De Novo Genome Project of Cupriavidus basilensis OR16

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Here we report on the complete genome sequence of Cupriavidus basilensis OR16 NCIMB BO2487. The genome of strain OR16 contains 7,534 putative coding sequences, including a large set of xenobiotics-degrading genes and a unique glucose dehydrogenase gene that is absent from other Cupriavidus genomes.

The genus Cupriavidus consists of metabolically diverse (chemooorganotrophic and facultative chemolithotrophic) organisms that inhabit various niches, like soil, root nodules, aquatic environments, and human clinical sources. Sugar utilization of Cupriavidus strains are limited to gluconate and fructose; surprisingly, glucose does not support growth. Cupriavidus environmental isolates are usually characterized by significant heavy metal resistance (5, 6), and a few of them are important xenobiotics degraders (3, 8, 9).

The first described Cupriavidus basilensis strain was isolated as a 2,6-dichlorophenol decomposer (13). Other isolates of this species were reported to degrade a wide variety of xenobiotics, including furfural, 5-hydroxymethyl furfural (7), bisphenol A (4), chlorophenols (14), and atrazine (12). The subject of our genome project, C. basilensis strain OR16, was isolated from a Hungarian pristine soil sample. It was identified by molecular taxonomy as C. basilensis. Regarding its metabolic properties, it was characterized as a good petroleum hydrocarbon-degrading and mycotoxin-degrading (aflatoxin B1 and T2 toxin) strain. A unique feature of this isolate, in contrast to all known Cupriavidus strains, is that it can use glucose as the sole carbon and energy source for growth.

Genome sequencing of C. basilensis OR16 was performed by combining the cycled ligation sequencing on the SOLiD 4 system (Life Technologies) with 454 FLX pyrosequencing (Roche). We generated 25,522,122 mate-paired (2 by 50-bp) reads on SOLiD along with 165,651 (≥360-bp) reads on 454 FLX, which altogether yielded >1,500-fold coverage. Assembly was performed using the Genomics Workbench 4.8 de novo plug-in and the Omixon Gapped SOLiD alignment 1.3.2 plug-in (2) provided by CLC Bio and Omixon, respectively, which generated 416 large (≥200-bp) contigs. Automatic annotation of the genome was performed with the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP; http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html), which utilizes GeneMark, Glimmer, and tRNAscan-SE searches. The uncompleted draft genome of C. basilensis OR16 consists of 8,546,215 bp, with a GC content of 41.2% and 7,534 putative coding sequences.

Until now, five Cupriavidus genome projects have been completed for representatives of the species C. necator, C. metallidurans, C. pinatubonensis, and C. taiwanensis (1, 6, 8, 10, 11). The sizes of these genomes range between 6.5 and 8.5 Mbp; thus, the genus belongs to a group of microbes which have a large genome.

The genome sequence of C. basilensis OR16 reveals an impressive catabolic potential, since several ring cleavage pathways for aromatic compounds were found, including catechol and protocatechuato ortho ring cleavage pathways, a catechol meta ring cleavage pathway, gentisate and homogentisate pathways, a hydroxyquinol pathway, a hydroquinone pathway, and a benzoylecoenzyme A pathway. Its survival under heavy metal stress conditions is ensured by genes encoding heavy metal transport/ detoxification proteins, such as copper-zinc-cadmium-chromate resistance proteins (copCD, a copper chaperone) and heavy metal efflux pumps (copper/heavy metal efflux P-type ATPases and CzcA family heavy metal efflux pumps).

Interestingly, besides an OprB glucose porin, a putative membrane-bound PQQ-dependent glucose dehydrogenase gene (OR16_10529) was also identified, which catalyzes glucose production from glucose. The presence of this gene is unique in strain OR16, as none of the other known Cupriavidus genomes encode it or its homologues, and this may account for the unusual glucose metabolism of strain OR16.

Nucleotide sequence accession numbers. The nucleotide sequence of C. basilensis strain OR16 has been deposited in DDBJ/EMBL/GenBank under accession number AHJE00000000. The version described in this paper is the first version, AHJE01000000.

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