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

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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.

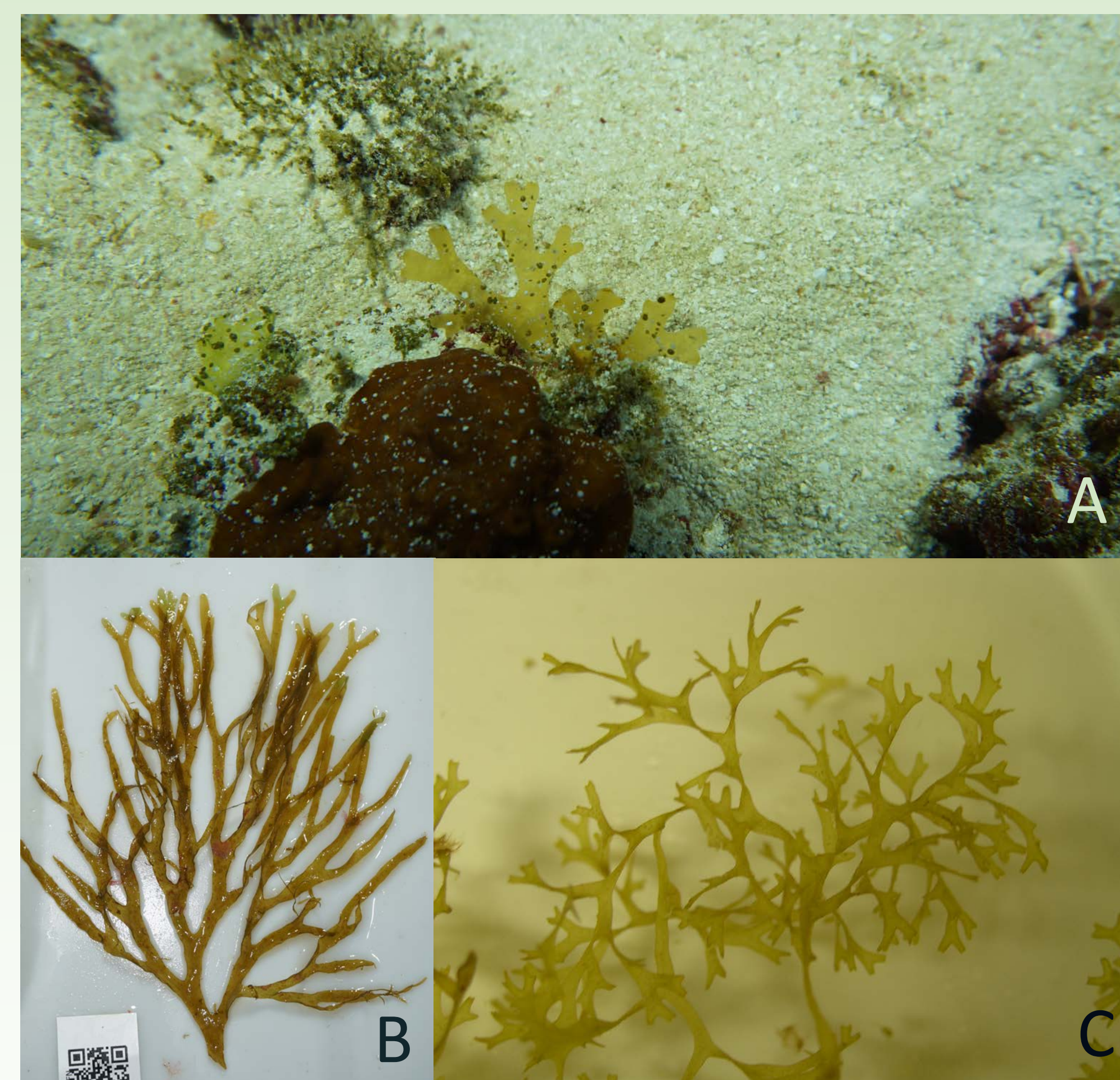


Fig 1. Photos of *Dictyota* specimens. (A) *Dictyota* sp. 2 (B) *Dictyota liturata* (C) *Dictyota acutiloba*

