Evolution of box jellyfish (Cnidaria: Cubozoa), a group of highly toxic invertebrates

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Cubozoa (Cnidaria: Medusozoa) represents a small clade of approximately 50 described species, some of which cause serious human envenomations. Our understanding of the evolutionary history of Cubozoa has been limited by the lack of a sound phylogenetic hypothesis for the group. Here, we present a comprehensive cubozoan phylogeny based on ribosomal genes coding for near-complete nuclear 18S (small subunit) and 28S (large subunit) and partial mitochondrial 16S. We discuss the implications of this phylogeny for our understanding of cubozoan venom evolution, biogeography and life-history evolution. Our phylogenetic hypothesis suggests that: (i) the last common ancestor of Carybdeida probably possessed the mechanism(s) underlying Irukandji syndrome, (ii) deep divergences between Atlantic and Indo-Pacific clades may be explained by ancient vicariant events, and (iii) sexual dimorphism evolved a single time in concert with complex sexual behaviour. Furthermore, several cubozoan taxa are either para- or polyphyletic, and we address some of these taxonomic issues by designating a new family, Carukiidae, a new genus, Copula, and by redefining the families Tamoyiidae and Tripedaliidae. Lastly, cubozoan species identities have long been misunderstood and the data presented here support many of the recent scientific descriptions of cubozoan species. However, the results of a phylogeographic analysis of Alatina moseri from Hawai‘i and Alatina mordens from Australia indicate that these two nominal species represent a single species that has maintained metapopulation cohesion by natural or anthropogenic dispersal.

Keywords: Cubozoa; box jellyfish; Irukandji; systematics; biogeography; phylogeography

1. INTRODUCTION

Although Cubozoa is the smallest class of Cnidaria, comprising some 50 described box jellyfish species, it is well known for several remarkable attributes. From the possession of complex eyes and associated visual capabilities (e.g. Nilsson et al. 2005), to extraordinary courtship and mating behaviour (e.g. Lewis & Long 2005), to extreme toxicity (e.g. Brinkman & Burnell 2009), there are many reasons why cubozoans catch the attention of the scientific community and public. Despite this interest, studies of cubozoan evolution have been hampered by a paucity of specimens in natural history museums preserved for both morphological and molecular investigation, as well as by their perceived lack of diversity. The last decade has seen more than a doubling in recognition of cubozoan species, but so far a robust phylogenetic framework for investigating the evolution of cubozoan diversity has been missing. We present a comprehensive phylogeny for Cubozoa and use it to discuss the evolution of venom, life history and biogeography.

2. MATERIAL AND METHODS

(a) Phylogenetic inference

A list of specimens used for this study is provided in the electronic supplementary material, table S1, including museum catalogue numbers where vouchers exist. Tentacle tissue was preserved in pure EtOH or saturated salt DMSO buffer (Dawson et al. 1998), from which DNA was extracted using organic phenol–chloroform extraction protocols according to the procedure outlined in Collins et al. (2008) or using the automated DNA isolation system AutoGenPrep 965 (AutoGen Inc., Holliston, MA, USA) following the manufacturer’s protocol. Ribosomal genes coding for partial mitochondrial 16S (16S) and near-complete nuclear 18S (small subunit; SSU) and 28S (large subunit; LSU) were amplified using the primers and protocols outlined in Cartwright et al. (2008) and Collins et al. (2008). PCR products were either sequenced by Cogenics (Houston, TX, USA) or at the Laboratory of Analytical Biology, Smithsonian Institution (Suitland, MD, USA). Trace files were assembled in Sequencher (v. 4.8; Gene Codes, MI) and subsequently aligned using Muscle (v. 3.7; Edgar 2004). Highly variable, poorly aligned regions were
removed from the final alignments using GBLOCKS (v. 0.91b; Castresana 2000) with the default parameters except that allowed gap positions were set to half. Nucleotide sequences were deposited in NCBI GenBank (electronic supplementary material, table S1) and alignments used for analyses were deposited in TreeBASE (treebase.org).

