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Bioactive metabolite produced from soil-based Streptomyces polyrhachis AS07 is isolated, characterised, and identified

Shraddha Walunj, ReetikeshPatel

***Corresponding author**

Shraddha Walunj, ReetikeshPatel,
Department of Biotechnology, The Institute of Science, India

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Abstract

The need to investigate new and potent antimicrobial agents from actinomycetes, which are frequently recognised for their capacity to produce a variety of antibiotics, is driven by the mounting stress created by antibiotic resistance. In this work, the secondary metabolite produced by the soil-dwelling strain Streptomyces polyrhachis AS07 is the main topic of investigation. Phylogenetic analysis and 16S rRNA sequencing techniques were used to identify the soil isolated strain. The Streptomyces sp. produced a sufficient output of secondary metabolites for evaluation of antibacterial capabilities in the correct laboratory settings. Propionic acid, palmitic acid, and other compounds with tetrazolic and monocarboxylic groups were found in high concentrations in the metabolite's Gas Chromatography Mass Spectrometry chromatogram as antimicrobial components. A wide variety of Gram-positive and Gram-negative microorganisms were examined using the antibacterial activity of the extracted metabolite was notable, with S. aureus being the target organism. With an IC50 value of 5.50 g/mL, it also showed potential antioxidant action. The metabolite successfully inhibited the ability of C. violaceum to sense quorums and showed the most antibiofilm action against B. subtilis. Additionally, the extract greatly reduced P. aeruginosa's capacity for swarming by up to 16.67%. In conclusion, the Streptomyces metabolite can be viewed as a powerful source of bioactive compounds for commercial production with a wide range of potential therapeutic uses.

Discussion

The 10 soil samples were successfully used to isolate the actinomycetes strain AS07, which was grown in pure culture on ISP-4 medium. When tested against all the test species, the isolated strain showed a sizable zone of inhibition. As a result, it was further chosen for experimental analysis. In order to show that AS07 was closely linked to the genus Streptomyces, the isolated strain's next-generation 16S rRNA sequencing analysis result was compared to all other accessible sequences in GenBank (NCBI, USA). The AS07 strain and Streptomyces camisole ZFG47 strain shared the most resemblance, according to the results of phylogenetic study (83%). The GC-MS technique was used to identify a number of ingredients found in the extracted metabolite. The secondary crude metabolite's GCMS chromatogram as a result included includes 28 peaks, each with a peak area and corresponding retention duration minutes.The secondary metabolic extract was exposed to a variety of microbial strains in order to assess the nature of the crude extract as a possible antibacterial agent. Certain numbers show that these organisms are more resistant to the test sample. Furthermore, the presence of antibiotic components discovered by GC-MS analysis may have contributed to the significant antibacterial activity that the metabolite isolated from Streptomyces species exhibited. A variety of biofilm-producing species were evaluated for resistance to the isolate's metabolite extract's anti-biofilm activity. The extracted material showed a positive antibiofilm effect on the test organisms that produced biofilms. Quorum's production of purple pigment from cultivated violacein. detection ofcommunication in A naturally occurring and easily recognised phenotype provided by Chroma bacterium violaceus aids in the assessment of anti-QS chemicals in test samples. The metabolite extract was examined using the Pseudomonas aeruginosa PA01 strain for the motility assay. The ability of the metabolite to hinder the migration of the bacteria decreases with increasing zone diameter and vice versa. In the presence of the metabolite derived from the soil bacteria Streptomyces polyrhachis, Pseudomonas aeruginosa displayed a 5 mm diameter swimming zone, suggesting 50% of the bacterium's swimming capabilities.

Conclusion

In our investigation, a Streptomyces strain was first isolated from soil, and then the strain's phylogenetic relationship was determined by next-generation 16S rRNA sequencing. Streptomyces polyrhachis produces metabolites that have significant antibiotic action against a variety of these pathogens, indicating that it may be a valuable source of powerful bioactive compounds for the treatment of difficult pathogenic microbes. Additionally, the metabolite had strong antioxidant

properties, significant anti-quorum sensing capabilities, and worked effectively as a biofilm creation inhibitor.

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