



Molecular and morphological characterization of *Amathia distans* Busk and *Amathia brasiliensis* Busk (Bryozoa: Ctenostomata) from the tropical and subtropical Western Atlantic

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Abstract

Morphological and molecular analyses have proven to be complementary tools of taxonomic information for the redescription of the ctenostome bryozoans *Amathia brasiliensis* Busk, 1886 and *Amathia distans* Busk, 1886. The two species, originally described from material collected by the ‘Challenger’ expedition but synonymized by later authors, now have their status fixed by means of the selection of lectotypes, morphological observations and analyses of DNA sequences described here. The morphological characters allowing the identification of living and/or preserved specimens are (1) *A. brasiliensis*: whitish-pale pigment spots in the frontal surface of stolons and zooids, and a wide stolon with biserial zooid clusters growing in clockwise and anti-clockwise spirals along it, the spirality direction being maintained from maternal to daughter stolons; and (2) *A. distans*: bright yellow pigment spots in stolonial and zooidal surfaces including lophophores, and a slender stolon, thickly cuticularized, with biserial zooid clusters growing in clockwise and anti-clockwise spirals along it and the spirality direction not maintained from maternal to daughter stolons. Pairwise comparisons of DNA sequences of the mitochondrial genes cytochrome c oxidase subunit I and large ribosomal RNA subunit revealed deep genetic divergence between *A. brasiliensis* and *A. distans*. Finally, analyses of those sequences within a Bayesian phylogenetic context recovered their genealogical species status.

Key words: redescription, genealogical species, COI, 16S rRNA, Vesiculariidae

Introduction

Amathia Lamouroux, 1812 is represented by approximately 33 extant described species of Bryozoa, distributed across all oceans (Bock 2010), and occurring in fouling, intertidal and subtidal habitats. While many of the species seem to be restricted to specific regions, at least eight are currently considered to be widespread (Bock 2010). Recent research relying on DNA sequence data has challenged the natural cosmopolitan status attributed to other bryozoan species (e.g. Davidson & Haygood 1999; Schwaninger 1999, 2008; Hoare *et al.* 2001; McGovern & Hellberg 2003; Mackie *et al.* 2006; Nikulina *et al.* 2007; Nikulina 2008; Hughes *et al.* 2008), classifying them instead as complexes of cryptic species, and/or recognizing events of bioinvasion responsible for their present widespread patterns of distribution. Specifically for *Amathia*, misidentifications, incomplete descriptions, and wrong taxonomic decisions leading to erroneous synonymies have underlined many previous references concerning several of its species, as reported by Chimonides (1987). This situation has not changed, as noted more than 20 years later by Souto *et al.* (2010). Additionally, there are still no DNA sequences available that might help to clarify their taxonomic status (only two sequences of ~70 base pairs of GRT-G1 retrotransposon gypsy-like reverse transcriptase, and the pseudogene LRT-L1 retrotransposon LINE-like reverse transcriptase, have been deposited in GenBank for *Amathia convoluta* Lamarck, 1816).

Recently, Vieira *et al.* (2008) listed four species of the genus as occurring in Brazilian waters: *Amathia brasiliensis* Busk, 1886, *Amathia crispa* Lamarck, 1816 (= *Amathia convoluta* Lamouroux, 1816, see d’Hondt 1983),