



Morphology and phylogeny of *Halamphora yongxingensis* sp. nov. (Bacillariophyta), a new marine benthic diatom isolated from Yongxing Island, South China Sea

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Abstract

Halamphora yongxingensis sp. nov., a marine benthic diatom isolated from an intertidal reef around the Yongxing Island, South China Sea (16° 58' 43.3" N, 112° 14' 41.7" E), is described in this study on the basis of light and electron microscopy. This diatom is also compared with related taxa such as *Halamphora subturgida* (Hustedt) Levkov and *Amphora subtropica* Wachnicka & Gaiser. In addition, phylogenetic analyses based on 18S rDNA and *rbcL* gene were also conducted. The results revealed that *H. yongxingensis* was clustered into the *Halamphora* clade, closely related to *Halamphora montana* (Krasske) Levkov. We discuss morphological differences between *H. yongxingensis* and *H. montana*.

Key words: 18S rDNA, diatom, *Halamphora yongxingensis*, phylogeny, *rbcL*, South China Sea, taxonomy

Introduction

The genus *Halamphora* (Cleve) Levkov (2009:165) was originally introduced as a subgenus of *Amphora* Ehrenberg ex Kützing (1844:107) but elevated to genus recently by Levkov (2009). *Amphora sensu lato* is a large genus widely distributed in continental, estuarine and marine environments. Cleve (1895) split *Amphora* into nine subgenera (*Amblyamphora*, *Amphora*, *Archiamphora*, *Calamphora*, *Cymbamphora*, *Diplamphora*, *Halamphora*, *Oxyamphora* and *Psammamphora*) based on frustule and valve outline, raphe position, stria type and girdle band striation. In the genus *Halamphora*, the chloroplast is H-shaped. Valve is asymmetric to the apical axis and symmetric to the transapical axis. The valve mantle is deep on the dorsal margin and shallow on the ventral margin. The dorsal fascia is usually absent. Proximal raphe ends are straight or dorsally deflected. In the internal view, the proximal raphe ends terminate at a single fused helictoglossa. Most of *Halamphora* species occur in marine or brackish water habitats (Spaulding 2011).

Benthic diatoms are widely used in aquaculture, such as abalone and sea cucumber culture, acting as inductors for larvae settlement and serving as the main food during the early juvenile stage (Kawamura *et al.* 1995, Ito & Kitamura 1997, Jouuchi *et al.* 2007). But different diatoms often exhibit profound differences in the effects of settlement and growth (Courtois de Viçose *et al.* 2010, Roberts & Lapworth 2001). Therefore, we need to know more detailed information on classification of the diatoms which were used as baits. Molecular tools play important roles in delimitation of diatom species and better understanding the phylogenetic relationships among diatom taxa (Kooistra *et al.* 2004, Rimet *et al.* 2011). Most molecular analyses have been conducted based on nuclear ribosomal DNA, mitochondrial genes (e.g. cytochrome oxidase subunit I (*cox1*) gene and cytochrome b (*cob*) gene) and chloroplast genes (e.g. the large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (*rbcL*) gene) (Evans *et al.* 2007, Alverson 2008).

When screening bait for *Stichopus horrens* Selenka (1867:316) in Yongxing Island, we found a new benthic

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