *Pseudomonas aeruginosa*, *P. putida*, and *P. stutzeri*, can use lactate as the sole carbon and energy source for growth (6, 7, 11, 15). NAD-independent L-lactate dehydrogenase (L-iLDH) and NAD-independent D-lactate dehydrogenase (D-iLDH) catalyze the oxidation of L-lactate and D-lactate into pyruvate, respectively. They play essential roles in the utilization of lactate in these species (6, 7, 14, 15). Some potential applications of L-iLDH and D-iLDH, such as 2-oxobutyrate production (4), pyruvate production (2, 5, 10, 19), and kinetic resolution of 2-hydroxy acids racemic mixtures (3, 8), have been also studied in recent years.

P. aeruginosa is a ubiquitous environmental bacterium that can cause disease in animals, including humans. As an opportunistic pathogen of humans, it can cause wound and burn infections as well as respiratory infections. *P. aeruginosa* is known for antibiotic resistance and has multiple virulence factors, enabling the formation of biofilms and infection of the multiple host species (16). *P. aeruginosa* XMG, a bacterium isolated from soil, can utilize lactate for growth (7). In a previous work, the *lldRPDE* operon, which comprises 4 genes, *lldR* (encoding a lactate-responsive regulator LldR), *lldP* (encoding a lactate permease), *lldD* (encoding an L-iLDH), and *lldE* (encoding a D-iLDH), was found in *P. aeruginosa* XMG. The regulation of the lactate utilization operon in *P. aeruginosa* XMG by the regulator LldR was also clarified (7).

Here, we present the draft genome sequence of *P. aeruginosa* XMG obtained using the Illumina GA system, which was performed by the Chinese National Human Genome Center at Shanghai in China with a paired-end library. The reads were assembled with VELVET (20), and the draft genome sequence was annotated by the RAST server (1). The functional description was determined using Clusters of Orthologous Genes (17), and tRNAs were predicted by tRNAscan-SE (13). The rRNAs were predicted by RNAmmer (12). The G+C content was calculated using the genome sequence.

The draft genome sequence of strain XMG comprises 6,454,576 bases, which was assembled into 226 contigs. It has a GC content of 66.4%. There are 61 predicted tRNAs and 5,933 protein-coding sequences (CDSs) (949-bp average length) in the genome sequence. The coding percentage is 78.2%, and 4,639 CDSs have functional predictions.

There are 565 subsystems represented in the genome sequence. The *lldRPDE* operon was annotated in the lactate utilization subsystem. Besides the lactate utilization operon, LldR also regulates the transcription of *ldhA* (encoding fermentative L-lactate dehydrogenase) and the *cgl1934-fruK-ptsF* operon (involved in fructose utilization) in *Corynebacterium glutamicum* (9, 18). The genes *ldhA*, *fruK*, and *ptsF* were found in the genome sequence of *P. aeruginosa* XMG. Thus, LldR might also regulate the transcription of those genes in strain XMG. Further analysis of the genome sequence might also provide other useful information related to *P. aeruginosa*, such as identifying genes involved in virulence, drug resistance, and aromatic catabolism.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession number [AJXX00000000](https://www.ncbi.nlm.nih.gov/nuccore/AJXX00000000). The version described in this paper is the first version, with accession number [AJXX01000000](https://www.ncbi.nlm.nih.gov/nuccore/AJXX01000000).

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