Metagenomics offers insight into marine sponge microbiomes

Sheila Podell
Jessica M. Blanton
Aaron Oliver
Michelle A. Schorn
Vinayak Agarwal
Jason S. Biggs
Bradley S. Moore
Eric E. Allen

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Abstract

Marine sponges and the microbial communities they host are critical to carbon and nutrient cycling in global reefs, and they often share unique, but poorly understood, symbiotic relationships. *Lamellodysidea* herbacea sponges, for example, obtain energy from photosynthetic *Hormosira* bacteria that live inside their bodies. These bacteria naturally produce compounds found in flame-retardant pollutants derived from consumer products. A new study describes how researchers are using metagenomics to understand how these creatures maintain a mutually beneficial relationship with sea sponges. Researchers obtained genetic material describing the relative abundance and metabolic capacities of 21 previously uncharacterized microbial populations associated with *Lamellodysidea* sponges. Analyses revealed genes coding for enzymes that break down halogenated aromatics, which could enable microbes to use pollutant-like compounds as carbon and energy sources. Future studies building off of this work could offer new insight into microbe–sponge relations and help scientists understand how these important cogs of the marine carbon cycle function together.