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Genome Sequence of a Strain of the Human Pathogenic Bacterium *Pseudomonas alcaligenes* That Caused Bloodstream Infection

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***Pseudomonas alcaligenes*, a Gram-negative aerobic bacterium, is a rare opportunistic human pathogen. Here, we report the whole-genome sequence of *P. alcaligenes* strain MRY13-0052, which was isolated from a bloodstream infection in a medical institution in Japan and is resistant to antimicrobial agents, including broad-spectrum cephalosporins and monobactams.**

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Pseudomonas alcaligenes is a Gram-negative aerobic rod belonging to the bacterial family *Pseudomonadaceae* and is a common inhabitant of soil and water. A recent study showed that *P. alcaligenes* is useful as a microbial inoculant for the biodegradation of toxic polycyclic aromatic hydrocarbons (1). *P. alcaligenes* has also been known as a rare opportunistic human pathogen (2). Based on 16S rRNA gene sequence analysis, *P. alcaligenes* was classified in the *Pseudomonas aeruginosa* group (3). However, little is known about the clinical importance of *P. alcaligenes* and its virulence factors, mainly because of the difficulties in identifying and distinguishing this bacterium from closely related *Pseudomonas* species in medical settings.

In this report, we announce the availability of the first draft genome sequence of *P. alcaligenes*. *P. alcaligenes* strain MRY13-0052 was recovered from a bloodstream infection in a medical institution in Japan in 2013 and was resistant to broad-spectrum cephalosporins and monobactams. Whole-genome shotgun (WGS) sequencing of strain MRY13-0052 was performed using the Roche 454 pyrosequencing platform (500-bp insert size). The reads were assembled *de novo* using Newbler Assembler version 2.3 (Roche). The draft genome sequence of MRY13-0052 consists of 237 contigs, yielding a total of 6,876,944 bp with an N_{50} contig size of 64,175 bp. The mean G+C content was 65.8%. A total of 6,190 coding DNA sequences were identified by the RAST server (http://rast.nmpdr.org) (4). The MRY13-0052 strain carried three class C β-lactamase genes that might confer resistance to β-lactam antibiotics. Any other acquired antimicrobial resistance genes in the WGS data were not detected using a Web-based tool, ResFinder version 1.3 (http://cge.cbs.dtu.dk/services/ResFinder/) (5).

Bacterial pathogens frequently use protein secretions to interact with their hosts. MRY13-0052 contains the type VI secretion system (T6SS) gene cluster and three genes that encode VgrG (valine glycine repeat G) translocator proteins (6). The T6SS, which is conserved among *Pseudomonas* species (7), delivers effectors into neighboring organisms, including bacteria and mammalian cells, leading to cytotoxicity and cell death in the targets (6). The MRY13-0052 strain furthermore contains a set of genes that encode proteins homologous to *P. aeruginosa* Tse1 (type VI effector 1) and Tsi1 (type VI immunity 1) (8) (66.9% and 48.8% identities, respectively). On the other hand, MRY13-0052 is devoid of the virulence-associated type III secretion system (T3SS) gene cluster, whereas a T3SS is the major virulence factor in animal and plant pathogenic *Pseudomonas* species, *P. aeruginosa*, and *Pseudomonas syringae* (9, 10). These data suggest that the T6SS might be an important virulence determinant in *P. alcaligenes* and that *P. alcaligenes* might partially share the same T6SS-dependent effector and immunity system with *P. aeruginosa*.

A more detailed report of the virulence phenotype of *P. alcaligenes* MRY13-0052 will be included in a future publication. A genome-wide comparison of *P. alcaligenes* with related *Pseudomonas* species, such as *P. aeruginosa*, *Pseudomonas mendocina*, and *Pseudomonas pseudoalcaligenes*, will facilitate additional comprehensive bioinformatic and phylogenetic analyses, thus expanding our understanding of fatal nosocomial infections caused by these opportunistic human pathogens.

Nucleotide sequence accession numbers. The WGS projects for *P. alcaligenes* MRY13-0052 have been deposited at DDBJ/EMBL/GenBank under the accession no. BATO00000000. The version described in this paper is the first version, BATO01000000.

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