

MOLECULAR DIVERSITY OF *PROCHLOROCOCCUS* WITHIN
PACIFIC COASTAL ISLAND SYSTEMS

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By

Carli A. Bober

Thesis Committee:

Zackary I. Johnson, Chairperson

Grieg Steward

Matthew Church

ABSTRACT

Prochlorococcus dominates oligotrophic, open-ocean ecosystems accounting for up to 40% of the photosynthetic biomass. *Prochlorococcus* is composed of genetically and physiologically distinct clades, or ecotypes, which occupy distinct niches. Although *Prochlorococcus* is generally considered to be an open-ocean microorganism, there is some evidence that it may be abundant in some coastal areas as well. To examine this in more detail, here I investigate the abundance and molecular diversity of *Prochlorococcus* in the vicinity of several Pacific Islands to determine how populations vary from offshore to onshore and whether nearshore populations are regulated by local or external processes. Using a combination of flow cytometry, quantitative PCR (QPCR), denaturing gradient gel electrophoresis (DGGE) and clone libraries, I show that in these tropical and sub-tropical coastal environments, *Prochlorococcus* is both abundant and diverse. In addition, some subpopulations identified in these coastal ecosystems were not found in the surrounding waters of the open ocean. Concentrations in Pacific island coastal waters of Hawaii, Aniwa, Futuna and Lord Howe average $\sim 10^4$ per mL and are comprised of both previously described and some novel lineages. The patterns of abundance and diversity of *Prochlorococcus* in these coastal island systems suggest that these populations are driven, in part, by internal dynamics and not the sole result of advection from offshore.