

1 **Systematics of ‘lithistid’ tetractinellid**
2 **demosponges from the Tropical Western**
3 **Atlantic – implications for phylodiversity**
4 **and bathymetric distribution**

5 **Astrid Schuster^{1,2}, Shirley A. Pomponi³, Andrzej Pisera⁴, Paco**
6 **Cárdenas⁵, Michelle Kelly⁶, Gert Wörheide^{1,7,8}, and Dirk Erpenbeck^{1,8}**

7 ¹**Department of Earth- & Environmental Sciences, Palaeontology and Geobiology,**
8 **Ludwig-Maximilians-Universität München, Richard-Wagner Str. 10, 80333 Munich,**
9 **Germany**

10 ²**Current address: Department of Biology, NordCEE, Southern University of Denmark,**
11 **Campusvej 55, 5300 M Odense, Denmark**

12 ³**Harbor Branch Oceanographic Institute, Florida Atlantic University, 5600 U.S. 1 North,**
13 **Ft Pierce, FL 34946, USA**

14 ⁴**Institute of Paleobiology, Polish Academy of Sciences, ul. Twarda 51/55, 00-818**
15 **Warszawa, Poland**

16 ⁵**Pharmacognosy, Department of Medicinal Chemistry, Uppsala University, Husargatan**
17 **3, 75123 Uppsala, Sweden**

18 ⁶**National Centre for Coasts and Oceans, National Institute of Water and Atmospheric**
19 **Research, Private Bag 99940, Newmarket, Auckland, 1149, New Zealand**

20 ⁷**SNSB-Bayerische Staatssammlung für Paläontologie und Geologie, Richard-Wagner**
21 **Str. 10, 80333 Munich, Germany**

22 ⁸**GeoBio-CenterLMU, Ludwig-Maximilians-Universität München, Richard-Wagner Str. 10,**
23 **80333 Munich, Germany**

24 Corresponding author:

25 Dirk Erpenbeck^{1,8}

26 Email address: erpenbeck@lmu.de

27 **ABSTRACT**

28 **Background** Among all present demosponges, lithistids represent a polyphyletic group with
29 exceptionally well preserved fossils dating back to the Cambrian. Knowledge of their recent
30 diversity, particularly in the Tropical Western Atlantic Ocean (TWA) where they are common
31 in deep waters, is scarce making any comparison between present and past major 'lithistid'
32 faunas difficult. In addition, the lack of sufficient molecular and morphological data hamper any
33 predictions on phylogenetic relationships or phylodiversity from this region. The Harbor Branch
34 Oceanographic Institute (HBOI, Fort Pierce, Florida) holds the largest collection of TWA lithistid
35 sponges worldwide, however, the majority remain to be taxonomically identified and revised.

36 **Methods/Principal Findings** In this study we provide sequences of 249 lithistid demo-
37 sponges using two independent molecular markers (28S rDNA (C1-D2) and *cox1* mtDNA). In
38 addition, a morphological documentation of 70 lithistid specimens is provided in the database
39 of the Sponge Barcoding Project (SBP). This integrated dataset represents the largest and
40 most comprehensive of the TWA lithistids to date. The phylogenetic diversity of 'lithistid'
41 demosponges in the Bahamas and Jamaica are high in comparison to other TWA regions;
42 Theonellidae and Corallistidae dominate the fauna, while Neopeltidae and Macandrewiidae are
43 rare. A new tetractinellid suborder, one new genus and several new species are recognized
44 and the Pacific 'lithistid' genera, *Herengeria* and *Awhiowhio*, are reported from the TWA for the
45 first time. The higher-taxa relationships of desma-bearing tetractinellids are discussed and
46 topics for revision suggested.

47 **Conclusion** This first integrative approach of TWA 'lithistid' demosponges contributes to a
48 better understanding of their phylogenetic affinities, diversity and bathymetric distribution pat-
49 terns within the TWA. As in the Pacific, the TWA 'lithistid' demosponges dominate deep-water
50 habitats. Deeper taxonomic investigations will undoubtedly contribute to a better comparison
51 between present major 'lithistid' faunas and their fossil record in the Mesozoic.