In addition to the alignments for each gene, all three were combined into a concatenated alignment. These four alignments were analysed using maximum parsimony (MP) in PAUP* (Swofford 2003) and maximum likelihood (ML) in RAXML (v. 7.0.3; Stamatakis 2006). MrModelTest (v. 2.3; Nylander 2004) was used to evaluate nucleotide substitution models for ML analyses. The concatenated dataset was partitioned by gene for analyses and number of invariant sites and gamma shape parameters were calculated separately for each partition in RAXML.

To establish the root of the cubozoan phylogeny, SSU and LSU sequences of both cubozoan taxa and outgroup taxa were aligned using MUSCLE, subsequently pruned using GBLOCKS and analysed with ML and MP using the criteria described above. Since the large divergence between ingroup and outgroup for the 16S gene does not allow for reliable alignment, we decided a priori not to analyse this marker using an outgroup.

In order to investigate the possibility of strongly supported character conflict among partitions in the combined datasets, we performed an incongruence length difference (ILD) test (Farris et al. 1995a,b) as implemented in PAUP*. The ILD test has often been used as a test of combinatoriality of datasets for phylogenetic analyses (e.g. Cunningham 1997), but interpretation of ILD test results has been the subject of debate (e.g. Barker & Lutzoni 2002).

(b) Alatina phylogeography
Mitochondrial 16S of seven specimens of Alatina mordens from Osprey Reef (Coral Sea, Queensland, Australia) and 19 specimens of Alatina moseri from Waikiki (O‘ahu, HI, USA) were amplified and sequenced using the same techniques as above (GenBank nos. GQ506980–GQ507005 associated with USNM voucher specimens). All sequences were aligned using MUSCLE and the beginning and end of the alignment were trimmed to the position at which the nucleotides for every specimen are known. A statistical parsimony haplotype network was calculated in TCS (v. 1.21; Castresana 2000) with the default parameters except that gaps treated as a fifth character state.

3. RESULTS
(a) Phylogeny of Cubozoa
The partition-homogeneity test, with 100 replicates, could not refute the null hypotheses of congruence among partitions in the combined datasets LSU/SSU with outgroup \((p = 0.38); \) electronic supplementary material, figure S1) and LSU/SSU/16S without outgroup \((p = 0.56); \) figure 1), suggesting the absence of strong conflict among partitions.

Phylogenetic analyses under both MP (not shown) and ML lead to highly congruent results, and node support is similar under both ML and MP (figure 1; electronic supplementary material, figures S1–S6). Both Chirodropida and Carybdeida are monophyletic clades with the root of Cubozoa falling in between the two in the SSU and combined LSU/SSU datasets with outgroup (electronic supplementary material, figures S1 and S3). Monophyly of Carybdeida is weakly contradicted in the LSU analysis (electronic supplementary material, figure S2); several deep nodes receive lower support when an outgroup is included in LSU analyses (compare figures S2 and S4, electronic supplementary material). In general, LSU and SSU analyses do not strongly disagree with one another; contradictory relationships are weakly supported (compare figures S2–S5, electronic supplementary material).

The fastest evolving marker, 16S (electronic supplementary material, figure S6), shows much congruence with both SSU and LSU (electronic supplementary material, figures S4 and S5). One point of difference involves Alatiniidae and Tripedaliidae. These families group together in the 16S-based phylogeny (electronic supplementary material, figure S6), as well as in SSU-based phylogeny without outgroup (albeit without support; electronic supplementary material, figure S5). This putative clade uniting Alatiniidae and Tripedaliidae seems surprising, but may be explained by nucleotide saturation. 16S evolves much more rapidly than both LSU and SSU, thus leading to higher degrees of nucleotide saturation that may confound signal at the deeper nodes. The addition of LSU data appears to overcome signal, artificial or otherwise, from 16S and SSU data. Indeed, a combined analysis of all three genes (figure 1) leads to a phylogenetic hypothesis that is most congruent with the LSU dataset. Despite the incongruence in the placement of Tripedaliidae between markers, the strongest support for its placement occurs in the combined analysis, where it is recovered as sister to Carybdeidae.

