

THE SEAGRASS *HALODULE* IN BERMUDA

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Introduction

The seagrass *Halodule bermudensis* den Hartog 1964 was described as an endemic Bermudian species. (See type location in Fig. 4)



Fig. 1. Leaf tips (above) and original specimen (right) of *H. bermudensis*. Scale for tips = 1 mm.

However, specimens of *Halodule* collected in Bermuda are more frequently referred to *Halodule wrightii* Ascherson. The taxonomic question of "what is *H. wrightii*?" is complicated by such things as the presence of two very distinct forms of *Halodule* on the herbarium sheets of the type material. Den Hartog (1964), among others, recognized that the original description of *H. wrightii* fit only one, the smaller, of these two forms. He described the larger form as *H. beaudettei* (den Hartog 1960)

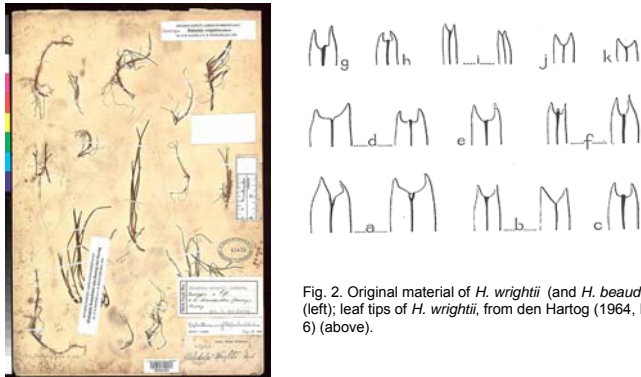


Fig. 2. Original material of *H. wrightii* (and *H. beaudettei*) (left); leaf tips of *H. wrightii*, from den Hartog (1964, Fig. 6) (above).

It is possible that both *H. wrightii* and *H. bermudensis* (Bernatowicz 1952, den Hartog 1964) have been found in Bermuda. However, no recent records of *Halodule* used morphology to establish a specific identity. *H. bermudensis* is now included in the IUCN red list (Livingstone, *et al.*, pers. comm.) as a data deficient taxon - one in need of additional study to determine both its taxonomic and biological status.

Leaf-tip morphology has been very important in the recognition of species of *Halodule*; however, it has been strongly criticized and described as highly variable within a species. More recently, molecular studies (Fig. 3) have been undertaken to document variability and evolutionary relationships among species of *Halodule*.

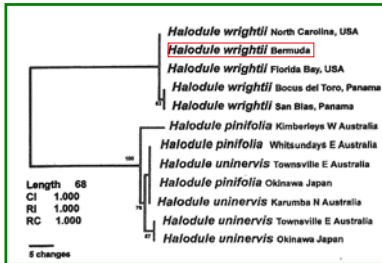


Fig. 3. ITS nuclear DNA sequence phylogram for *Halodule* from Waycott *et al.* (2006).

In many taxa ITS is a heterozygous, multi-copy gene, requiring cloning to establish the range and limits of variation within a population. In this analysis, Bermuda populations of *Halodule* have the same sequence as populations from North Carolina and Florida Bay, and all these are different from populations from the Caribbean coast of Panama. For each of these locations, only one sequence is reported in Waycott *et al.* (2006).

Methods

In order to provide additional information on the morphological and molecular characteristics of *Halodule* species found in Bermuda, new material was acquired in 2008. The *rbcl* chloroplast gene was sequenced primarily because comparative data for other populations were available (Les *et al.* 1997); it is also variable within the genus but does not require cloning. Sequence and leaf-tip data were acquired and co-recorded for every rhizome studied.

Results

Comprehensive benthic surveys done between 2006 and 2009 show that *Halodule* in Bermuda is a widespread, shallow-water organism found both inshore and at offshore reef-associated sites (Figs 4 & 5). When sediment conditions and light levels are adequate for supporting seagrass beds, the density of *Halodule* in the beds is probably controlled by nutrient availability.

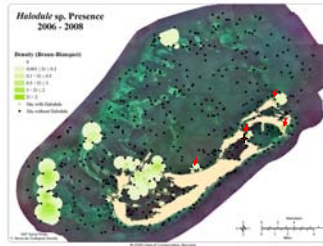


Fig. 4. Present distribution of *Halodule* in Bermuda; sample locations for genetic and leaf tip material; and type location for *H. bermudensis*.

