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The *Cylindrobulla* / *Ascobulla* complex—unraveling problems in identification and adding to *Cylindrobulla* diversity (Gastropoda, Heterobranchia, Sacoglossa) by describing a new species

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Abstract

Sacoglossa (Gastropoda: Heterobranchia) are generally considered a monophyletic group, previously associated within the now defunct “Opisthobranchia”, but now basally located within Panpulmonata. In the light of this new phylogenetic hypothesis, detailed knowledge of the most basal groups within Sacoglossa is of paramount importance. This study focuses on the genus *Cylindrobulla*, which is usually considered the most basal group within the Sacoglossa from a morphological point of view, because it does not share the typical elongate radula teeth of all other Sacoglossa. We describe a new species, *Cylindrobulla schuppi* sp. nov., and provide data on its food. We reexamined and clarify the radula of the type species *C. beaulti*, review the genus with all other valid species, provide new characters to aid in the proper identification of species within this genus, compare it to the very similar genus *Ascobulla*, present a determination key using external characters to ensure proper identification of the two similar genera, and discuss phylogenetic relationships within the shelled sacoglossan, the Oxynoacea.

Key words: Food, barcoding, *rbcl*, *tufA*, Oxynoacea, character analysis, phylogeny

Introduction

The Sacoglossa comprises a group of marine heterobranchs that feed on algae using a modified radular tooth that allows them to suck out algal cell sap (Jensen 1996a). Many sacoglossan species are known to sequester chloroplasts from their algal food and maintain them for weeks to months (kleptoplasty) (e.g., Rumpho *et al.* 2000; Evertsen *et al.* 2007; Händeler *et al.* 2009; see also reviews of Rumpho *et al.* 2011 and Wägele and Martin 2013). Numerous species are capable of “stealing” secondary metabolites from their food sources (kleptochimistry) for their own chemical defense (e.g., Cimino & Ghiselin 1998; Marín & Ros 2004).

The affiliation of Sacoglossa within Heterobranchia has changed often in recent years, certainly due to taxon and gene selection (see e.g., Jensen 2011), but was recently included in the new taxon Panpulmonata (see Schrödl *et al.* 2011) based on earlier analyses including several genes and with good support values (e.g., Dinapoli and Klussmann-Kolb 2010; Jörger *et al.* 2010, Göbbeler & Klussmann-Kolb 2011, Wägele *et al.* 2014). Kocot *et al.* (2013) and Zapata *et al.* (2014) confirmed this affiliation by genomic analyses. Sacoglossa is generally considered monophyletic (Wägele & Klussmann-Kolb 2005; Jörger *et al.* 2010; Dayrat *et al.* 2011; Kohnert *et al.* 2013; see Wägele *et al.* 2014), although the relative positions of groups within this taxon remain disputed (Jensen 1996a, b; Händeler & Wägele 2007; Händeler *et al.* 2009; Maeda *et al.* 2010, Jensen 2011). The most basal group within the Sacoglossa has been debated for many years and varies according the methods used for phylogenetic analysis. The taxa with characters considered as rather basal and plesiomorphic compared to taxa within the former Opisthobranchia, (large shells, no rhinophores, but see also Brenzinger *et al.* 2013) are *Cylindrobulla* Fischer, 1857, and *Ascobulla* Marcus, 1972, which appear almost identical in morphology. *Cylindrobulla* has been excluded from Sacoglossa in the past (Jensen 1996a; 1996b) mainly based on the presence of a radula with a broad median tooth not adequately adapted for piercing and sucking, whereas *Ascobulla* and all other sacoglossan species have a

published by Verbruggen *et al.* (2009) in GenBank. According to AlgalBase, this species is not distributed in the Atlantic, or even in the Caribbean Sea. *Halimeda opuntia* sequences differ from our sequences by about 6%, indicating a different species. We are not able to sort out the taxonomy of *Halimeda* species; however, this might be necessary in future for correct food identification by barcoding.

When comparing *Cylindrobulla* and *Ascobulla* with the remaining oxynocean taxa based on morphology alone, these two genera are still very close. This sharply contrasts the molecular data as was already depicted by Maeda *et al.* (2010). Unlike Händeler *et al.* (2009), who deliberately chose *Cylindrobulla* as outgroup for their phylogenetic analysis (based on the strong differences in the radula), Maeda and coworkers considered the genus as member of the ingroup and used a caenogastropod as the outgroup. In their results, as in ours, *Cylindrobulla* and *Ascobulla* are not closely related. *Cylindrobulla* is not the basal group in either analysis, but it is rendered the most basal taxon within the Oxynoacea in the four gene analysis. This implies that *Cylindrobulla* either has secondarily evolved a broad radula tooth that is not able to penetrate cell walls in a similar way as all other sacoglossans do, or that the piercing form has evolved twice in Sacoglossa (in Oxynoacea and Plakobranchacea). We consider the results on paraphyly of *Ascobulla* and Juliidae in the analysis based on mitochondrial genes alone as an artefact, probably due to the high substitution rate of these markers and especially the 3rd position in the CO1 gene.

Jensen (2011) recently doubted the close affinities of Siphonariidae with Sacoglossa as suggested by multi-locus analyses and considered their morphological similarities as homoplasies. It is known that outgroup selection as well as taxon sampling and the selection of genes has a great effect on molecular analyses. We therefore do not consider our results as a final conclusion of oxynocean phylogeny.

This study summarizes and adds considerably to our knowledge of two morphologically similar genera, *Cylindrobulla* and *Ascobulla*. Nevertheless, many gaps in the morphological data matrix solidify this report as a preliminary one and suggest that proper assessment, especially of the taxa *C. systemma* and *C. souverbiei*, as well as of all recent *Ascobulla* species, is still warranted.

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