Genome-guided exploration of marine *Streptomyces* sp. and *Nocardiopsis* sp. for their biosynthetic and drug-development potential

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Abstract

Actinomycetes are prolific producers of bioactive natural compounds, making them valuable targets for discovering novel therapeutics in the face of rising antimicrobial resistance. This study investigated the biosynthetic potential of Actinomycetes isolated from marine sponge and sediment samples collected along the west coast of India. Whole-genome sequencing of six isolates generated high-quality Illumina assemblies, and BLAST- and phylogeny-based analyses identified A01 and A96 as Nocardiopsis sp., while A03, A45, A57, and A90 grouped with Streptomyces. Genome mining revealed that Streptomyces sp. A57 carried the highest number of biosynthetic gene clusters (28 BGCs). Terpene clusters were detected in all Streptomyces genomes, and the ectoine was conserved across both genera. Several predicted BGCs showed low similarity to known clusters, indicating the presence of unexplored biosynthetic pathways with potential for novel metabolite production. These findings highlight the rich genomic diversity of marine Actinomycetes and underscore their promise as reservoirs for future drug discovery. Further work integrating genomics with metabolomics will aid in experimentally characterizing these predicted metabolites.

Keywords: Actinomycetes, Secondary metabolites, *Streptomyces*, *Nocardiopsis*, Bioactive compounds