52 INTRODUCTION

53 Among all present demosponges, lithistids represent a palaeontologically important polyphyletic
54 group, with exceptionally well preserved fossils dating back to the Cambrian (e.g. Pisera, 2002;
55 2006), and several relict genera represented in living faunas today (e.g. Lévi, 1991; Pisera, 2002;
56 Kelly, 2007; Kelly et al., 2003). Several key 'lithistid' demosponge faunas are relatively well
57 known: 1) 'lithistid' demosponges are dominant components of seamount communities on the
58 Norfolk Ridge and in the South-West Pacific (e.g. Lévi, 1991; Kelly, 2000, 2007; Schlacher-
59 Hoenlinger, Pisera and Hooper, 2005; Kelly et al., 2007), and their inventory, morphological
60 identification and molecular systematics has been the focus of several studies (e.g. Schlacher-
61 Hoenlinger, Pisera and Hooper, 2005; Schuster et al., 2015); 2) large 'lithistid' assemblages are
62 reported from continental shelves and caves of the North-East Atlantic (e.g. Carvalho, Pomponi
63 and Xavier, 2015), and from seamounts in the Mediterranean (e.g. Maldonado et al., 2015).

64 However, the present-day lithistid species and their phylogenetic diversity in several marine
65 bioregions including the Western Indian Ocean, Subantarctic regions including South Africa,
66 Northern Pacific and Tropical Western Atlantic (TWA) are incompletely understood. While
67 'lithistid' demosponges in the TWA are reported from continental shelves, caves and slopes by
68 Van Soest and Stentoft (1988), Reed and Pomponi (1997), and Pomponi et al., (2001), and many
69 earlier reports of individual species (e.g. Sollas, 1888), the fauna is still poorly known with few
70 descriptions and no molecular data. This greatly limits the understanding of their phylogenetic
71 relationships, diversity and evolution.

72 Desma-bearing demosponges, historically referred to as 'lithistid' demosponges, form a
73 polyphyletic group. Molecular systematics now group the majority of 'lithistid' demosponges
74 (11 out of 13 families) to the order Tetractinellida Marshall, 1876. Eight of these families are

75 assigned to the suborder Astrophorina Sollas, 1887 and three to the suborder Spirophorina *sensu*
76 Morrow and Cárdenas 2015 (Cárdenas et al., 2011; Morrow and Cárdenas, 2015; Schuster et al.,
77 2015). Schuster et al. (2015) showed several ‘lithistid’ families such as Pleromidae Sollas, 1888,
78 Desmanthidae Topsent, 1894 and Scleritodermidae Sollas, 1888 to be polyphyletic, and Corallis-
79 tidae Sollas, 1888, Theonellidae von Lendenfeld, 1903 and Phymatellidae Schrammen, 1910 to
80 be monophyletic. However, the systematic affinities for families such as e.g. Siphonidiidae von
81 Lendenfeld, 1903, Azoricidae Sollas, 1888 and Neopeltidae Sollas, 1888, remain obscure due to
82 few molecular data available, and hence, only 21 out of 40 ‘lithistid’ genera were evaluated in
83 Schuster et al. (2015). The same study indicated that several spicule types convergently evolved
84 within this sponge group. The families Scleritodermidae and Siphonidiidae were suggested to
85 form a separate clade within Tetractinellida, but outside the two suborders Astrophorina and
86 Spirophorina (Kelly Borges and Pomponi, 1994; Schuster et al., 2015). With the discovery and
87 description of a new tetractinellid family Stupendidae Kelly and Cárdenas, 2016, a sister group
88 relationship of Stupendidae to a clade consisting of rhizomorine-desma-bearing Scleritodermidae,
89 Siphonidiidae and Azoricidae Sollas, 1888 was recently indicated (Kelly and Cárdenas, 2016).
90 However, understanding the higher taxonomic relationships within Tetractinellida including its
91 lithistid lineages is still hindered by incomplete taxon sampling and sequencing of key taxa such
92 as Thrombidae Sollas 1888 or *Gastrophanella* Schmidt, 1879 (e.g. Kelly Borges and Pomponi,
93 1994; Cárdenas et al., 2011).

