Baseline assessment of coral-associated microbial communities
PI: Craig Nelson, Assistant Researcher of Oceanography, UH Mānoa
Co-I: Emilia Sogin, Max Planck Institute for Marine Microbiology, Bremen, Germany

Project Summary
Microbial symbiotic partners mediate biochemical transformations that contribute to host performance, thereforealtering the trajectory of individual survival and ecosystem function. Consequently, these communities are essential components of many marine ecosystems including coral reefs, where microbial partners re-cycle organic molecules, such as carbon, nitrogen and sulfur, to mobilize nutrients in oligotrophic waters. For instance, tropical reef-building corals, which provide essential habitat for a mosaic of plants and animals, partner with a diverse community of prokaryotic and eukaryotic organisms (including viruses, bacteria, Archaea, fungi and dinoflagellates). These microbial partners influence the health, trajectory and survival of corals, thereby altering the function of reef communities and the services they provide.

Our project aims to describe the presence and abundance of Prokaryotes (e.g., bacteria and Archaea) associated with 9 common coral species found in the waters off of Moorea, French Polynesia as part of a larger effort in describing the role of microbial partners on coral reefs. We successfully sequenced 16S rDNA sequencing libraries of V3-V4 region for 41 different individuals spanning 4 genera (Fig. 1). Our data indicate different coral species and genera have strong structuring in their Prokaryotic assemblages, suggesting these communities are host specific (Fig. 2).

Shifts in climatic and environmental conditions likely alter microbial communities and their functions. Therefore, future ecological changes may prompt coral hosts, each with a different Prokaryotic assemblage, to experience varied physiological performance. The data from this project will serve as a baseline measurement of coral-associated microbial communities along a fringing reef in the South Pacific Ocean. Future collections can be compared to these data to determine how changing climatic conditions influence the relationship between corals and their microbial symbionts.

Fig. 1. Coral-associated Prokaryotic communities. Bar plot shows the relative abundance of the top 100 OTUS (Operational Taxonomic Units) of the dataset pooled by coral species.
Fig. 2. nMDS ordination showing the community structure of coral-associated Prokaryotic communities. ANOSIMS comparison of coral species indicates the model is capturing 79% of the variation in community structure and that coral species have significantly different bacterial communities.