**METHODS**

*Study Design and Location*

Individual colonies of *Montipora capitata* were tagged and sampled to determine the spatial variability of *Symbiodinium* clades C and D found in colonies from different habitats. All corals were sampled from Kāne’ohe Bay, located on the east side of O’ahu in Hawai’i, USA. Corals were tagged with medium-sized yellow cattle tags throughout Kāne’ohe Bay (Fig. 1). Colonies at five patch reefs and three fringing reefs were tagged in each of the northern, central and southern regions of the bay with an additional submerged reef south of the Hawai’i Institute of Marine Biology. At each patch reef, 30 colonies were tagged; 10 colonies each from windward slope, top and leeward slope with depth recorded using a depth gauge. Given the lack of leeward slope on fringing reefs, 20 colonies were tagged at each site; 10 colonies each from the top and slope. At the tops of the patch reefs and the fringe sites most colonies were between 0 and 1 meter depth. Along the windward and leeward slopes, colonies were tagged randomly at a depth from 0.5 meters to 15 meters. Reefs lacking colonies from depths greater than 5 meters were re-visited and five additional colonies were sampled. Depth was later adjusted according to differences in mean sea level using NOAA’s daily tide tables for Moku o Lo’e, Kāne’ohe Bay at 6-minute intervals. In total, 16 patch reefs and 9 fringing reefs were sampled across Kāne’ohe Bay resulting in a sample size of 707 colonies. Tagging, photographing and sampling of colonies took place between 7 June 2016 and 12 August 2016.

*Sample Collection and Processing*

Ten weights with attached floats were randomly cast from the surface across a distance of approximately 20 meters on each reef area (top and both slopes). The closest colony of *M. capitata* in proximityto each float was tagged and sampled. Each sample consisted of a small branch fragment (~4-5cm) taken from the tip of a branch located at the top of the colony. *In situ* photographs with an included scale bar and color standard were taken of each colony. The coral fragment was subsampled for a tissue biopsy shortly after collection (never greater than 1.5 hours), which was placed in 500μL DNA buffer (5M NaCl, 0.5M EDTA) with 1% sodium dodecyl sulfate (SDS). The remaining fragment was immediately frozen in liquid nitrogen and archived at -80°C in the laboratory. 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 (qPCR) was used to analyze the symbiont community of each collected sample. Based on amplification of the internal transcribed spacer region (ITS2), sequences of *Symbiodinium* clades C and D resulted from existing clade-level primers and probes (Cunning et al. 2013). All samples were assayed with primers of both clades C and D in duplicate 10μL reactions on a StepOnePlus platform (Applied Biosystems) for 40 cycles. Parameters were set at a fluorescence threshold of 0.01 and a baseline interval of cycles 15-22. The StepOnePlus software produced the target symbiont ratio of clade C to D in each sample, normalized for fluorescence intensity and locus gene copy number. Symbiont clades detected in only one qPCR reaction were not considered. The proportion of clade C dominance was calculated from the clade C to D ratio by the formula [(C:D)/(C:D+1)]. The resulting proportion of clade D dominance was then calculated by the formula 1-[(C:D)/(C:D+1)]. Based on the proportion values of clades C and D, the dominant symbiont type was determined. If a colony possessed both symbiont clades, designated as a mixture, the clade present in higher proportion was noted as CD or DC accordingly.

*Data Analysis*

Chi-Squared tests were used to assess differences in colony color morph, dominant symbiont clade and symbiont community mixtures between reef areas, bay areas and reef types. To estimate the probability of occurrence of color morph, dominant symbiont and symbiont community mixture as a function of increasing depth, logistic regressions of generalized linear models were used. Depth was standardized according to differences in mean sea level using daily tide tables for Moku o Lo’e, Kāne’ohe Bay at 6-minute intervals.

Distribution of c to d:

* across habitat types,
* across bay regions,
* across depths
* in different color morphs