Diversity of the brown alga Dictyota between deep and shallow reefs of Hawaii

Mary Ade  
*Augustana College, Rock Island Illinois*

Rachael M. Wade  
*University of Hawaii, Manoa*

Heather L. Spalding  
*University of Hawaii, Manoa*

Alison R. Sherwood  
*University of Hawaii, Manoa*

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Diversity of the brown alga *Dictyota* between deep and shallow reefs of Hawai‘i

Mary T. Ade, Rachael M. Wade, Heather L. Spalding, and Alison R. Sherwood

Department of Botany, University of Hawai‘i at Mānoa

**INTRODUCTION**

- Mesophotic coral ecosystems (MCEs) have been shown to house higher levels of endemism and new species compared to shallow reefs. [1,2]
- Previous findings suggest MCEs have potential to serve as refugia for shallow water species. [1,2]
- Little is known about species’ boundaries within shallow and deep reefs due to a lack of research on MCEs until recent years. [1,2,5]
- *Dictyota* is a globally distributed genus of algae, known to inhabit both temperate and tropical waters. We use *Dictyota* as a case study to examine connectivity between shallow and deep algal assemblages. [3,4,6]
- Varied depth and temperatures in the abundant reefs of the main and northwestern Hawaiian islands make it an ideal location for studying the connectivity of shallow and deep reefs.

**OBJECTIVES**

- To investigate the distribution and species identity of the brown alga *Dictyota* in the Hawaiian Islands and any differences between deep and shallow reef environments.

**HYPOTHESES**

- If trends illustrated by other mesophotic studies hold true, then the deep and shallow *Dictyota* assemblages will differ due to environmental disconnectivity. [1,5]
- If these trends do not hold true, there should be no difference in assemblages between depths.

**METHODS**

- Live algae samples were collected between September 2012 and June 2016 by technical divers and the *Pisces IV* submarine between depths of 133 - 35m across the Main (MHI) and Northwestern Hawaiian islands (NWHI).
- Genomic DNA was extracted from 19 *Dictyota* specimens and stored at -20 °C.
- A portion of the chloroplast gene marker (rbcL) was sequenced to reconstruct a molecular phylogeny and determine species identity.
- These sequences were used to run maximum likelihood analyses with bootstrapping.
- 20 gross macroscopic characters and 13 microscopic feature were used to identify species.

**RESULTS**

- Of the 19 samples, six were successfully amplified and sequenced.
- There are six distinct lineages. Two are exclusively shallow, two are found in both depths, and two are exclusively deep.
- The two deepwater *Dictyota* lineages could not be identified and are likely new records or species.

**CONCLUSIONS**

- While some species were collected from a deep or shallow environment exclusively, others inhabited both environments, suggesting connectedness, to a degree. This contrasts with the null hypothesis that shallow and deepwater reefs are fully distinct [1].
- Two deepwater species did not cluster with anything known and did not match descriptions in any current dichotomous keys for *Dictyota* and therefore are likely new to science.
- Many of the DNA samples were not successfully sequenced. There is likely more unique algal diversity in the MCEs to be discovered.
- Future research on exploring reef connectivity should include a broader sampling, due to a lack of algae collected from shallow water reefs of the NWHI and low success with DNA amplification.

**REFERENCES**


**ACKNOWLEDGEMENTS**

- This work was supported by an NSF REU Site award (no. DB1560491), “Undergraduate Research Experiences in DNA-Based Discoveries in Hawai‘i’s Biodiversity,” to Stuart Donachie and Stephanie Kraft-Terry at the University of Hawai‘i at Mānoa.
- Funding and support for mesophotic macroalgal collections was from the National Oceanic and Atmospheric Administration (NOAA) Office of National Marine Sanctuaries (Papahānaumokuākea Marine National Monument), NOAA Center for Sponsored Coastal Ocean Research (NA07NOS4780188, NA07NOS5780187, NA07NOS4780190, NA07NOS5780189), NOAA Coral Reef Conservation Program (NA05OAAM4301108, NA09OAAM430219), NOAA’s Deep Sea Coral Research and Technology Program, NOAA Undersea Research Program’s Hawai‘i Undersea Research Laboratory (HURL; MCO-17 and HCO-08), NOAA’s Office of Ocean Exploration, and the National Fish and Wildlife Foundation.
- Thanks to Shabbin Hsu and the staff at ASGPB for sequencing the samples used in this research.