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Morphological reassessment and molecular assessment of *Sargassum* (Fucales: Phaeophyceae) species from the Gulf of California, Mexico

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Abstract

Systematic molecular studies have not been performed on ecologically important brown algae (*Sargassum*) in the Gulf of California, Mexico, where 42 specific and infraspecific names have been recorded within this genus. We conducted phylogenetic analyses of nuclear ribosomal ITS and mitochondrial *cox*1 and *cox*3 sequences, along with detailed morphological observations of *Sargassum* collected in the Gulf of California. We confirmed the presence of six species, five previously described—*S. herporhizum*, *S. horridum*, *S. johnstonii*, *S. lapazeanum*, and *S. sinicola*, as well as the newly described *Sargassum ulixei* sp. nov. which is characterized by terete primary axes arising from the stipe, lanceolate to elliptical sessile ecostate blades with smooth margins, cryptostomata, ellipsoidal vesicles with a short mucron, and cylindrical to ellipsoidal receptacles. The individual analyses and subsequent phylogenetic analysis recognized two groups previously described by Dawson, one as *Sargassum* and other as *Horridum*. Our studies suggest that the Gulf of California is a region with endemic *Sargassum* species, and is clearly distinguished from the Pacific side of Baja California, where recently introduced species are common. Based on phylogenetic relationships, we propose two geographical origins for the *Sargassum from* the Gulf of California: a first group originating from the proto-Gulf, related to species from the northern hemisphere (including five species); and a second group, containing *S. sinicola*, introduced when the southern end opened at a later stage.

Keywords: Gulf of California, molecular markers, morphology, phylogeny, *Sargassum*, new species, new synonyms

Introduction

In the Gulf of California, originated in the early Late Miocene (Ledesma-Vázquez 2002, Ledesma-Vázquez & Carreño 2010), *Sargassum* species produce a large amounts of biomass (Norris 2010). Their ecological organization resembles that of a forest because they produce a canopy that acts as a habitat for diverse assemblages of epiphytic algae/microinvertebrates and understory algae, invertebrates, and fish (Soto-Mardones *et al*. 1999, Brusca *et al*. 2005, Enriquez-Andrade *et al*. 2005). *Sargassum* forests are reproductive and nursery areas of fishery-related species (Aburto-Oropeza *et al*. 2008) and endangered species such as the green turtle *Chelonia mydas*. Thus, these are critical habitats for coastal management and species conservation (Witherington *et al.* 2012).

Historically, some names applied to the *Sargassum* species from the Gulf of California were proposed by Setchell and Gardner (1924) who described 15 new species, and Setchell (1937) who described three more. Dawson (1944) reviewed the taxonomy of the genus and proposed a reduction to ten species (as well as one form) based on morphological features, and proposed two new species. Dawson (1944) also organized supraspecific taxonomic categories due to the difficulty in identification to the species level, as informal "groups" *Johnstonii* Dawson (1944: 239), *Lapazeanum* Dawson (1944: 241), *Sinicola* Dawson (1944: 245), and *Herporhizum* Dawson (1944: 249). Later, Taylor (1945) reported six species, including *Sargassum brandegeei* Setchell & Gardner (1924: 736), *Sasrgassum howellii* Setchell (1937: 132), *Sargassum pacificum* Bory de Saint-Vincent (1828: 123) and *Sargassum liebmannii* Agardh (1847: 8) for Maria Islands, without comparing all these species to others from the region.

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patterns and formed new currents that flow along the east Pacific coast (Kessler 2006, Kirby *et al.* 2008). Once the taxonomy and phylogeny of *Sargassum* from the Gulf of California are clear, we will be able to infer their relationships with Mexican Pacific and Central American Pacific *Sargassum* species using morphological and molecular data in order to understand distributions, phylogeny relationships and the diversity of the genus.

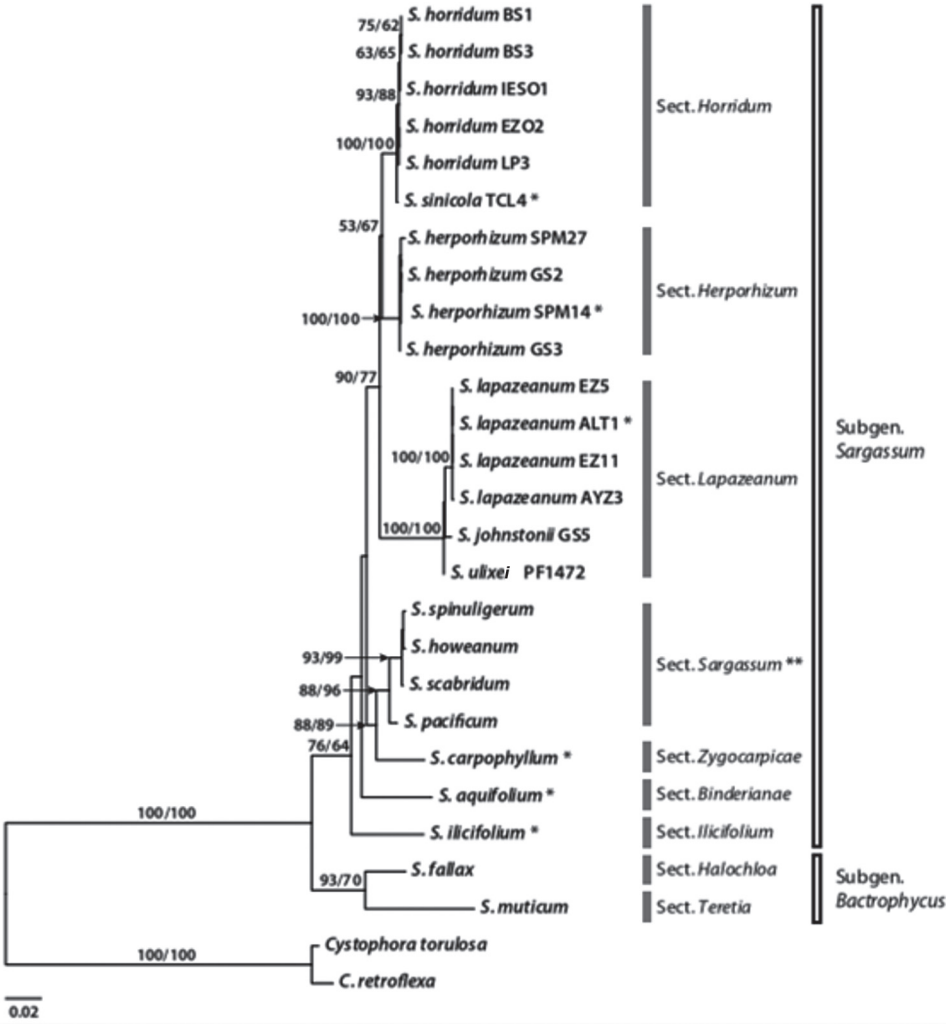

FIGURE 9. Maximum likelihood concatenated tree of *Sargassum* inferred from ITS2+*cox*1+*cox*3 sequences. Bootstrap values are indicated for ML/MP when over 50%. An asterisk indicates the type of each section, while two asterisks denote the type of each subgenus.

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