94 Aside from the report of ‘lithistids’ in some specific island regions of the TWA, such as
95 Barbados (Van Soest and Stentoft, 1988), the Bahamas (Maldonado and Young, 1996; Reed
96 and Pomponi, 1997), Cuba (Pisera, 1999) the deep Florida shelf (Pisera and Pomponi, 2015),
97 and chemotaxonomic studies (Kelly-Borges et al. 1994) the most comprehensive taxonomy
98 based survey comprising nearly all island groups in the TWA was conducted by Pomponi
99 et al. (2001). The main focus of a study of Pomponi et al. (2001) was the documentation
100 of biodiversity and bathymetric distributions of ‘lithistids’, thus no morphological species
101 descriptions, sequences or phylogenetic affinities of these specimens were included. Although
102 Pomponi et al. (2001) concluded that ‘lithistids’ are an important and dominant group of deep,
103 hard-bottom habitats in the TWA, no comprehensive integrative taxonomic approach using
104 molecular and morphological data has yet been made to evaluate this large and unique collection
105 of TWA ‘lithistid’ demosponges, which is to a large extent unidentified and awaits taxonomic
106 revision. Their study was based on 36 expeditions and 450 submersible transects led by the
107 Harbor Branch Oceanographic Institute (HBOI) from 1984 to 2000, and aimed to provide an
108 inventory of the biodiversity and bathymetric distribution of TWA ‘lithistids’. As a result, 28
109 ‘lithistid’ species representing 18 genera and 9 families were reported from the TWA. However,
110 knowledge of the TWA ‘lithistid’ fauna still remains comparatively poorly known, but crucial
111 for a better knowledge of their global diversity and their comparison to the Mesozoic ‘lithistids’.

112 The present study presents the first molecular systematic attempt to evaluate a large part of
113 the extensive HBOI ‘lithistid’ collection (\approx 250 specimens) by means of generating independent
114 molecular markers (*cox1* and 28S, C1-D2 region) from material collected between 1985 and
115 2011. Complementary to this we included *in situ* and SEM pictures of 71 taxa into the SBP. This
116 study includes samples from almost all island groups in the TWA (Fig. 1) from depths ranging
117 between 2 and 950 m, covering different geomorphological zonations as described in Reed and
118 Pomponi (1997). The phylogenetic affinities of 31 out of the 35 ‘lithistid’ Tetractinellida genera
119 are reconstructed. Furthermore, our results reveal a new clade including all rhizoclone desma
120 bearing lithistids plus Stupendidae and Thrombidae, and document potential new genera/species
121 and occurrences for the TWA. With this systematic groundwork the molecular phylogeny of
122 eight island regions in the TWA and the relative abundance and bathymetric distribution patterns
123 of 218 samples representing nine desma-bearing families are analysed and discussed suggesting

124 that the present-day ‘lithistid’ fauna is as diverse as the fauna from the Mesozoic.

125 MATERIALS AND METHODS

126 Specimen collection and identification

127 Between 1995 and 2011, sponge samples were collected from the Tropical Western Atlantic
128 (TWA) by the *Johnson-Sea-Link (JSL) I* and *II* submersibles operated by the HBOI, Fort Pierce,
129 Florida and by scuba diving during several expeditions to the Bahamas, Cuba, Florida Keys,
130 Curaçao, Turks and Caicos, Puerto Rico, Honduras, Jamaica, Guadeloupe, Gulf of Mexico
131 and Bonaire (Fig. 1). These expeditions aimed to conduct a biodiversity inventory and collect
132 samples for biomedical research focused particularly on sponges, octocorals and algae. Various
133 habitats from the fore reef slopes and escarpments to the deep shelf slopes were sampled using
134 either a claw, suction tube or scoop in depths from 0–1000 m. Sponge samples from this
135 collection, were pre-identified by S.P. and M.K., and frozen and/or stored in 70% ethanol. For
136 comparison, additional material from the Southwest Pacific (New Caledonia and New Zealand),
137 and Indo-Pacific region, in the National Institute of Water and Atmospheric Research (NIWA)
138 collection in Auckland and its invertebrate collection (NIC) in Wellington, New Zealand, were
139 subsampled for molecular investigations. This material included subsamples of tetractinellids,
140 which were collected by scuba diving during several expeditions across the Indo-Pacific and New
141 Zealand, led by the Coral Reef Research Foundation (CRRF) in Republic of Palau, identified
142 by M.K. Six specimens (three *Geodia* spp. and three *Cinachyrella* spp.) from Jamaica and
143 Norway were added from the Bavarian State Collection of Zoology (ZSM) in Munich, Germany
144 (identification by Helmut Lehnert). Detailed information for all novel samples sequenced is
145 provided in the Supplementary Material.

