

## "The microbiome of keratose marine sponges: spatiotemporal dynamics and functional attributes"

Rodrigo Costa

Microbial Ecology and Evolution Research Group, Centre of Marine Sciences, Algarve University, Portugal

Marine sponges harbour complex microbial communities of ecological and biotechnological importance. In spite of their putative relevance to host functioning, in-depth knowledge of sponge microbiome stability over space and time is scarce. Furthermore, only recently have we been able to address the functional features of these chemically complex microbial assemblages owing to pivotal advances in (single cell) genomics, metagenomics, and analytical chemistry. Here, I approach keratose sponges (i.e., lacking mineral spicules and possessing an organic fibers skeleton instead), as a model group in the study of the marine sponge microbiome. 454-pyrosequencing profiling of sponge-derived 16S rRNA gene amplicons reveals that prokaryotic communities in keratose species are dominated by the bacterial phyla *Actinobacteria*, *Acidobacteria*, *Proteobacteria*, *Poribacteria*, PAUC34f, *Chloroflexi* and *Bacteroidetes*, along with ammonia-oxidizing archaea in the *Thaumarchaeota* phylum. At the approximate "species" level (operational taxonomic units defined at 97% 16S rRNA gene sequence similarity) half a gram of one keratose specimen hosts hundreds of bacterial species - the vast majority of which are difficult to cultivate - and dozens of fungal and archaeal species. The structure of these assemblages is shaped by the host species and highly stable over space and time, in spite of a measurable, transient sponge microbiota composed of less abundant phylotypes. Primer-less, shotgun sequencing of these symbiotic consortia highlights a unique microbial assemblage that sharply differs from seawater and sediment microbial communities not only in terms of phylogenetic composition, but also because of the markedly higher incidence of Clustered Regularly Interspaced Palindromic Repeats (CRISPRs) and reduced viral abundance in the symbiotic consortium, among other features. Several bioactive terpenoids and polyketides have been retrieved from keratose sponges. Current genome mining of hard-to-culture symbionts captivated in the laboratory strengthens the hypothesis of a symbiotic origin of these compounds. It further holds promise in shedding new light on the life strategies of "biphasic" (i.e., occurring both in sponges and seawater) alphaproteobacterial clades retrieved from these hosts.