

The phylum Chloroflexi and clade SAR202 dominate the microbiome of two marine sponges living in an extreme environment

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Abstract

The adaptation of marine sponges to their environment is often attributed to the specific composition of their bacterial communities. In this study, we assessed the bacterial microbiome of two dominant sponges, *Rhabdastrella globostellata* and *Hyrtilos erectus*, living in the Bouraké lagoon (New Caledonia), where abiotic conditions reach extreme values of temperature, pH, and oxygen during low tide. Scuba divers collected sponge specimens and sediment and seawater samples at 2-3m depth. The bacterial communities were studied using 16S rRNA metabarcoding, and variations between the two sponges were compared using Principal Component Analyses (PCA) biplots. The phylum Chloroflexi and clade SAR202 appeared dominant in both sponge species reaching an average relative abundance of 41.2% and 53.2% in *H. erectus* and 53.2% and 78.7% in *R. globostellata*, respectively, while they were absent in sediments and seawater. Principal Component Analyses (PCA) explained 70.9% (phyla) and 86.6% (clade) showing that the bacterial community's structure in both sponges is driven by Chloroflexi. This study is the first report of such a noteworthy relative abundance of Chloroflexi and SAR202 has been described in the microbiome of marine sponges. As these bacteria are known to play key roles in sponge nutrition and fitness, their high abundance strongly suggests an adaptive response to the extreme environmental conditions of the Bouraké lagoon.

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