(b) Alatina phylogeography
The final alignment of Alatina 16S sequences contained 545 sites; of the 28 variable characters, 10 were parsimony informative. We found 20 unique haplotypes and uncorrected pairwise distances among haplotypes did not exceed 1.84 per cent. The haplotype network (figure 2) shows that haplotypes of both A. moseri and A. mordens are not reciprocally monophyletic and appear inter-digitated. The most common mt16S haplotype \((n = 4)\) was found in two specimens of each A. moseri and A. mordens.

4. DISCUSSION
(a) Phylogenetic analyses and signal
Since evolutionary rates differ from gene to gene, some incongruence among topologies using different gene trees is not surprising. Combined analysis of all genes should lead to a better estimate of the evolutionary relationships of taxa compared with single-gene analyses (Gadagkar et al. 2005). We find alignment quality to be much improved for the ingroup when excluding highly divergent outgroup taxa. Thus, combined analysis excluding outgroup taxa (figure 1) should represent the best estimate of evolutionary relationships in Cubozoa to date.

Previous phylogenetic analyses of Medusozoa (Collins 2002; Collins et al. 2006) were limited in their sampling within Cubozoa. Increased taxon sampling lends itself to begin investigating several questions concerning the evolution of cubozoan toxicity, behaviour and biogeography. Further, it becomes clear that the taxonomic framework at the family level sensu Daly et al. (2007) is inconsistent with a phylogenetic approach to taxonomy.
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Chiropsalmidae, Tamoiyidae and Carybdeidae are probably para- or polyphyletic. Consequently, we amend the diagnoses of several taxa or designate new taxa to establish monophyly (changes reflected in figures and table). However, we choose to leave Chiropsalmidae unchanged, as we are missing several chirodropid genera in our analyses.

(b) Toxicity

The evolution of venom in Cubozoa is of significant interest, as many cubozoans are known to be highly toxic (e.g. Williamson et al. 1996), resulting in major costs to public health and the tourism industry, particularly in Australia (e.g. Bailey et al. 2003). Efforts have led to the characterization of some venom components of a few cubozoan species (see Brinkman & Burnell 2009 for a review) and the development of an antivenom for the deadly cubozoan Chironex fleckeri (see Currie 2003). In order to enhance data interpretation and risk management, a historical framework providing a clear understanding of species identities and systematics is vital. In addition to retrospective interpretation of venom data, the phylogenetic framework we present here is relevant for phylogenetic forecasting. That is, close relatives of a highly toxic species are more likely than not highly toxic as well.

Toxicity varies from species to species with some being completely harmless to humans while others can cause death within minutes. The chirodropid C. fleckeri is considered the most lethal jellyfish known (Wiltshire et al. 2000). Not surprisingly, its close relative Chironex yamaguchii has caused human fatalities in Japan and the Philippines (Fenner & Williamson 1996; Fenner 1997 (both as Chiropsalmus quadrigatus); Lewis & Bentlage 2009). By contrast, Chiropsalmus and Chironex species are considered much less dangerous (but see Bengtson et al. 1991). Differences in toxicity among chirodropids may be explained by differences in the amount of tentacle surface area, and consequently, the amount of venom that can be delivered (see Nagai 2003). Interestingly, an unvouchered tissue specimen from Palau appears to be closely related to C. yamaguchii from Japan, raising questions about the toxicity and identity of this chirodropid.

