



Draft Genome Sequence of a Granaticin-Producing Strain of *Streptomyces parvus* Isolated from a Roman Tomb in the Necropolis of Carmona, Spain

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ABSTRACT *Streptomyces parvus* strain C05 was isolated from the walls of a Roman tomb located in Carmona, Seville, Spain. Subsequent studies determined the capability of this strain for producing granaticins. Here, we report the 8.7-Mbp draft genome sequence for this bacterium.

The phylum *Actinobacteria* is common in caves (1). Microclimatic conditions as well as the availability and nature of nutrients are critical elements for the biogeochemical processes carried out by different members of this group in subterranean environments (2–4), being especially relevant in the biodeterioration of cultural heritage (5).

The Circular Mausoleum is a small tomb located in the Roman Necropolis of Carmona, Spain. This tomb presents abundant and unusual violet stains affecting the mural paintings. A bacterium initially identified as *Streptomyces* sp. C05 was isolated from these stains and produced a violet pigment in the laboratory. Chemical analysis identified several granaticins as the source of the violet pigments (6). rRNA 16S and multilocus sequence analysis (MLSA) identified this bacterium as a strain of *Streptomyces parvus* (5). Granaticins exhibited antibacterial activity against Gram-positive bacteria and are synthesized by other *Streptomyces* species, such as *S. vietnamensis* and *S. violaceoruber*, but the type strain of *S. parvus*, NRRL B-1455, does not have the ability to synthesize granaticins (5, 7, 8).

Streptomyces parvus strain C05 was cultivated in tryptone soy agar incubated at 30°C. Genomic DNA isolation from this bacterium was carried out using the Marmur method (9) with modifications. The DNA concentration measurement was quantified with an Invitrogen Qubit 2.0 fluorometer. Genomic DNA was sequenced using 250-bp paired-end reads on an Illumina HiSeq platform by means of a Nextera XT library prep kit. A total of 2,183,823 reads were generated with a median insert size of 515 bp.

The read quality was checked with FastQC 0.11.5 (10). Reads were adapter trimmed using Trimmomatic 0.36 with a sliding window quality cutoff of Q15 (11). *De novo* assembly for this draft genome was performed using SPAdes 3.11.1 (12) with the “careful” option to reduce mismatches and short indels, and annotations were carried out using the NCBI Prokaryotic Genome Annotation Pipeline (13), with Sma3s (14) for functional annotations using the UniProt bacterium database with the “uniprot” option and antiSMASH (15) for secondary metabolite biosynthesis gene cluster prediction. A total of 729 contigs were obtained with a mean coverage of 29.94×. The N_{50} value was 28,163, and the largest contig was 102,255 bp. The genome size was 8,755,172 bp with an average G+C content of 71.4%. A total of 8,111 genes were detected, with 17 rRNA and 66 tRNA genes predicted.

Streptomyces sp. strain C05 was closely related to *Streptomyces parvus* NRRL B-1455^T (GenBank accession number [VXCD00000000](https://www.ncbi.nlm.nih.gov/nuclseq/VXCD00000000)). The relatedness was assessed by calculating the average nucleotide identity with the BLAST and MUMmer algorithms using

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the JSpeciesWS Web service (16). Average nucleotide identity using BLAST (ANIb) and MUMmer (ANIm) between C05 and type strains presented values of 95.50% and 96.86%, respectively, suggesting that the *S. parvus* type strain and C05 belong to the same species.

The prediction of secondary metabolite clusters using antiSMASH corroborated the granaticin production since its genome presented 86% of the granaticin biosynthesis gene cluster described in *S. violaceoruber* (GenBank accession number [AJ011500](#)), in addition to 54 biosynthetic gene clusters involved in the production of different bioactive compounds. Therefore, the results obtained in former *in vitro* studies (5, 6), along with the prediction of secondary metabolites derived from *in silico* analysis carried out for *Streptomyces parvus* C05, promote the exploration of subterranean environments as a prolific source for biocompounds of biotechnological interest (17).

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [VSZQ00000000](#). The version described in this paper is the first version, VSZQ01000000. BioProject and raw data are available at the accession numbers [PRJNA562075](#) and [SRR10059654](#), respectively.

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