

ID: W2475445983

TITLE: Microbiome Composition and Diversity of the Ice-Dwelling Sea Anemone, *Edwardsiella andrillae*

AUTHOR: ['Alison E. Murray', 'Frank R. Rack', 'Robert Zook', 'Michael Williams', 'Mary L. Higham', 'Michael Broe', 'Ronald S. Kaufmann', 'Marymegan Daly']

ABSTRACT:

*Edwardsiella andrillae* is a sea anemone (Cnidaria: Anthozoa: Actiniaria) only known to live embedded in the ice at the seawater interface on the underside of the Ross Ice Shelf, Antarctica. Although the anatomy and morphological characteristics of *E. andrillae* have been described, the adaptations of this species to the under-ice ecosystem have yet to be examined. One feature that may be important to the physiology and ecology of *E. andrillae* is its microbiome, which may play a role in health and survival, as has been deduced in other metazoans, including anthozoans. Here we describe the microbiome of five specimens of *E. andrillae*, compare the diversity we recovered to that known for temperate anemones and another Antarctic cnidarian, and consider the phylogenetic and functional implications of microbial diversity for these animals. The *E. andrillae* microbiome was relatively low in diversity, with seven phyla detected, yet included substantial phylogenetic novelty. Among the five anemones investigated, the distribution of microbial taxa varied; this trait appears to be shared by many anthozoans. Most importantly, specimens either appeared to be dominated by Proteobacteria-affiliated members or by deeply branching Tenericute sequences. There were few closely related sequence types that were common to temperate and Antarctic sea anemone microbiomes, the exception being an *Acinetobacter*-related representative. Similar observations were made between microbes associated with *E. andrillae* and an Antarctic soft coral; however, there were several closely-related, low abundance Gammaproteobacteria in both Antarctic microbiomes, particularly from the soft coral, that are also commonly detected in Southern Ocean seawater. Although this preliminary study leaves open many questions concerning microbiome diversity and its role in host ecology, we identify major lineages of microbes (e.g., diverse deep-branching Alphaproteobacteria, Epsilonproteobacteria, and divergent Tenericutes affiliates) that may play critical roles, and we highlight the current understanding and the need for future studies of sea anemone-microbiome relationships.

SOURCE: Integrative and comparative biology

PDF URL: <https://academic.oup.com/icb/article-pdf/56/4/542/6758553/icw095.pdf>

CITED BY COUNT: 21

PUBLICATION YEAR: 2016

TYPE: article

CONCEPTS: ['Biology', 'Sea anemone', 'Ecology', 'Microbiome', 'Anthozoa', 'Anemone', 'Cnidaria', 'Phylogenetic diversity', 'Gammaproteobacteria', 'Coral', 'Phylogenetics', 'Paleontology', 'Bioinformatics', 'Biochemistry', '16S ribosomal RNA', 'Gene', 'Bacteria']