In contrast to the notion that chirodropids represent the most lethal box jellies, haemolytic activity of purified toxin proteins appears lower in C. yamaguchii (Nagai et al. 2002; as C. quadrigatus) than in Alatina sp. (Nagai et al. 2000a; as Carybdea alata) and highest in Carybdea brevispada (Nagai et al. 2000b; as C. rastoni [sic]). Similarly, lethal doses of venom appear much lower in C. brevispada when compared with Alatina sp. and C. yamaguchii (Nagai 2003). Note, however, that these haemolytic assays do not appear to have been standardized among treatments, potentially making direct comparisons unreliable. Nonetheless, Bailey et al. (2005) also reported higher haemolytic activities in a species of Carybdea compared with two chirodropid species. However, haemolytic activity does not appear to be the lethal factor in the venoms investigated (Bailey et al. 2005), and haemolytic proteins represent only a fraction of the proteins present in cubozoan venom (Chung et al. 2001).

Sequencing of haemolytic proteins demonstrated two carybdeid and three chirodropid protein toxins to display

Figure 1. Maximum likelihood topology (under GTR + I + G) of the combined nuclear LSU, SSU and mitochondrial 16S dataset. The alignment contains 5546 characters (LSU, 3292 characters; SSU, 1777 characters and 16S: 486 characters), of which 4369 are invariant and 936 parsimony informative. ML/MP parametric bootstrap support values (1000 replicates) are indicated on each node; if only one value is given it applies to both ML and MP. Less than symbol, bootstrap support of which 4369 are invariant and 936 parsimony informative. ML/MP parametric bootstrap support values (1000 replicates) are indicated on each node; if only one value is given it applies to both ML and MP. Less than symbol, bootstrap support less than 50; dark grey, Indo-Pacific; light grey, Atlantic/Caribbean; a, includes SE Atlantic and b, both nominal species indicated on each node; if only one value is given it applies to both ML and MP.
Several cubozoan species are known to cause a set of symptoms called Irukandji syndrome. Initially, Irukandji syndrome was attributed to Carukia barnesi whose sting causes a sharp prickling sensation without visible injury (Barnes 1964). Systemic effects are delayed by minutes causing a sharp prickling sensation without visible injury. Since its original description, the syndrome has been reported from, or attributed to, other cubozoans: Morbakka (Fenner et al. 1985), Tamoya (Morandini & Marques 1997), Malo (Gershwin 2005a, 2007), Alatina (Yoshimoto & Yanagihara 2002 (as C. alata); Gershwin 2005b; Little et al. 2006) and Gerongia (Gershwin & Alderslade 2005).

Usually Irukandji syndrome in cubozoans other than Carukia is referred to as Irukandji-like syndrome (or as Morbakka syndrome by Morbakka; Fenner et al. 1985). Irukandji-like syndrome shares the same basic symptoms of classic Irukandji syndrome, but may be less severe in some species or even more severe in others. For example, a more severe case causing a fatality off North Queensland, Australia, was attributed to C. barnesi's close relative Malo kingi (Fenner & Hadok 2002; Gershwin 2007; but see Bailey 2003). Thus far, very little is known about the mechanism(s) underlying Irukandji syndrome. Thorough toxicological studies of Irukandji-causing species from disparate clades should clarify the function and nature of the syndrome.

While disparate clades in Cubozoa contain Irukandji-causing species, all are part of Carybdeida. Irukandji syndrome is particularly well documented for species of Tamoyoidea sensu Daly et al. (2007). Interestingly, Tamoya consistently falls outside Tamoyoidea (figure 1; electronic supplementary material, figures S1–S6) and is easily distinguishable from its other genera, Carukia, Malo, Gerongia and Morbakka. Hence, we amend the meaning of Tamoyoidea Haeckel, 1880 to contain all those carybdeid medusae that possess frown-shaped rhopaliar niche ostia lacking rhopaliar horns (type genus Tamoya Muller, 1859). We propose the new family Carukiidae, with type genus Carukia Southcott, 1967, to contain those carybdeids that lack gastric filaments and possess frown-shaped rhopaliar niche ostia with rhopaliar horns (genera Carukia, Malo Gershwin, 2005, Gerongia Gershwin & Alderslade, 2005 and Morbakka Gershwin, 2008). Both Tamoyoidea sens. nov. and Carukiidae branch after Carybdeidae and Tripedaliidae, while Alatinoa represents the earliest diverging carybdeid clade (Caribdea marsupialis may be misidentified; see below). This topology suggests that the last common ancestor of Carybdeidae probably possessed the mechanism(s) underlying Irukandji syndrome (figure 3). Further, the ability to cause Irukandji syndrome may have been lost in the lineage leading to Carybdeidae and Tripedaliidae (figure 3; a species of Caribdea was linked to Irukandji syndrome (Little et al. 2006), but this attribution appears unconfirmed (Gershwin 2006a)). A syndrome described as Irukandji-like may be caused by a couple of non-cubozoan species (e.g. Fenner et al. 1996 (Stomolophus nomurai); Fenner 1998 (Gonionemus and Physalia)), but homology will remain obscure until the mechanism(s) underlying the syndrome are clarified.

