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Genome Sequence of *Acinetobacter calcoaceticus* PHEA-2, Isolated from Industry Wastewater▽

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Genome analysis of *Acinetobacter calcoaceticus* PHEA-2 was undertaken because of the importance of this bacterium for bioremediation of phenol-polluted water and because of the close phylogenetic relationship of this species with the human pathogen *Acinetobacter baumannii*. To our knowledge, this is the first strain of *A. calcoaceticus* whose genome has been sequenced.

The *Acinetobacter* genus belongs to the gamma subclass of proteobacteria, which are widespread in nature and can be obtained from soil and water, but they are also recognized as significant pathogens in hospital environments (8, 11). *Acinetobacter* isolates are nutritionally versatile, and they often display natural competence that may be the mechanism for horizontal gene transfer by which acinetobacteria achieve genetic diversity (3). *Acinetobacter calcoaceticus* and *Acinetobacter baumannii* are genotypically closely related and phenotypically difficult to distinguish (5). The nucleotide sequences of the genomes of six clinical *A. baumannii* isolates have been established, but there was no *A. calcoaceticus* genome available for comparison (1, 3, 7, 12).

A. calcoaceticus PHEA-2 was originally isolated from industrial wastewater in China because of its ability to use phenol as the sole carbon source (13–15). In this report, raw reads of the strain genome were generated by using Illumina GA (Solexa) and assembled with the SOAP *de novo* software (9). Based on the reference genome of *A. baumannii* AYE (12), a draft genome of PHEA-2 was completed. Closure of the 115 gaps was finished by PCR and prime walking by using the routine Sanger method. Contigs and PCR products were assembled using the sequence assembly program (Phrap). Coding sequences (CDSs) were predicted using GLIMMER (4). Putative ribosomal-binding sites and tRNA genes were identified using the ribosome binding site (RBS) finder (6) and tRNAscan-SE (10). The rRNA operons and transposons were revealed by BLASTN (2). Tandem repeats shorter than 2,000 nucleotides (nt) were predicted by the Tandem Repeats Finder (Trf) software (http://tandem.bu.edu/trf/trf.html) and RepeatMasker (http://www.repeatmasker.org/).

A. calcoaceticus PHEA-2 has a single circular chromosome of 3,862,530 bp and an average G+C content of 38.8%. The chromosome of PHEA-2 contains 3,599 putative coding sequences (938-bp average length, 87.5% coding density), of which 3,095 have functional predictions. The genome encodes 69 tRNAs, representing all amino acids and two rRNA operons. COG analysis for strain PHEA-2 predicts 96 genes involved in signal transduction. Strain PHEA-2 has many two-component systems, including 15 predicted histidine kinase-associated CDSs (HPKs), 30 response regulator receiver proteins (RRs), and two hybrid proteins with both histidine kinase and response regulatory domains for sensing and responding to dynamic environmental conditions. Consistent with its abilities to mineralize various aromatic compounds, three different major pathways for the catabolism of these compounds, i.e., the catechol (*cat*), protocatechuate (*pca*), and phenylacetate (*pha*), are predicted in PHEA-2. The clustering of these catabolic genes and their high G+C contents (47.4%, 50.8%, 51.4%, and 49.1%) support the hypothesis that the four catabolic regions in the PHEA-2 genome were acquired by horizontal gene transfer. In general, industry wastewater is an extreme and hostile habitat where various xenobiotic compounds, including heavy metals, have toxic effects on microbial activity. Analysis of the complete genome sequence of PHEA-2 revealed many clues for the basis of its stress tolerance. It also offers opportunities for exploiting the biotechnological potential of the genus *Acinetobacter*.

Nucleotide sequence accession number. The complete nucleotide sequence of *A. calcoaceticus* PHEA-2 has been deposited in GenBank under accession number CP002177.

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