RESULTS

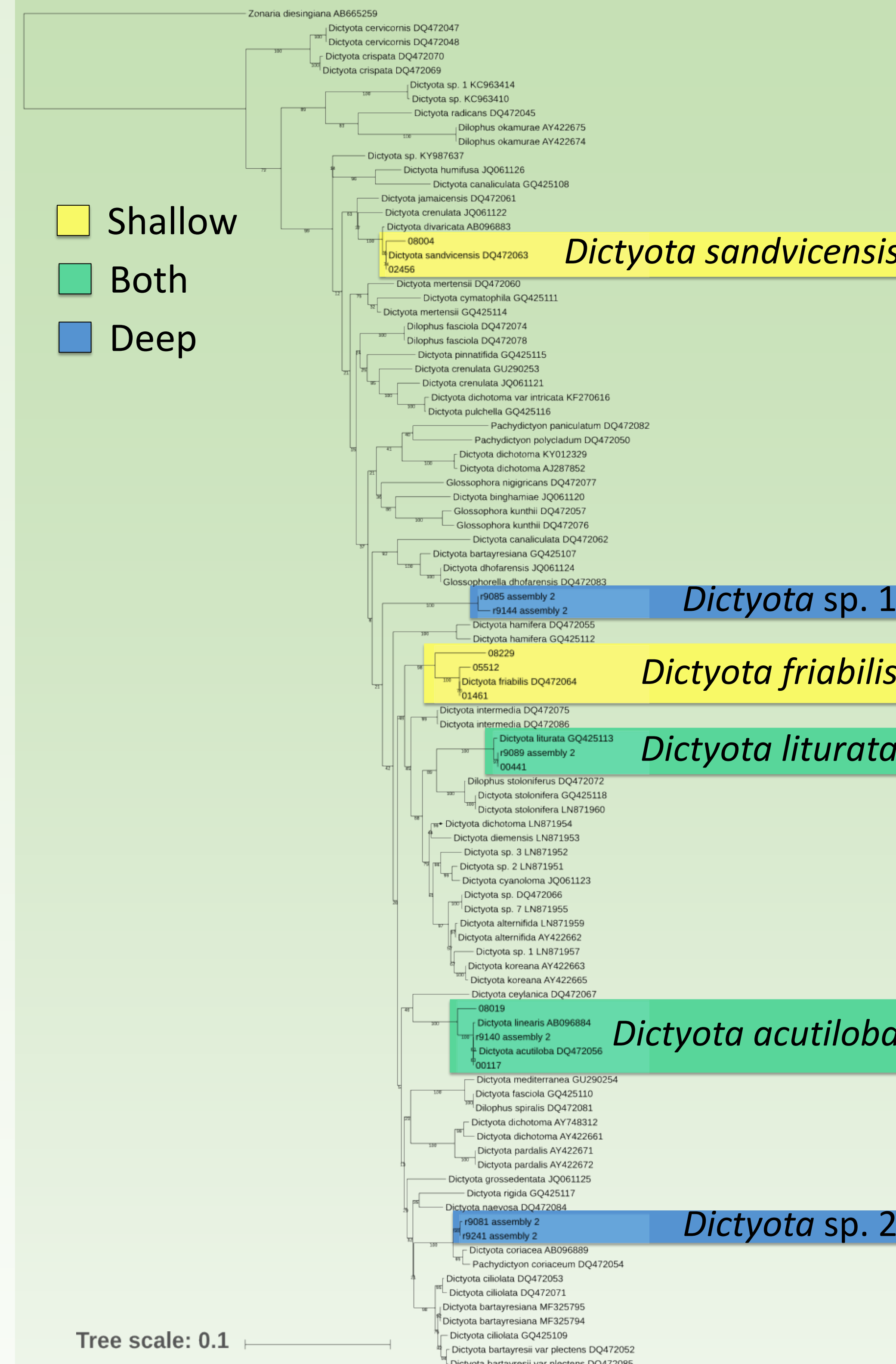


Fig 2. *rbcl* Maximum Likelihood estimated phylogeny of *Dictyota*. Nodal values represent bootstrap support.