Even with a robust phylogeny, several problems hamper cubozoan venom studies. Difficulties in extracting venom, the use of whole tentacle tissue instead of isolated nematocysts and contradictory results among research groups (Brinkman & Burnell 2009 and references cited therein) need to be addressed. Furthermore, toxins have been reported to differ among different body parts of specimens and possibly different ontogenetic stages (Brinkman & Burnell 2009 and references cited therein). Finally, taxonomic uncertainties and resulting misidentification may impede toxicological research. For example, the number of bioactive proteins isolated from C. marsupialis from the Mediterranean...
(Rottini et al. 1995) differs from that of the same nominal species from the Caribbean (Sanchez-Rodriguez et al. 2006) leading to the interpretation of intraspecific venom variation. However, true C. marsupialis from the Mediterranean is easily distinguishable from its congeners in the Caribbean (i.e. Carybdea xaymacana and Carybdea auct. xaymacana) by their gastric phacellae. The existence of C. marsupialis in the Caribbean is most probably an example of taxonomic confusion.

Our working hypothesis with increased taxon sampling supports the preliminary finding that Carybdea sivickisi is more closely related to Tripedalia cystophora than it is to any species of Carybdea (Collins 2002; Collins et al. 2006). To retain monophyly of Carybdea, we designate the new genus Copula to accommodate Carybdea sivickisi Stiasny, 1926; the name is in reference to the well-documented courtship behaviour and sexual dimorphism (see below). We amend the meaning of Tripedaliidae Conant, 1897 to contain all carybdeids that display sexual dimorphism of the gonads, produce spermatophores and in which at least the males possess subgastral sacs/seminal vesicles (see Hartwick 1991).

Species of both Carybdeidae and Alatinidae appear to be ovoviviparous and eggs are fertilized internally after female medusae have taken up sperm released into the water column during spawning aggregations (Studebaker 1972; Arneson 1976). Neither courtship behaviour nor sexual dimorphism appears to be present in these two families. Further, embryos are released within minutes to hours after fertilization (Studebaker 1972; Arneson 1976). To our knowledge, reproductive strategies of both Tamoyidae sens. nov. and Carukiidae remain undocumented. In Chirodropida, Yamaguchi & Hartwick (1980) reported external fertilization for medusae of both Carybdea fleckeri and Chiropsella bronzie (as Carybdea quadrigatus). While information from Carukiidae and Tamoyidae are needed, it appears that internal fertilization is a synapomorphy of Carybdeida. Further, we suggest that sexual dimorphism evolved a single time concomitant with complex sexual behaviour (figure 3).

