

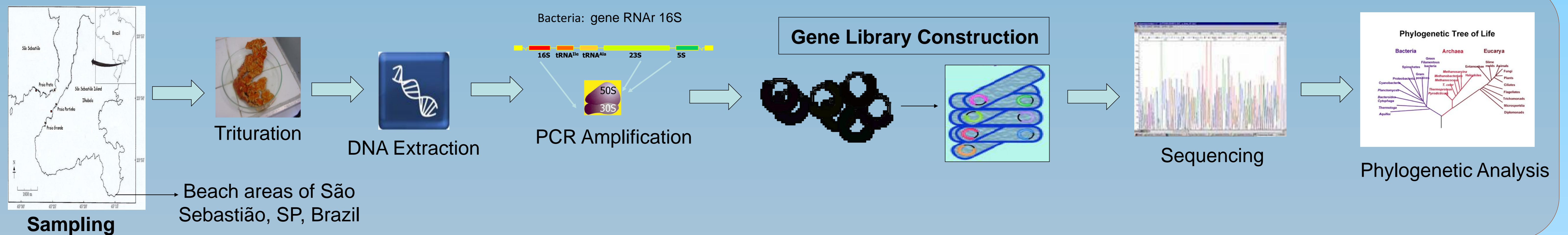
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**Key words:** Bacterial Communities, Gene Libraries, Marine Sponge

