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MARINE BACTERIAL EXTRACTS FROM RESTINGA ECOSYSTEMS AS POTENTIAL ANTI-BIOFILM AGENTS AGAINST *Pseudomonas aeruginosa* VIA CO-CULTURE STRATEGIES

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Infectious diseases remain a major global health burden, accounting for nearly 20% of worldwide deaths (Martens et al., 2017). The declining efficacy of antibiotics against bacterial pathogens is mainly driven by intrinsic, acquired, and adaptive tolerance, with biofilm formation being one of the most critical adaptive defenses. Biofilms are linked to approximately 80% of chronic infections (Rather et al., 2021), notably chronic wound infections often caused and aggravated by the Gram-negative pathogen *Pseudomonas aeruginosa*. Addressing these challenges requires exploring novel sources of antimicrobial agents. Since oceans cover around 70% of Earth's surface, marine ecosystems represent an underexplored reservoir of bioactive molecules. Their long evolutionary history has generated vast biodiversity and unique adaptive strategies, enabling the production of chemically diverse metabolites. Among them, marine-derived bacteria are particularly promising as producers of secondary metabolites with potential anti-biofilm applications. In this study, 65 supernatants were obtained from mono-cultures of environmental marine bacteria isolated from the Restinga ecosystems on the South coast of Rio Grande do Sul, and 65 additional supernatants were produced through co-culture with the human pathogen *Pseudomonas aeruginosa* PA01. This work aimed to evaluate, using mixed-culture strategies, the scope and limitations of secondary metabolite production in inhibiting bacterial growth and biofilm formation by *Pseudomonas aeruginosa* ATCC 27853. Based on biological activity results, six supernatants were selected for secondary metabolites extraction: four from mono-culture (5M, 31M, 39M, 42M) and two from co-culture (12C, 15C). Then, anti-bacterial and anti-biofilm assays were also performed. Notably, regardless of cultivation strategy 12C showed bacterial growth inhibition by over 50%, while others selected extracts exhibited anti-biofilm activity more than 85%. 16S rRNA sequencing was performed to identify the promising marine-derived bacteria. The authors thank the support from their institutions, and the financial support of CAPES, CNPq, FAPERGS and the REDE MaRe (Rede de Pesquisa dos Ecossistemas Mangue e Restinga).

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