In general, cubozoan distributions are not well documented on intermediate geographical scales (e.g. provinces, states or countries) owing to a lack of sampling, which hampers biogeographic enquiries at this scale (see Bentlage et al. 2009 for a possible strategy to address this issue). However, on larger scales (e.g. ocean basins) several patterns emerge in light of our results. In particular, we uncovered numerous deep divergences among Indo-Pacific and Atlantic clades (figure 1).
In Chirodropidae, the genus *Chiropsalmus* is exclusively Atlantic, whereas the congeneric *Chiropsella* is from the Indo-Pacific groups with the exclusively Indo-Pacific *Chironex* (family Chirodropidae). Similarly, what had been recognized as *Tamoyiidae* (*Tamoyiidae sens. nov. plus Carukiidae*) can also be divided geographically: *Tamoyiidae* is restricted to the Atlantic and the described species of *Carukiidae* are known from Australia and Japan, but probably range throughout the Indo-Pacific (Cleland & Southcott 1965; B. Bentlage 2009, unpublished notes). The pattern within *Alatiidae* and *Tripedaliidae* is unclear owing to limited taxon sampling. Both sampled species of *Tripedaliidae*, *Copula sivickisi* and *T. cystophora*, can be found in all three oceans and future studies should seek to determine if these species are truly circumtropical or flocks of regional species.

Our densest sampling is in *Carybdea*, but unfortunately, relationships among Indo-Pacific and Atlantic/Caribbean taxa lack support, so it is unclear whether there are deep divergences separating lineages into exclusively Atlantic/Caribbean and Indo-Pacific clades (figure 1). Nonetheless, integrating phylogeny and taxonomic investigations suggests that *Carybdea* spp. are more restricted in their geographical distributions than has been recognized by most workers. For example, *C. saymacana* has been sampled from both the Caribbean and Western Australia, but deep divergence indicates crypticism in this nominal species. Similarly, *Carybdea rastoni* has traditionally been viewed as having a wide distribution with occurrence records from South Australia, Hawai‘i and Japan among others. Our sampling shows that this is also a case of numerous species being united under the same name. Examination of the specimens suggests that *C. rastoni* can be distinguished morphologically (Gershwin & Gibbons 2009; B. Bentlage 2009, unpublished notes). Rather than having cryptic species in the sense that they are indistinguishable morphologically, this appears to be a case in which species have been proposed historically (*C. rastoni* Haacke, 1886 (South Australia), *C. brevipedalis* Kishinouye, 1891 (Japan) and *Carybdea arborifera* Maas, 1897 (Hawai‘i)) but subsequently synonymized and/or disregarded.

Discovering that widespread nominal *Carybdea* spp. represent geographically isolated species assemblages indicates that these medusae do not exchange genetic material across large bodies of open water. Hence, we suppose that speciation in the genus is largely driven by vicariance. Dispersal events, however, cannot be ruled out as a source to account for diversification. For instance, *C. arborifera* probably arose in Hawai‘i after long-range dispersal; islands have existed at the present position of the Hawaiian Islands from at least the late Paleocene onwards, but were always remote (Carson & Clague 1995).

The inability to cross open ocean habitats is most likely a widespread phenomenon in Cuboza, as most species appear to inhabit near shore habitats above the continental shelves (i.e. the neritic zone). Considering this, deep divergences between Atlantic and Indo-Pacific clades of Cuboza may be explained by ancient vicariant events. Unfortunately fossil jellyfishes are rare, leading to uncertainty in dating cladogenetic events (Cartwright & Collins 2007). However, fossils that possibly represent cubozoans have been discovered from the upper Jurassic (*Quadrumedusina quadrata* Haackel, 1869), upper Carboniferous (*Anthracomedusa turnbulli* Johnson & Richardson 1968) and the middle Cambrian (*Cartwright et al.* 2007). Given their neritic habitat, cubozoans probably diversified as a result of plate movements in concert with eustatic sea-level fluctuations; the splitting of Pangea could have provided the setting for this.

