

## DIVERSITY ANALYSIS OF THE BACTERIAL COMMUNITY ASSOCIATED WITH THE MARINE SPONGE *Drasmodon reticulata*

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### Abstract:

Sponges have been the focus of great interest due to the fact that they form close associations with a variety of microorganisms and represent a rich source of biologically active compounds. In spite of their biotechnological potential, a clear picture of microbial diversity in such hosts is not available. This work aimed to investigate the bacterial community inhabiting the marine sponge *Drasmodon reticulata* using culture-independent methods. Sponge samples were collected in beach areas of São Sebastião city (SP, Brazil), sterilized and triturated for subsequent DNA extraction. Fragments of 16S rDNA were PCR-amplified and used to construct a clone library. A total of 117 clones were successfully sequenced and identified by SIMO RDP database. Approximately 50% (59 clones) were affiliated to Cyanobacteria, a known sponge-associated phylum. Proteobacteria was the second most abundant phylum with 49 clones (42%), and other groups included Bacteroidetes (4%), Actinobacteria (2%) and Lentisphaerae (1%). These results revealed a diversity scenario very different from the one obtained in a recent study published by our research group [1], in which microbial communities from the same marine sponge were analyzed by using cultivation methods. The latter showed high abundance of the phylum Firmicutes (53%), followed by Actinobacteria (27%). The comparison between both studies demonstrates that cultivation and culture-independent methods are complementary, since they enable the recovery of different groups from the environment. Analyses performed using the Dotur program enabled us to classify the sequences into 41 distinct OTU's at the species level ( $D \leq 0.03$ ). Diversity (Shannon index) and richness analyses (Chao and Ace estimators) revealed that the bacterial diversity observed in the sample and the total phylotype richness of the bacterial community associated with the marine sponge are high. Nonetheless, the diversity observed in the 16S rDNA library is still an underestimate of the total bacterial diversity present in the environment, and further sampling would yield an increased observed diversity. [1] Menezes, C.B.A. et al. 2009. Microbial diversity associated with algae, ascidians and sponges from the north coast of São Paulo state, Brazil. **Microbiol. Res.**, doi:10.1016. **Financial support: FAPESP.**

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