- 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 connectivity, 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.

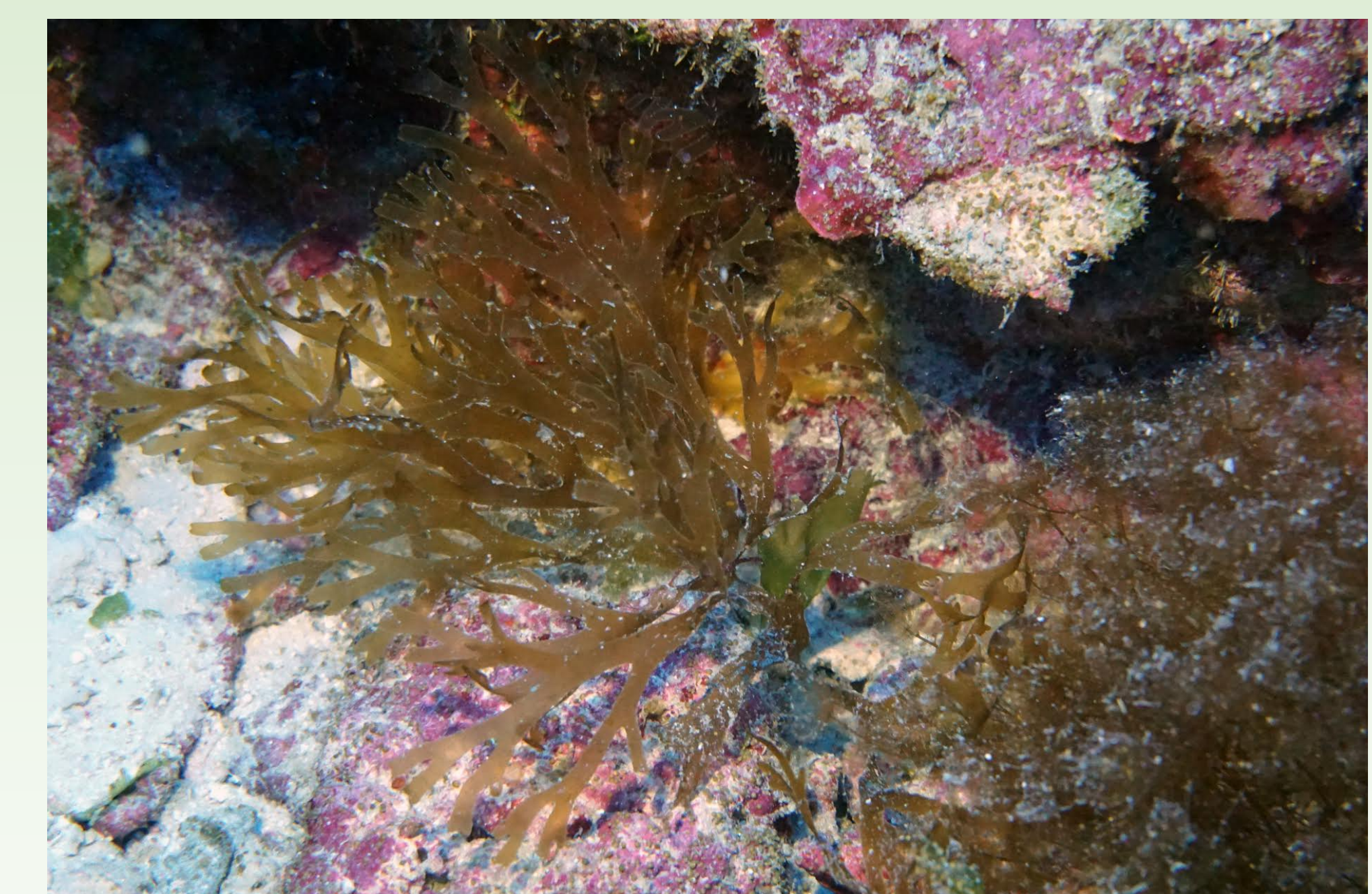


Fig 3. Photo of *Dictyota* sample NWHI-423 Unsuccessfully amplified deepwater sample of unknown identity.

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