In contrast to the general pattern described above, we have evidence for a pelagic cubozoan. The genus *Alatina* is represented with several nominal species in the Pacific (see Gershwin 2005b) from which we sampled *A. moseri* Mayer, 1906 and *A. mordens* Gershwin, 2005 from or nearby their type localities (Hawai‘i and the Coral Sea, respectively). We found no genetic divergences corresponding to geographical locality; in fact both ‘species’ share at least one 16S haplotype (figure 2). Additionally, no clear pattern differentiating the two populations exists. Rather, the haplotype network reflects a well-mixed population with regular gene flow. Inspection of specimens (including Hawaiian-type material USNM 22308, 22311 and 29632) and study of its original description (Mayer 1906) demonstrates that *A. moseri* has been present in Hawai‘i at least since the beginning of the twentieth century. The initial discovery of *Alatina* spp. in Australia seems not as well documented as is true for many marine invertebrates from this continent.

In contrast to other cubozoans, *Alatina* spp. live at or close to the edge of the continental shelf (Arneson & Cutress 1976; as *C. alata*) and have been obtained from great water depths before (e.g. Morandi 2003; as *C. alata*). It seems that *A. moseri* can only be encountered in shallow waters several days after the full moon (e.g. Thomas et al. 2001; Yanagihara et al. 2002; both as *C. alata*) when individuals congregate to spawn; the same is true for *A. mordens* (T. Carrette & J. Seymour 2008, personal communication). Furthermore, it has been suggested that individuals of *Alatina* spp. live up to 12 months (Arneson & Cutress 1976). Hence, it seems quite possible that *Alatina* spp. have an oceanic lifestyle and are able to maintain cohesive metapopulations across ocean basins.

Our investigation of historic specimens demonstrates that *A. moseri* was present in Hawai‘i more than a century ago. An early introduction of *A. moseri* into Hawai‘i is possible, but it seems unlikely that this would have occurred from the Coral Sea, given that ship traffic from Australia to Hawai‘i was probably low at the time and the observed genetic signal would suggest multiple introductions rather than a single one. Considering the possible effect World War II naval traffic had on the spread of marine organisms (e.g. Coles et al. 1999), *A. moseri* may conversely have been introduced into the Coral Sea. Indeed, it is conceivable that *A. moseri* was introduced into the Coral Sea from Hawai‘i and prior to that into Hawaiian waters from yet another location. However, considering the life cycle of *A. moseri* (and the synonymous *A. mordens*), we find dispersal by natural means a more viable explanation of the pattern we observe. Investigation of additional *Alatina* spp. may show that some of these also represent artificial taxonomic units.

(e) *Carybdea marsupialis*: a model organism misidentified?

We recover *C. marsupialis* together with *A. moseri* as the sister group to the remaining carybeids. This placement
appears surprising considering the stark morphological differences between Carybdea spp. and Alatina spp. (compare Gershwin & Gibbons 2009 with Gershwin 2005b). Specimens of C. marsupialis for this and other studies (Collins 2002; Collins et al. 2006) are derived from a polyp culture at the museum of the University of Hamburg, Germany. To our knowledge these polyps were originally obtained by B. Werner some 40 years ago in La Parguera, Puerto Rico (A. C. Arneson 2008, personal communication) and used for life cycle studies (e.g. Werner et al. 1971; Straehler-Pohl & Jarms 2005). Alatina spp. can be found in Puerto Rico, and considering the placement of C. marsupialis as a close relative of a member of Alatinaeidae, it is possible that the culture in Hamburg actually contains the polyp stage of a species of Alatina rather than Carybdea. Since this particular culture has served as the stock for several important experiments on Carybdea development (e.g. Stangl et al. 2002; Fisher & Hofmann 2004; Straehler-Pohl & Jarms 2005), it is vital to confirm the identification of the polyps by either rearing medusae to adulthood or collecting fresh material from the Caribbean for genetic comparisons. Inclusion of C. marsupialis from close to its type locality in Italy in future phylogenetic studies should also help shed light on this issue.

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ENDNOTE

1The name Carybdea brevipedalia is not in widespread usage, but its original description and type locality (Kishinouye 1891) demonstrate that it is the senior synonym of the name Carybdea marmorata, 1906 recently used as valid in Gershwin (2006b) and Gershwin & Gibbons (2009).

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