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GENOME ANNOUNCEMENT

Draft Genome Sequence of the Volatile Organic Compound-Producing Antarctic Bacterium *Arthrobacter* sp. Strain TB23, Able To Inhibit Cystic Fibrosis Pathogens Belonging to the *Burkholderia cepacia* Complex

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***Arthrobacter* sp. strain TB23 was isolated from the Antarctic sponge *Lissodendoryx nobilis*. This bacterium is able to produce antimicrobial compounds and volatile organic compounds (VOCs) that inhibit the growth of other Antarctic bacteria and of cystic fibrosis opportunistic pathogens, respectively. Here we report the draft genome sequence of *Arthrobacter* sp. TB23.**

Volatile organic compounds (VOCs) are a class of heterogeneous molecules that are synthesized by various organisms, and the function, for most of them, has not been clarified. There is, however, increasing evidence that supports the idea that VOC production is a common strategy that is widespread among distantly related bacteria (3). Particularly interesting is the novel finding that several Antarctic bacteria affiliated with diverse genera (both Gram positive and Gram negative) and isolated from diverse ecological niches (sponges, seawater, and sediments) produce VOCs (7). The analysis of VOC profiles performed using gas chromatography–solid-phase microextraction technology also revealed that these VOCs belong to quite different chemical classes, including sulfur compounds (8). The biological significance of VOC production by Antarctic bacteria is still unknown, but it has been recently demonstrated that many sponge-associated Antarctic bacteria possess the ability to inhibit the growth of other Antarctic strains (4). Furthermore, these bacteria are also effective toward some human opportunistic pathogens. Indeed, some Antarctic bacteria are able to specifically inhibit the growth of *Burkholderia cepacia* complex (Bcc) strains (7). Bcc strains are among the most dangerous pathogens in immunocompromised patients, such as those affected by cystic fibrosis (CF) (6), and are known to be resistant to several antibiotics (1, 2). It is also noteworthy that the ability to inhibit the growth of Bcc bacteria is related to the production of VOCs (7, 8). One of the most interesting Antarctic bacteria is *Arthrobacter* sp. strain TB23, a strain isolated from a sponge affiliated with the species *Lissodendoryx nobilis*, which exhibited a very high inhibitory activity toward both other Antarctic and Bcc strains (4, 7). Therefore, the knowledge of the genome of this strain represents the first mandatory step toward the identification of the metabolic pathways responsible for new antimicrobial molecule production.

Herein we report the draft genome sequence of *Arthrobacter* sp. strain TB23. The TB23 genome was sequenced using Illumina HiSeq2000, and the 16,927,441 reads (101 bp long) were first trimmed with SolexaQA. The resulting reads, having an average length of 63 bp, were assembled using ABySS software version 1.3.4 ($k = 50$). The assembled genome was 3,542,528 bp long, distributed into 104 contigs (>1,000 b; average length, 34,062 bp), displaying an overall GC content of 63.32%, a rather high but expected value for a genome of a member of the *Actinobacteria*.

Genome annotation was performed using the RAST annotation system and allowed the identification of 3,298 open reading frames (ORFs), 46 tRNA, and 6 rRNA operons. Of the 3,298 ORFs, 2,418 (73%) were assigned to at least one of the Clusters of Orthologous Groups (9) families.

The presence of antibiotic and secondary metabolite biosynthesis genes was checked with antiSMASH (5), and that work revealed that the *Arthrobacter* sp. TB23 draft genome sequence harbors three interesting gene clusters, including a type III polyketide synthase (PKS), a nonribosomal peptide synthetase gene, and terpene biosynthetic genes, respectively. A deeper functional annotation of the predicted ORFs also revealed that the genome contains the full gene set responsible for the biosynthesis of the terpenoid backbone trough the non-mevalonate 2-C-methyl-D-erythritol 4-phosphate/1-deoxy-D-xylulose 5-phosphate pathway.

Nucleotide sequence accession numbers. The results of this whole-genome shotgun project have been deposited at DDBJ/EMBL/GenBank under the accession number ALPM00000000. The version described in this paper is the first version, ALPM01000000.

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Arthrobacter sp. TB23 belongs to the Italian Collection of Antarctic Bacteria of the National Antarctic Museum (CIBAN-MNA, Italy).

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