Pseudomonas extremaustralis 14-3b presents genes involved in the synthesis of different polyhydroxyalkanoates, in tolerance and degradation of pollutants, and in microaerobic metabolism. Several genomic islands were detected. Genetic machinery could contribute to the adaptability to stressful conditions. This is the first genome sequence reported from a Pseudomonas isolated from cold environments.

Pseudomonas extremaustralis 14-3T was isolated from a temporary pond in Antarctica (8). This strain shows high heat, cold, and oxidative stress resistance (3, 4) in association with accumulation of large amounts of polyhydroxybutyrate (PHB), a type of polyhydroxyalkanoate (PHA). This polymer is synthesized from octanoate but not from glucose (1). Here, we report the genome sequence of P. extremaustralis 14-3b (DSM 25547), a natural derivative of the type strain able to produce PHB from both octanoate and glucose.

The sequence was obtained using a whole-genome shotgun strategy with a Roche 454 GS Titanium pyrosequencer at INDEAR, Argentina. Assembly was done by using Newbler version 2.5.3 with the -urt option with 20× genome coverage, generating 113 large contigs. The draft genome was 6,587,033 bases in length, with a mean GC content of 60.66%. Genome annotation was done using the standard operating procedures for prokaryotic annotation from the RAST server (5). A total of 5,934 coding sequences (CDS) and 62 structural RNAs (49 tRNAs) were predicted. Annotation covered 500 RAST subsystems (49%), while 1,516 CDS (26%) were classified as encoding hypothetical proteins.

The P. extremaustralis genome showed a well-developed antioxidant defense system that include five catalases, one cytochrome c peroxidase, and two alkyl hydroperoxide reductases. This strain is able to use nitrate as an alternative electron acceptor (9); in concordance, its genome was found to have 18 genes related to nitrate metabolism. Genes involved in nitrate, nitric oxide, and nitrous oxide reduction were present. Genes that code for nitrite reductases, with the exception involved in osmotic resistance, vitamin biosynthesis, PHB and exopolysaccharide metabolism, and proteins related to transport systems. We have described that PHB biosynthesis genes are located in a GI (2). Genome analysis showed other three genes involved in PHA metabolism in the same GI. Pseudomonas species typically have the phaC1Z2DIF cluster, which is responsible for synthesis of medium-chain-length PHA. In P. extremaustralis, these genes were also detected, but phaI and phaF were not located downstream of phaD due to the insertion of seven open reading frames with high similarity to those found in the betaproteobacteria.

The overall genome analysis revealed a high potential for adaptability to extreme environmental conditions.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AHIP00000000. The version described in this paper is the first version, AHIP01000000.

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