

Genome-Scale Analysis of *Streptomyces Caatingaensis* CMAA 1322 Metabolism, a New Abiotic Stress-Tolerant Actinomycete

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Abstract : Extremophilic microorganism are adapted to biotopes combining several stress factors (temperature, pressure, radiation, salinity and pH), which indicate the richness valuable resource for the exploitation of novel biotechnological processes and constitute unique models for investigations their biomolecules (1, 2). The above information encourages us investigate bioprospecting synthesized compounds by a novel actinomycete, designated thermotolerant *Streptomyces caatingaensis* CMAA 1322, isolated from sample soil tropical dry forest (Caatinga) in the Brazilian semiarid region (3-17°S and 35-45°W). This set of constrating physical and climatic factores provide the unique conditions and a diversity of well adapted species, interesting site for biotechnological purposes. Preliminary studies have shown the great potential in the production of cytotoxic, pesticidal and antimicrobial molecules (3). Thus, to extend knowledge of the genes clusters responsible for producing biosynthetic pathways of natural products in strain CMAA1322, whole-genome shotgun (WGS) DNA sequencing was performed using paired-end long sequencing with PacBio RS (Pacific Biosciences). Genomic DNA was extracted from a pure culture grown overnight on LB medium using the PureLink genomic DNA kit (Life Technologies). An approximately 3- to 20-kb-insert PacBio library was constructed and sequenced on an 8 single-molecule real-time (SMRT) cell, yielding 116,269 reads (average length, 7,446 bp), which were allocated into 18 contigs, with 142.11x coverage and N50 value of 20,548 bp (BioProject number PRJNA288757). The assembled data were analyzed by Rapid Annotations using Subsystems Technology (RAST) (4) the genome size was found to be 7,055,077 bp, comprising 6167 open reading frames (ORFs) and 413 subsystems. The G+C content was estimated to be 72 mol%. The closest-neighbors tool, available in RAST through functional comparison of the genome, revealed that strain CMAA1322 is more closely related to *Streptomyces hygroscopicus* ATCC 53653 (similarity score value, 537), *S. violaceusniger* Tu 4113 (score value, 483), *S. avermitilis* MA-4680 (score value, 475), *S. albus* J1074 (score value, 447). The *Streptomyces* sp. CMAA1322 genome contains 98 tRNA genes and 135 genes copies related to stress response, mainly osmotic stress (14), heat shock (16), oxidative stress (49). Functional annotation by antiSMASH version 3.0 (5) identified 41 clusters for secondary metabolites (including two clusters for lanthipeptides, ten clusters for nonribosomal peptide synthetases [NRPS], three clusters for siderophores, fourteen for polyketide synthetase [PKS], six clusters encoding a terpene, two clusters encoding a bacteriocin, and one cluster encoding a phenazine). Our work provide in comparative analyse of genome and extract produced (data no published) by lineage CMAA1322, revealing the potential of microorganisms accessed from extreme environments as Caatinga" to produce a wide range of biotechnological relevant compounds.

Keywords : caatinga, streptomyces, environmental stresses, biosynthetic pathways

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