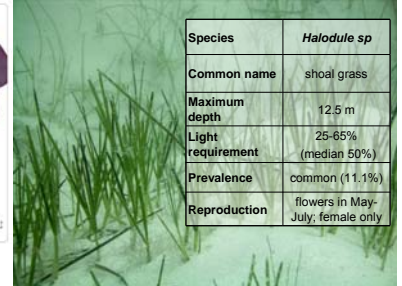


Fig. 5. Ecology of *Halodule* in Bermuda.

All leaf tips examined had a distinct mid-projection and two small lateral teeth; blade width about 1 to 1.4 mm (Figs 6 & 7). This leaf tip morphology is not like either *H. bermudensis* or typical *H. wrightii* (Figs 1 & 2), but is more like what has been described for *H. beaudettei* (see den Hartog 1964).

#rhizome fragments (# leaf tips)	Mean tip width (mm)	Midrib projection	Midrib projection lateral teeth	#lateral teeth	Laterals, inner sides
31 (191)	Mean - 1.13 Max - 1.38 Min - 0.98	Present	longer, rarely subequal (2.6%)	Normally 2, rarely 1 (4.7%) or none (.5%)	Concave - larger laterals - straight - smaller laterals

Fig. 7. Summary of leaf tip forms for all tips examined.

Fig. 6. Range of leaf tip forms for 4 locations in Bermuda; shoots collected recently from the type location of *H. bermudensis* had tips most like *.

The DNA sequence for the *rbcl* chloroplast gene of Bermuda specimens is unique (Fig. 8), compared to a number of populations of *Halodule* from the Caribbean and US east coast.

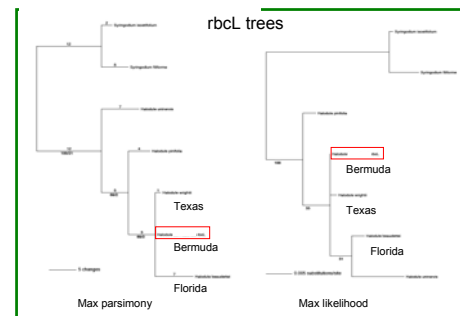


Fig. 8. Maximum parsimony and maximum likelihood phylograms for *rbcl* gene for populations of *Halodule*. The unique sequence for the Bermuda population is one base pair different from the Texas population identified as *H. wrightii* and seven base pairs different from a Florida population identified originally as *H. beaudettei* and later as *H. wrightii*. The differences among these populations are small, but robust. In ML and Bayesian analyses, the Florida population was the sister to a population of *H. pinifolia*. Bootstrap (of 10,000 reps) are on both trees and Bremer values are shown on the single MP tree.

Conclusions

- *Halodule* is common and thriving in Bermuda, but leaf-tip morphology does not indicate this is *H. bermudensis* or *H. wrightii*, as either was originally described; typical *H. bermudensis* was not found at the type location of the species and it may no longer occur in Bermuda
- *rbcl* sequence is unique and consistent for the Bermuda population, slightly different from a Texas population identified as *H. wrightii* and much more different from a Florida population identified as *H. beaudettei*; the difference between the Texas and Florida populations are slightly greater than between the Florida and Bermuda populations
- *rbcl* sequence combined with ITS sequence data indicate there may be as many as four distinct populations of *Halodule* in the Gulf of Mexico-Caribbean-Floridian-Bermudian region
- A few more sequences from a few more locations/populations would add greatly to the resolution of specific diversity of *Halodule* in the Atlantic; morphology, location and genetics must be co-recorded to maximize information content

Bibliography

Bernatowicz, A.J. 1952. Bull. Mar. Sci. Gulf Carib. 2:338-345; den Hartog, C. 1960. Pacif. Natur. 15:1-8; den Hartog, C. 1964. Blumea 12 (2):289-312; Les, D. H. *et al.* 1997. Syst. Bot. 22 (3):443-463; Waycott, M. *et al.* 2006. In Larkum, A.W.D. *et al.*: Seagrasses: biology, ecology and conservation, 25-50.