

MACROECOLOGY MEETS MACROEVOLUTION: EVOLUTIONARY NICHE DYNAMICS IN THE SEAWEED *HALIMEDA*

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Because of their broad distribution in geographic and ecological dimensions, seaweeds (macroalgae) offer great potential as models for marine biogeographic inquiry and exploration of the interface between macroecology and macroevolution. This study aims to characterize evolutionary niche dynamics in the common seaweed genus *Halimeda*, use the observed insights to gain understanding of the biogeographic history of the genus, and predict habitats that can be targeted for discovery of species of special biogeographic interest.

The evolutionary history of the genus is characterized using molecular phylogenetics and relaxed molecular clock analysis. Niche modeling is carried out based on macroecological data derived from global satellite imagery with Maximum Entropy techniques. Evolutionary niche dynamics are inferred through application of ancestral character state estimation.

A nearly comprehensive molecular phylogeny of the genus was inferred from a six-locus dataset. Macroecological niche models showed that species' distribution ranges are considerably smaller than their potential ranges. We show strong phylogenetic signal in various macroecological niche features.

The evolution of *Halimeda* is characterized by conservatism for tropical, nutrient-depleted habitats, yet one section of the genus managed to invade colder habitats multiple times independently. Niche models indicate that the restricted geographic ranges of *Halimeda* species are not due to habitat unsuitability, strengthening the case for dispersal limitation. Niche models identified hotspots of habitat suitability of Caribbean species in the East Pacific Ocean. We propose that these hotspots be targeted for discovery of new species separated from their Caribbean siblings since the Miocene rise of the Central American Isthmus.