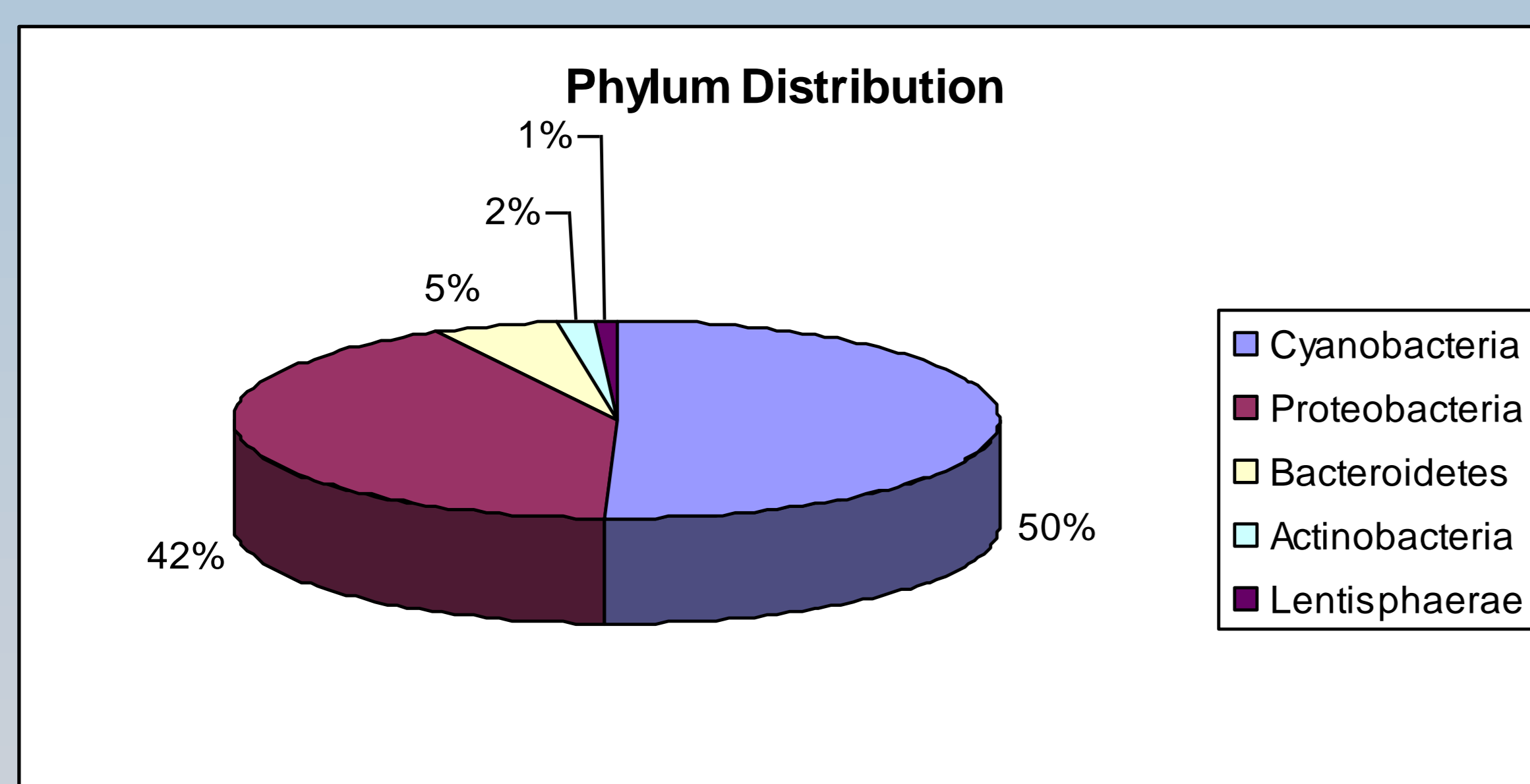
## INTRODUCTION

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, antifungal, 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 *Drummacidon reticulata* using cultivation-independent methods.

