

Host specificity of fungal communities in marine sponges

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Abstract

Sponges are engaged in intimate symbioses with a diversity of microorganisms from all three domains of life. Bacterial and archaeal communities associated with marine sponges are relatively well-known. Marine fungi, in general, are far less studied in comparison to their terrestrial counterparts. Consequently, the identification of fungi associated with marine organisms and the understanding of their ecological significance is in its infancy. Within an integrative study of the microbial community associated with marine sponges, we assessed the fungal diversity in two sympatric sponge genera across the Mediterranean and the Caribbean Sea. We deep-sequenced ITS2 and 18S rRNA marker genes in the sponge species *Dysidea avara* and *Dysidea etheria*, and compared the results to those in the sponges *Aplysina aerophoba* and *Aplysina cauliformis* as well as seawater. Using both marker genes, we found a compositional difference in the fungal communities between sponge and seawater samples. However, it was only with the ITS2 marker gene that we observed fungal communities following a host-specific pattern, with sponge species significantly differentiating fungal community composition. We found a high diversity of putatively novel taxa in the seawater, and an enrichment of these taxa in sponge samples, indistinctive of the sponge genus. We proposed putative fungal symbionts for each sponge species which constitute good candidates for future efforts to understand the functional roles that mediate the interactions with their hosts.