

Genome-resolved metagenomics provides novel insights into chitin turnover, metabolic specialization, and niche partitioning in the octocoral microbiome

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Octocorals (Octocorallia, Cnidaria) are an integral part of benthic marine ecosystems. They increase habitat complexity and biodiversity and play key roles in coastal food chains. They are found in association with various microorganisms. Our previous work showed that the octocoral microbiome is distinct from the environmental surroundings, host genus-specific, and undergoes complex structural changes in the transition to the dysbiotic state [1]. However, the role of bacterial symbionts that populate octocorals is still poorly understood. To shed light on their metabolic capacities, we examined 66 high-quality metagenome-assembled genomes (MAGs) spanning 30 prokaryotic species, retrieved from microbial metagenomes of three octocoral species and seawater [2].

Symbionts of healthy octocorals were affiliated with the taxa Endozoicomonadaceae, Candidatus Thioglobaceae, Metamycoplasmataceae, unclassified Pseudomonadales, Rhodobacteraceae, unclassified Alphaproteobacteria and Candidatus Rhabdochlamydiaceae. Phylogenomics inference revealed that the Endozoicomonadaceae symbionts uncovered here represent two species of a novel genus unique to temperate octocorals, here denoted Candidatus Gorgonimonas eunicellae and Candidatus Gorgonimonas leptogorgiae. Their genomes revealed metabolic capacities to thrive under suboxic conditions and high gene copy numbers of serine-threonine protein kinases, type III-secretion system, type IV-pili, and ankyrin-repeat proteins, suggesting excellent capabilities to colonize, aggregate, and persist inside their host. Contrarily, MAGs obtained from seawater frequently lacked symbiosis-related genes.

All Endozoicomonadaceae symbionts harbored endo-chitinase and chitin-binding protein-encoding genes, indicating that they can hydrolyze the most abundant polysaccharide in the oceans. Other symbionts, including Metamycoplasmataceae and Candidatus Thioglobaceae, may assimilate the smaller chitin-oligosaccharides resulting from chitin breakdown and engage in chitin deacetylation, respectively, suggesting possibilities for substrate cross-feeding and a role for the coral microbiome in overall chitin turnover. We also observed sharp differences in secondary metabolite production potential between symbiotic lineages. Specific Proteobacteria taxa may specialize in chemical defense and guard other symbionts, including Endozoicomonadaceae, which lack such capacity.

We identify a thus-far unanticipated, global role for Endozoicomonadaceae symbionts of corals in the processing of chitin, a major component of the natural zoo- and phytoplankton feed of octocorals. We conclude that niche partitioning, metabolic specialization, and adaptation to low oxygen conditions among prokaryotic symbionts likely contribute to the plasticity and adaptability of the octocoral holobiont in changing marine environments. These findings bear implications for our understanding of symbiotic relationships in marine environments and benthic ecosystem functioning. They may further guide the formulation of new culture media, targeting elusive symbionts of marine animals.

[1] Keller-Costa et al., 2021, Microbiome, 9, 1-21

[2] Keller-Costa et al., 2022, Microbiome 10, 151