

**TITLE:** GENOMIC ANALYSIS OF SECONDARY METABOLITES AND ANTIMICROBIAL ACTIVITY OF *Streptomyces* sp.

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**INSTITUTIONS:** 1.CENTRO PLURIDISCIPLINAR DE PESQUISAS QUÍMICAS, BIOLÓGICAS E AGRÍCOLAS - CPQBA, UNICAMP (AV. ALEXANDRE CAZELLATO, 999, PAULÍNIA-SP, BRAZIL); 2.MOTIVA BIOINFORMÁTICA ME (SERTÃOZINHO-SP, BRAZIL); 3.INSTITUTO DE BIOLOGIA - UNICAMP (R. MONTEIRO LOBATO 255, CAMPINAS-SP, BRAZIL)

**ABSTRACT:**

The genus *Streptomyces* host species known for producing a diversity of secondary metabolites with antimicrobial activity. These compounds are related to classes of natural products like Non-Ribosomal Peptides (NRPs) and the Polyketides (PKs). This study aims to verify if the *Streptomyces* sp. isolated from Antarctica is capable to produce antimicrobial compounds and use the genomic analysis to find gene clusters associated with the production of antimicrobials. The *Streptomyces* sp. was isolated from salp, a planktonic tunicate, collected in Punta Plaza, King George Island, Antarctica, during the austral summer of 2010. The strain was isolated in M1 medium prepared with artificial sea water at 28 °C. After 30 days of bacterium cultivation in stationary conditions, the crude extract was obtained from liquid-liquid extraction with ethyl acetate solvent. The strain was tested for antimicrobial activity and could inhibit the bacteria *Staphylococcus aureus* ATCC 6538, *Bacillus subtilis* ATCC 6051, *Micrococcus luteus* ATCC 4698, *Neisseria meningitidis* (strains B4, C2135, WATCC and YUSA) and the yeast *Candida albicans* ATCC10231, with MIC ranging from 0,25 to 2,0 mg.mL<sup>-1</sup>. The genome sequencing of the *Streptomyces* sp. was performed with paired-end library sequenced using the HiSeq2500 system and assembled resulting in sequences with a total length of 6,968,465 bp in 49 contigs. Open reading frames (ORFs) were predicted comprising 6,547 coding sequences (CDSs) and the genome was annotated resulting in 399 subsystems. The analysis of secondary metabolites by antiSMASH and natural products by NaPDoS indicated 30 gene clusters, 8 NRPS, 6 type-1-PKS, 1 type-3-PKS, 1 NRPS-type1-PKS and 2 bacteriocins. Gene clusters related to the antibiotics and antifungal were identified in the genome, as the polypeptide antibiotic Bacitracin, the macrolide antibiotic Chlorothricin, the antibiotic Rifamycin, the antifungal and antiprotozoal Amphotericin, the antifungal Candicidin with activity against *C. albicans*. In vitro assays showed that the bacterium was able to produce antimicrobial compounds and the analysis of clusters related to the production of PKs and NRPs indicated potential antimicrobial compounds produced by the *Streptomyces* sp. strain. This study highlights the need for bioprospecting in extreme environments, such as Antarctica.

**Keywords:** Antimicrobial activity, Natural products, Polyketide, Non-Ribosomal Peptide, *Streptomyces*

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