

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



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## INTRODUCTION

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 with cytotoxic, antibacterial, antiviral or anti-inflammatory activities. The ecological associations which occur between the microorganisms and marine substrates have been greatly neglected and, in spite of their biotechnological potential, a clear picture of microbial diversity in hosts such as marine sponges is not available. This work aimed to investigate the composition and structure of the bacterial community inhabiting the marine sponge Dragmacidon reticulata using cultivation-independent methods.

### **MATERIAL AND METHODS**



#### **RESULTS AND DISCUSSION**



Approximately 50% (59 clones) were affiliated to Cyanobacteria, a known sponge-associated phylum. Proteobacteria was the second most abundant phylum (42%). These results revealed a diversity scenario very different from the one obtained in a recent study published by our research group [Menezes et al., 2009], 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 demonstrated that cultivation-dependent and independent methods are complementary, since they enable the recovery of different groups from the environment. Analyses performed using the Mothur program enabled us to classify the sequences into 45 distinct OTU's at the species level (D≤0.03). Proteobacteria was the most diverse group, presenting 28 OTUs, while the phylum Cyanobacteria, which had the highest abundance, was classified into 8 OTUs only. 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.

80 Uncultured bacterium clone Gven\_N16 (GU118510) \*Coral

Uncultured *Marinovum* sp. clone SHWH\_night (FJ744930) 100 Clone H3\_2 OTU 13 (1) Uncultured bacterium clone SHFG606 (FJ203199) Clone H1\_1 OTU 12 (1) Thalassobius sp. D7024 (FJ161330) Uncultured bacterium clone FATNROCT034 (GU185196) **Clone C6\_1** OTU 8 (1) <sup>–</sup> Uncultured *Loktanella* sp. clone NdSurf107 (FJ753163) **Clone E4\_1** OTU 7 (1) Roseobacter denitrificans strain NBRC15277 (DQ915623) **Clone G1\_1** OTU 11 (1) 98 Clone E4\_2 OTU 21 (1) Uncultured marine bacterium clone BM1-1-77 (FJ825845) **Clone H3\_1** OTU 20 (2) Roseovarius aestuarii strain SMK-122 (EU156066) Uncultured alpha proteobacterium clone HAL-T-16 (EU350873) <sup>99<sup>I</sup></sup> Clone C2\_1 OTU 10 (1) Uncultured Rhodobacteraceae (FN582321) **Clone B8\_2** OTU 19 (1) Marine bacterium (isolate SRF3) (AJ002565) **Clone C4\_1** OTU 9 (1) <u>99</u> Uncultured alpha proteobacterium clone C8W\_100 (HM057657) **Clone H11\_2** OTU 17 (1) Uncultured alpha proteobacterium clone HG145 (FN582322) <sup>39L</sup> Clone A11\_2 OTU 18 (1) 100 Uncultured bacterium clone S23\_913 (EF572814) Clone H4\_1 OTU 23 (1) 99 Uncultured bacterium clone S25\_719 (EF574375) **Clone B3\_1** OTU 14 (2) Uncultured marine bacterium clone D92\_03 (AY923017) <sup>100</sup> Clone F5\_1 OTU 22 (1) Erythrobacter ishigakiensis (AB363004)





Proteobacteria