



## ***DIVERSITY OF THE FUNGAL MICROBIOME ASSOCIATED WITH ECHINODERMS FROM SÃO SEBASTIÃO (SÃO PAULO), TOWARDS METABOLOMICS***

**Julia Farias Ikenaga**<sup>1,2\*</sup>, Matheus Gotha<sup>2</sup>, Cauê Arantes Wagner Zuccarino<sup>2</sup>, Kleyton Junior Gomes de Moraes<sup>2</sup>, Roberto Gomes de Souza Berlinck<sup>2</sup>

[juliaikenaga@gmail.com](mailto:juliaikenaga@gmail.com)

1-Department of Genetics and Evolution, Federal University of São Carlos, São Carlos 13565-905, Brazil 2- São Carlos Institute of Chemistry, University of São Paulo (USP), São Carlos 13566-590, Brazil

Marine organisms have acquired chemical adaptations that provide them protection against different predators, as well as chemical cues for environmental adaptation. These chemicals are secondary metabolites which are produced and/or accumulated when marine macroorganisms are exposed to stressful situations, and present an array of bioactivities. Frequently these compounds are produced by microorganisms associated to macroorganisms. Echinoderms (sea-stars, holothurians or sea cucumbers, and brittle stars) are marine invertebrates that participate directly in the marine nutrient cycling processes, and typically provide complex triterpene saponins as secondary metabolites. Much less investigated are fungi associated with echinoderms, in particular from echinoderms' viscera. The few studies developed have shown that secondary metabolites produced by fungi associated with echinoderms are remarkably unique both structurally and biologically. The present investigation aimed at the isolation identification of fungal strains associated with echinoderms' viscera collected on the coast of São Sebastião (SP, Brazil), as well as to evaluate their production of secondary metabolites under different culture conditions. Nineteen of such fungal strains were grown in different media, which were extracted with EtOAc, the extracts defatted and subjected to a solid-phase extraction pre-purification. Analysis of fractions was performed by HPLC-UV-MS, UPLC-HRMS and UPLC-MS/MS. Metabolomics analysis was performed using GNPS, MetaboAnalyst 6.0 and SIRIUS 4. Among the detected secondary metabolites, some were brominated, and the majority are assigned as polyketides, sesquiterpenes, and aromatic compounds. Results of this investigation will be presented and discussed.

**Keywords:** *marine biotechnology, microbial metabolism, marine diversity, fungi*

**Acknowledgements:** to FAPESP, CAPES and CNPq for the financial support.

