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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Citreicella aestuarii* Strain 357, a Member of the *Roseobacter* Clade Isolated without Xenobiotic Pressure from a Petroleum-Polluted Beach

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***Citreicella aestuarii* 357 is a member of the *Roseobacter* clade that was isolated without xenobiotic pressure from an oil-polluted sand sample from the Galician coast (Spain). Its genome sequence suggests an organoheterotrophic metabolism, including a wide catabolic potential for aromatic hydrocarbons.**

Bacteria from the *Roseobacter* clade are common in seawater and sediments. Roseobacters are also associated with marine algae and metazoans (1). They are considered generalist, metabolically versatile, mixotrophic bacteria that are able to obtain carbon and energy by chemoorganotrophy, photoheterotrophy, and/or chemolithotrophy (5). The relevant role that roseobacters play in marine ecosystems has led to large efforts in terms of genome analysis (2). So far, more than 40 genomes have been sequenced, including a single representative of the genus *Citreicella* (isolate SE45).

Isolate 357 was obtained by plating on marine broth agar an oil-polluted sand sample obtained from Praia da Seda beach (Galicia, Spain) after the *Prestige* tanker accident in Spain. The isolate was identified by 16S rRNA gene sequencing as *Citreicella aestuarii* (98.9% sequence similarity to type strain AD8), which was further confirmed by DNA-DNA hybridization (76% relatedness). Strain 357 is catalase and oxidase positive, and it is able to oxidize thiosulfate and reduce nitrate. Cells are motile rods with a single polar flagellum.

Genome sequencing was done using the 454 GS FLX Titanium system. A total of 395,325 reads were assembled using Newbler v. 2.3. A draft genome of 180 contigs over 500 bp in size was obtained. Genome annotation and analysis were done using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html), the KEGG Automatic Annotation Server (4), and the Pathway Tools program (3). The genome of strain 357 was 4,598,615 bp in length (30-fold coverage), presented a high G+C content (62.8%), showed a coding density of 87.6%, and contained 4,573 coding sequences and 44 tRNA genes. Although a single contig harboring the entire rRNA operon was obtained, the 136-fold coverage of individual reads suggested the presence of four copies of each rRNA gene. Genome analysis suggested the presence of at least 76 plausible transposases belonging to 11 different insertion sequence families and 9 integrase-like proteins.

Putative genes that cover all of the major metabolic pathways were found, including the glycolysis; tricarboxylic acid cycle; pentose phosphate; Entner-Doudoroff; and amino acid, purine, and pyrimidine biosynthesis pathways. Genome analysis revealed that strain 357 is able to generate ATP via oxidative phosphorylation and has the putative genes for both aa_3- and cbb_3-type cytochrome *c* oxidases. In addition, its genome codes for putative sulfite-oxidizing chemolithotrophy (*sox* genes), carbon monoxide oxidation (*cox* genes), nitrate reduction to ammonia, and sulfate and thiosulfate reduction to H_2S.

The genome of strain 357 has 51 genes involved in flagellar assembly and chemotaxis (*che*, *flg*, *flh*, *fli*, and *mot* genes). It also contains more than 240 genes related to two-component systems and to ABC transporters. Other transport systems, such as a type IV secretion system and the Sec pathway, were also detected.

Finally, more than 120 protein-coding genes possibly involved in the metabolism of aromatic compounds (i.e., benzoate, toluene, xylene, and naphthalene) were found in the genome of *C. aestuarii* 357. Although strain 357 was isolated without xenobiotic pressure, the data are consistent with the polluted environment from which it was isolated and suggest a wide catabolic potential that is currently being evaluated.

Nucleotide sequence accession numbers. This Whole-Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. AJKJ00000000. The version described in this paper is the first version, AJKJ00000000.1.

ACKNOWLEDGMENTS

L.Y.S.-S., I.B.-G., and J.M.P.-V. were supported by grants from the Santander Bank, the Government of the Balearic Islands (FSE cofunding), and the Spanish Science and Education Ministry, respectively. J.A.C.-O. was supported by a fellowship from the Fundación Ramón Areces. B.N. and R.B. acknowledge the financial support of the Spanish MINECO through projects CTM2008-02574/MAR and CTM2011-

Received 13 July 2012 Accepted 17 July 2012

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doi:10.1128/JB.01261-12

24886 (with FEDER cofunding) and the Acciones Integradas program (FR2009-0106). J.A. thanks the Commissariat à l'Energie Atomique et aux Energies Alternatives and the Ministère des Affaires Etrangères et Européennes, République Française (Partenariat Hubert Curien, Picasso Program), for financial support.

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