The role of bacteria in marine animal hosts: The good, the bad, and the commensal

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Marine animal holobionts harbor complex microbial communities which include a diversity of prokaryotes (bacteria and archaea), microeukaryotes, and viruses. In contrast to the terrestrial realm where numerous powerful examples of functionally well characterized host-microbe interactions exist, our understanding of marine host-microbe interactions is much less developed. Due to the challenges associated with working with marine non-model animal systems, substantial effort has been channeled into the study of associated microbial community dynamics using metabarcoding approaches, while functional work is mainly biased towards pathogenic interactions. Here I present work on the ecology of two distinct examples of marine animal-associated microbes: the functional group of nitrogen fixers (diazotrophs) and the ubiquitous bacterial family Endozoicomonadaceae, which exhibits a spectrum of lifestyles depending on their host identity. Recent work on these microbial groups demonstrates the importance of environmental context in interactions and lifestyles of marine microbes. This work further highlights that knowledge of microbial functions is critical to understanding health and resilience of their marine animal hosts, especially in the context of rapidly accelerating global change.