



***METABOLOMIC PROFILE OF MARINE BACTERIA CULTIVATED UNDER  
CONDITIONS THAT MIMIC THE EFFECT OF CORAL BLEACHING***

**Mariana Rocha**<sup>1\*</sup>, Ana Paula Muche Schiavo<sup>1</sup>, Bianca Del Bianco Sahm<sup>2</sup>, Leticia Veras  
Costa Lotufo<sup>2</sup>, Anelize Bauermeister<sup>1</sup>

[mari\\_rocha.12@usp.br](mailto:mari_rocha.12@usp.br); [anelize@iq.usp.br](mailto:anelize@iq.usp.br)

1-Instituto de Química da Universidade de São Paulo, Av. Professor Lineu Prestes, 748, São Paulo, SP, Brazil. 2- Instituto de Ciências Biomédicas da Universidade de São Paulo, Av. Professor Lineu Prestes, 2415, São Paulo, SP, Brazil

Coral reefs are extremely diverse ecosystems, essential for the life of countless marine species, and of great economic importance to coastal communities. However, the maintenance of these ecosystems is being threatened by damage caused by the rising of the ocean surface water temperatures and acidification, both reflections of the climate changes caused by global warming. Understanding the impacts of these environmental changes on corals microbiome is essential for finding ways to mitigate the bleaching. Corals harbor a diverse range of microorganisms that form their holobiont, making it essential to investigate how the microbiota and its metabolic products can be affected under stressful environmental conditions. Therefore, this study aims to isolate and cultivate bacteria associated with the coral *Mussismilia hispida*, a coral widely spread in Brazilian coast, in order to investigate the metabolites produced by the associated microorganisms and evaluate the effect on their production under conditions that mimic coral stress, such as variations in temperature and pH. To date, 119 bacteria strains have been isolated based on their morphological aspect, as well as colony color and shape. The investigation of their metabolites production and the taxonomic identification are still ongoing. Metabolite analysis has been performed on an ultra-high-performance liquid chromatography coupled with mass spectrometry (UHPLC-MS), applying an untargeted method. The data will be analyzed in GNPS (Global Natural Products Social Molecular Networking) platform and the microbeMASST tool. The authors thank the support from their institution, the Coordination of Superior Level Staff Improvement (CAPES) for the fellowship, and FAPESP for the grant (process 2024/05211-4).

**Keywords:** metabolomics, natural products, specialized metabolites, chemical ecology, marine microorganisms.

