

## Draft Genome Sequence of *Bizionia argentinensis*, Isolated from Antarctic Surface Water

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**A psychrotolerant marine bacterial strain, designated JUB59<sup>T</sup>, was isolated from Antarctic surface seawater and classified as a new species of the genus *Bizionia*. Here, we present the first draft genome sequence for this genus, which suggests interesting features such as UV resistance, hydrolytic exoenzymes, and nitrogen metabolism.**

*Bizionia argentinensis* JUB59<sup>T</sup> belongs to the marine clade of the family *Flavobacteriaceae* (1). Members of this clade are widespread in marine environments, from the tropics to polar oceans, where they play an important role in the mineralization of organic matter (2). Whole-genome sequencing of strain JUB59<sup>T</sup> was performed using the Roche 454 GS FLX system. A shotgun analysis with a 34× coverage was performed, resulting in 405,465 high-quality reads with an average length of 277.1 bases. Sequences were assembled using Newbler, and 107 contigs were obtained. Gene prediction was performed using Glimmer 3.0. rRNAs and tRNAs were predicted using rRNAmmer (7) and tRNAscan-SE (10), respectively. Each gene was annotated through BlastP searches against the Swiss-Prot, COG, and KEGG databases. Also, hmmerScan was performed against Pfam and Tigrfam. Finally, SignalP was performed to predict signal peptides. Analysis of the unclosed draft genome shows a coding density of 85.09% and a GC content of 33.77%. A total of 3,195 open reading frames (ORFs) were predicted, of which 979 were assigned as hypothetical proteins. A total of 1,583 were assigned to COG classes, and 1,195 were assigned to KEGG pathways.

The *Bizionia argentinensis* JUB59<sup>T</sup> genome contained genes for a complete tricarboxylic acid cycle, glycolysis, and a pentose phosphate pathway. The genome sequence also revealed that JUB59<sup>T</sup> is a denitrifying facultative anaerobic bacterium capable of assimilatory-dissimilatory nitrite re-

duction and uses NO<sub>2</sub><sup>-</sup> as the electron acceptor, a capacity that has been only rarely reported for *Flavobacteriaceae* members (6). All genes related to the denitrification process were found on the genome except for nitrate reductase. In particular, reduction of NO<sub>2</sub><sup>-</sup> to NO is catalyzed by a copper-containing nitrite reductase. By the assimilatory route, NO<sub>2</sub><sup>-</sup> is reduced by a nitrite reductase (ammonia forming), and ammonia is then used as a source of nitrogen for amino acid biosynthesis. Consistent with the high levels of UV-B irradiance determined by the latitude but also by the presence of a spring ozone hole (4), the genome contains 3 photolyase genes and complete DNA repair systems. In addition, the bacterial genome presented genes involved in the biosynthesis of carotenoids and xanthophylls. In particular, a copy of a β-carotene hydroxylase that catalyzes the production of β-cryptoxanthin and zeaxanthin, pigments detected previously in other Antarctic *Flavobacteria* (5) but not in members of the genus *Bizionia*, was found (3, 8, 9). According to the permanent low ambient temperature, the genome also presented a set of genes coding for the biosynthesis of unsaturated fatty acids. Another interesting feature of *B. argentinensis* is its ability to release peptidases to the environment in order to degrade surrounding compounds. We have found 24 genes belonging to Pfam or Tigrfam, peptidase families that also have signal peptides. This fact could permit us to extend the relevant ecological role in natural carbon cycling attributed to other marine *Bacteroidetes* to this Antarctic member of the genus *Bizionia*.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/

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GenBank under the accession number AFXZ00000000. The version described in this paper is the first version, AFXZ01000000.

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