**INTRODUCTION**

Coral reef habitats are among the most biologically diverse ecosystems on the planet. Large assemblages of coexisting organisms form these ecologically crucial environments, which provide cumulative services unquantifiable in value. The rugosity and structural framework characteristic of coral reefs is due to the calcification of hard corals in the order Scleractinia. Such calcification is made possible by the formation of an endosymbiosis with photosynthetic dinoflagellates of the order Scleractinia.

**METHODS**

*Study Design and Location*

Colonies of *Montipora capitata* across Kāne’ohe Bay, O’ahu, Hawai’i, USA were tagged and sampled in order to analyze the spatial variability of *Symbiodinium* clades. Corals were tagged on patch reefs and fringing reefs in the northern, central and southern regions of Kāne’ohe Bay (Figure \_). Five patch reefs and three fringing reefs were tagged in each region of the bay. At each patch reef, 30 colonies were tagged; 10 colonies each from windward slope, top and leeward slope. Along the windward and leeward slopes, colonies were tagged along a depth gradient. Given the lack of leeward slope on fringing reefs, 20 colonies were tagged at each site; 10 colonies each from the top and slope. Tagging and sampling of colonies took place between 7 June 2016 and \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_. In total, 15 patch reefs and 9 fringing reefs were sampled across Kāne’ohe Bay resulting in a sample size of n=630 colonies. Fragments from each colony were frozen in liquid nitrogen and archived for future use in DNA extraction and collaborative efforts analyzing biogeochemistry and energetics in Kāne’ohe Bay.

*Colony Tagging and Sample Collection*

Ten weights with attached floats were randomly deployed at each area of the reef. The closest colony of *Montipora capitata* in proximity to each float was tagged and a small branch fragment (~4-5cm) was removed. *In situ* photographs were taken of each colony for color morph and size analysis by visual assessment. Tissue biopsies were taken from each collected fragment and placed in 500μL DNA buffer (5M NaCl, 0.5M EDTA) with 1% sodium dodecyl sulfate (SDS) and the remaining fragment was frozen in liquid nitrogen to be stored at -80°C as an archive for future analyses. DNA was extracted from each sample biopsy following a modified CTAB-chloroform protocol (dx.doi.org/10.17504/protocols.io.dyq7vv).

*Symbiodinium Community Analysis*

Quantitative PCR was used to analyze the symbiont community in each collected sample. Based on amplification of internal transcribed spacer (ITS2),clade C and D *Symbiodinium* sequences resulted from existing clade-level primers and probes. All samples were assays of both clade C and D *Symbiodinium* in duplicate 10μL reactions on a StepOnePlus platform (Applied Biosystems) for 40 cycles with a relative fluorescence threshold of 0.01 and baseline interval of cycles 15-22. The target symbiont ratios of symbiont clade C to D in each sample, normalized for fluorescence intensity and locus gene copy number, were produced by the StepOneplus software.