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Draft Genome Sequence of *Microbacterium* sp. Strain Alg239_V18, an Actinobacterium Retrieved from the Marine Sponge *Spongia* sp.

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ABSTRACT Here, we describe the draft genome sequence of *Microbacterium* sp. strain Alg239_V18, an actinobacterium retrieved from the marine sponge *Spongia* sp. Genome annotation revealed a vast gene repertoire involved in antibiotic and heavy metal-resistance, and a versatile carbohydrate assimilation metabolism with potential for chitin utilization.

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Microbacterium spp. are aerobic, Gram-positive actinobacteria found in diverse environments (1)—including marine habitats such as deep-sea sediments (2, 3), seawater (4), bivalves (5), and marine sponges (6–8)—and possess the ability to produce pharmaceutically important natural products such as the bioactive compound glucosylmannosyl-glycerolipid (7). Although several *Microbacterium* genomes are publicly available, most derive from terrestrial sources and very few represent host-associated strains. *Microbacterium* spp. are among the prevalent actinobacteria cultivated from marine sponges (9, 10), but little is known about their functional features and possible roles in this interaction. To increase our understanding of the metabolic potential of these marine sponge associates, we report here the draft genome sequence of *Microbacterium* sp. strain Alg239_V18, cultivated from the marine sponge *Spongia* sp. sampled off the coast of Algarve, South Portugal. Genomic DNA of *Microbacterium* sp. strain Alg239_V18 was extracted with the Wizard genomic DNA purification kit (Promega Corporation, Madison, WI, USA) after cultivation and purification of the colony on VXA medium (double-strength VL55 medium (11) supplemented with 0.05% xylan and solidified with agar) and subsequent overnight growth in liquid VX medium. Genome sequencing was performed at Mr. DNA (Shallowater, TX, USA) on an Illumina MiSeq device using paired-end, 2 × 301-bp libraries. Sequencing depth was 0.97 Gb, leading to 298× coverage of the genome, which was assembled *de novo* into 22 *Microbacterium* contigs with the NGen DNA assembly software by DNAStar, Inc. The resulting draft genome sequence was annotated with the Rapid Annotations Using Subsystems Technology (RAST) prokaryotic genome annotation server (version 2.0) using standard procedures (12). Secondary metabolite- and antibiotic-encoding gene clusters were predicted with antiSMASH (13) and NapDos (14).

The genome is 3,228,018 bp in length, featuring a GC content of 69.4% and 3,061coding sequences, in addition to five rRNAs and 45 tRNAs. *Microbacterium* sp. strain Alg239_V18 displayed 98.8% 16S rRNA gene similarity with its closest relative, *M. aquimaris* JS54-2(T), isolated from seawater (4). Genome annotation displayed a broad range of genes possibly involved in antibiotic (e.g., fluoroquinolones) and heavy metal resistance (e.g., arsenic, cobalt, copper, and mercury); the latter observation is consis-

tent with the recent isolation of several *Microbacterium* strains from heavy metal–contaminated soils (15). A diversified carbohydrate metabolism can be inferred from the annotated genome, encompassing multiple genes involved in the assimilation of various mono-, di-, and oligosaccharides, and 17 genes related to chitin and N-acetylglucosamine utilization. Using antiSMASH, we found a putative tetraterpene biosynthetic gene cluster displaying similar architecture to that of *M. testaceum* StLB037, in addition to one type III polyketide synthase gene cluster resembling that of *M. yannicii* PS01. Curiously, terpene classes such as furanoterpenes, furanosesterterpenes, and sesterterpenes are regularly retrieved from *Spongia officinalis*, and some display biofilm-inducing capacities (16). The search for natural product domains using NaPDoS retrieved a putative modular KS domain similar to that involved in the biosynthesis of candicidin, an antifungal compound usually obtained from the actinobacterium *Streptomyces griseus* and applied in the treatment of candidiasis.

Accession number(s). This draft genome sequence of *Microbacterium* sp. strain Alg239_V18 was deposited in the European Nucleotide Archive (ENA) (http://www.ebi.ac.uk/ena) under the accession numbers FMSE01000001 to FMSE01000022. The study identification number is PRJEB15584.

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