## MATERIAL AND METHODS

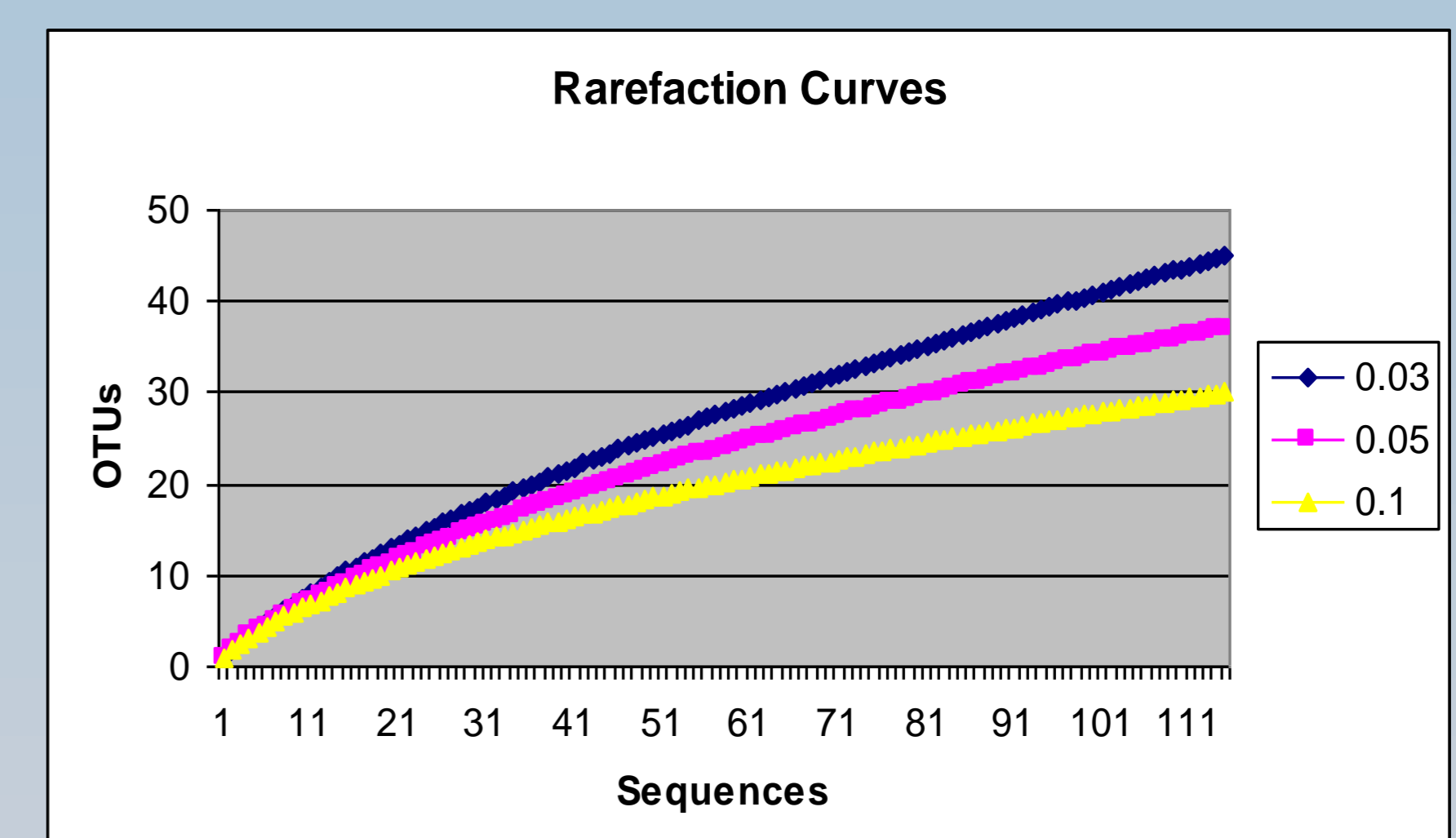


## RESULTS AND DISCUSSION

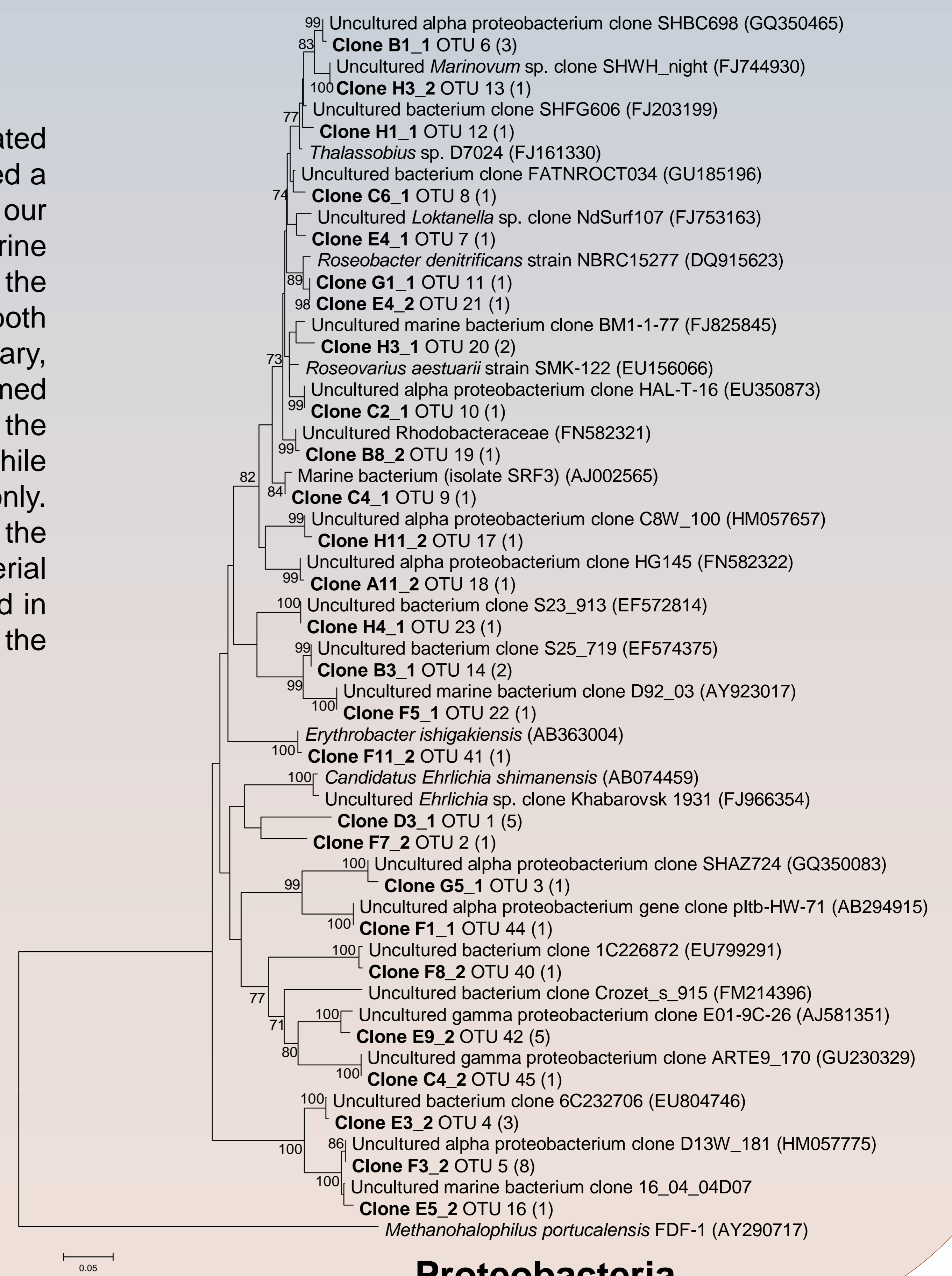
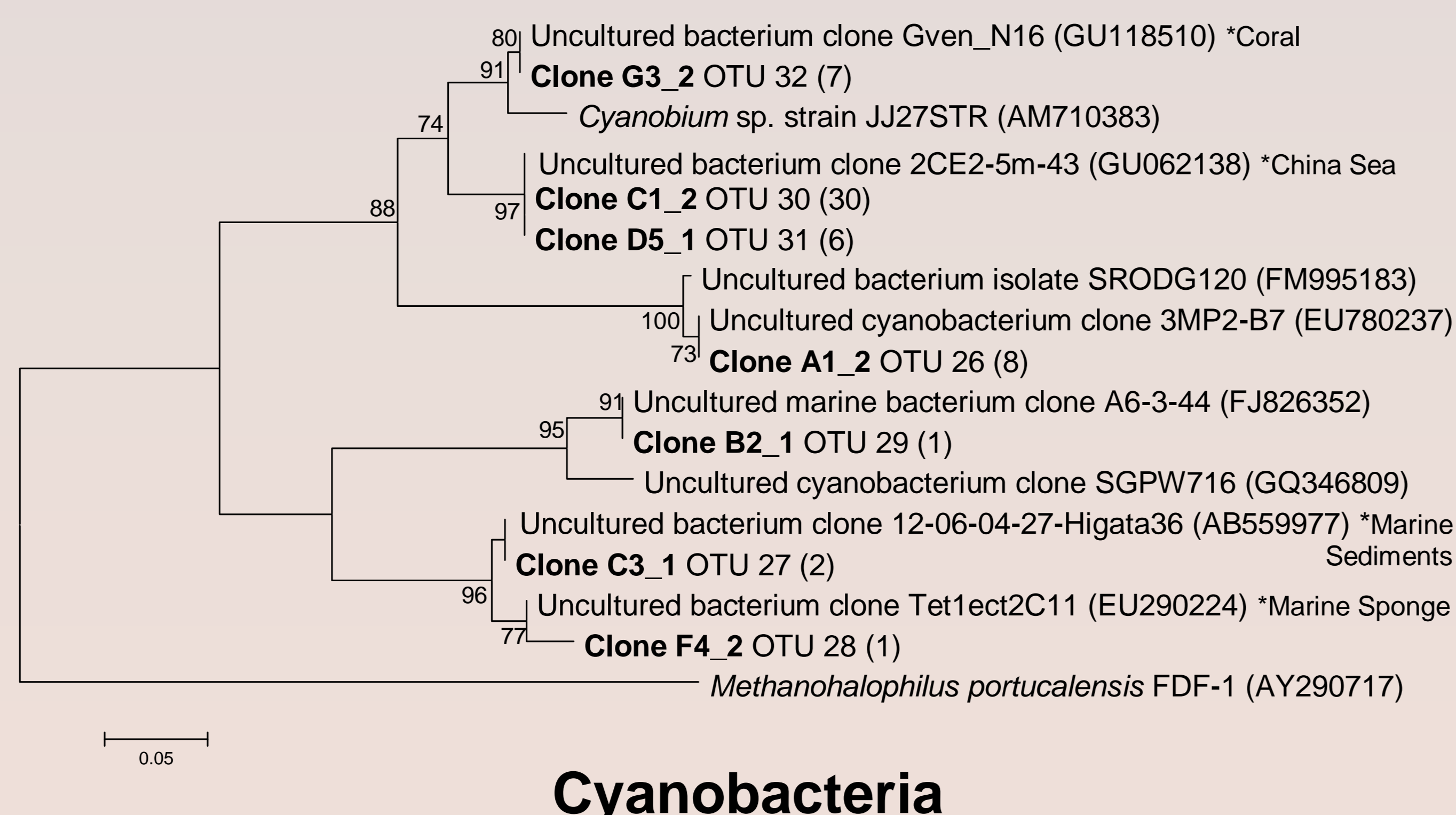


### Mothur Analysis

Chao	Ace	Shannon	Simpson
144.2	271	3.11	0.084



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 ( $D \leq 0.03$ ). 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.



**Cyanobacteria**

**Proteobacteria**