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Genome Sequence of Radiation-Resistant *Modestobacter marinus* Strain BC501, a Representative Actinobacterium That Thrives on Calcareous Stone Surfaces

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Here we report the full genome sequence of *Modestobacter marinus* strain BC501, an actinobacterial isolate that thrives on stone surfaces. The generated chromosome is circular, with a length of 5.57 Mb and a G+C content of 74.13%, containing 5,445 protein-coding genes, 48 tRNAs, and 3 ribosomal operons.

The genus *Modestobacter* was amended to accommodate aerobic non-spore-forming and typically psychrotolerant actinobacteria of the family *Geodermatophilaceae* (6) and the order *Frankiales* (7). These actinobacteria are able to grow on oligotrophic medium as irregular orange-red or pink colonies during initial growth, turning later to a black color. Morphologically, *Modestobacter* grows as short rods or cocci, tending to aggregate and form short and multiseptated filaments multiplying by swarming buds. Three species have been defined: *Modestobacter multiseptatus* (5), *M. versicolor* (8), and *M. marinus* (11). Type strains from the three species were originally isolated from an Antarctic surface regolith from the Linnaeus Terrace (1,600 m) in the Asgard Range/Transantarctic Mountains, a biological soil crust collected from the Colorado Plateau (United States), and deep-sea sediment (2,983 m) collected from the Atlantic Ocean, respectively.

Several isolates of *M. multiseptatus*, most of which have now been reclassified as *M. marinus* according to Xiao et al. (11), have been shown to be predominant in the first two millimeters of calcarenite stone surfaces characterized by high solar radiation, rapid and wide temperature shifts, and low water and nutrient availability (3). Based on their particular and rich esterase pool, members of the *Modestobacter* genus are assumed to have access to various trace carbon sources on stone surfaces characterized by low organic carbon availability (2). Moreover, *Modestobacter marinus* strain BC501 was reported to be highly resistant to desiccation and to gamma- and high-energy UV radiations (3) compared to its close relative *Blastococcus saxosidens* strain DD2, recovered from the deeper part of the stone material (1, 3).

The genome was determined for *M. marinus* strain BC501, isolated from a white marble surface in Carrara, Tuscany, Italy (9), and maintained in Luedemann medium (4). The finished genome is a single circular molecule obtained from 7,529 Sanger reads, 677,271 454 single reads, 154,757 454 mate-paired reads, and 11,973,162 Sol-exa reads (3 runs) for an overall 230-fold coverage. It contains 5,570,930 bases, with a G+C content of 74.13%. There are 5,445 protein-coding genes, 3 rRNA operons, and 48 tRNA genes.

The genome sequence of *M. marinus* BC501 contains several genes in multiple copies, such as *coxSML* (carbon monoxide dehydrogenase), *dnaj* (chaperone Hsp40), *kata* (manganese-containing catalase), *mcrA* (mitomycin radical oxidase), *ohrR* (or-

ganic hydroperoxide resistance transcriptional regulator, MarR family), *recQ* (DNA helicase), *soxABDG* (sarcosine oxidase), *trxAB* (thioredoxin reductase), *trwC* (conjugative relaxase), and *uvrACD* (UV resistance).

Nucleotide sequence accession number. The *M. marinus* BC501 genome sequence and annotation data have been deposited in EMBL under the accession number [FO203431](https://www.ebi.ac.uk/ena/entry/FO203431). Complete data are also available in the MicroScope platform (10) (<https://www.genoscope.cns.fr/agc/microscope>, GeoScope project).

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