146 Undetermined samples from the TWA (all HBOI subsamples) were identified to the genus
147 level according to their phylogenetic position relative to known species. Based on this, we
148 selected 71 samples with distinct genotypes for a deeper morphological investigation. For
149 those taxa we examined deck pictures, and prepared thick sections as well as spicule and
150 skeleton stubs for scanning electron microscopy (SEM). We used the methodology outlined
151 in Pisera and Pomponi (2015) to illustrate and evaluate morphological characters. Based on
152 this, 249 specimens could be identified to genus and/or species level. Morphological docu-
153 mentation for the 71 representative specimens are provided in the Sponge Barcoding Project
154 (SBP) (<http://www.spongebarcoding.org/>). SEM stubs and spicule slides including thick sections
155 are deposited at the Bavarian State Collection for Paleontology and Geology (BSPG) Munich,
156 Germany under accession numbers XXXX.

157 Molecular investigations

158 Genomic DNA was isolated from small pieces of sponge tissue preserved in 70% ethanol
159 using a modified protocol of the DNeasy (Qiagen) Blood and Tissue Kit, which included an
160 additional centrifugation step just before transferring the lysate to the spin column. A Nano-Drop
161 1000 Spectrophotometer (Thermo Scientific) was used to quantify the isolated genomic DNA.
162 Amplification of a fragment of the mitochondrial cytochrome c oxidase subunit I (*cox1*, partial
163 ≈ 659 bp) was performed using the primers dgLCO1490 and dgHCO2198 (Meyer, Geller and
164 Paulay, 2005). Additionally, a fragment of an unlinked nuclear ribosomal gene (28S; partition
165 C1-D2, 768-832 bp) was amplified using the forward C1’ASTR (Cárdenas et al., 2010) and
166 the reverse universal D2 (Lê, Lecointre and Perasso, 1993) primers. Both amplifications follow
167 the PCR protocol and settings outlined in Schuster et al. (2015). Amplification success was
168 checked on a 1.5% agarose gel. For the majority of the 28S fragments we observed an additional
169 non-specific shorter band at ≈ 650 bp, which was subsequently identified as originating from
170 a bacterial template. Therefore, separation of double bands and PCR clean-up was performed

171 using a modified freeze-squeeze method (Tautz and Renz, 1983), as described in Schuster et al.
172 (2015). For sequencing of the 28S fragment, 6 μ l of the remaining supernatant from the clean-up
173 was used with the PCR primers and BigDye Terminator v3.1 (Applied Biosystems, Forster City,
174 CA, USA) chemicals. For sequencing of *cox1* we used a 1:10 dilution of the PCR products
175 together with the PCR primers and BigDye Terminator v3.1 chemicals. Sequencing was carried
176 out on an ABI 3730 Genetic Analyzer at the Sequencing Service of the Department of Biology
177 (LMU München). Sponge origin of novel sequences were tested by BLAST searches against
178 NCBI GenBank (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>). Raw trace files were post- processed
179 by base-calling using CodonCode Aligner v.3.7.1.1 (CodonCode Corporation). Geneious®
180 v.8.1.8 (<http://www.geneious.com>, Kearse et al., 2012) was used for the assembly of forward and
181 reverse reads. Sequences will be deposited at the European Nucleotide Archive (ENA) and the
182 SBP under accession numbers #1794 to #2108.

183 **Phylogenetic reconstructions**

184 Alignments were generated separately for *cox1* and 28S using MAFFT v.7 under the L-INS-I
185 algorithm (Kato and Standley, 2013) because of heterogeneous taxon sampling and moderate
186 sequencing success of *cox1*. Saturation of both markers was evaluated using Xia's test (Xia et al.,
187 2013) as implemented in DAMBE v5.1.5 (Xia, 2013) which compares an estimated substitution
188 saturation index (Iss) to a critical substitution saturation index (Iss.c). For the *cox1* dataset,
189 sequences of *Halichondria panicea* (Pallas, 1766) (subclass: Heteroscleromorpha Cárdenas,
190 Pérez and Boury-Esnault, 2012, order Suberitida Schmidt, 1870) and *Aplysina aerophoba* (Nardo,
191 1833) (subclass Verongimorpha Erpenbeck et al., 2012, order Verongiida Bergquist, 1978) were
192 chosen as outgroups. For the 28S dataset sequences of the order Sphaerocladina were chosen as
193 outgroup. All outgroups have been used in earlier phylogenetic studies on tetractinellids (see
194 e.g. Schuster et al., 2015; Kelly and Cárdenas, 2016). The final *cox1* alignment comprised 307
195 sequences of which 122 are newly generated sequences for this study. The alignment was 635
196 bp long, of which 295 bp were constant, 40 bp were parsimony uninformative and 300 bp were
197 parsimony informative. The final 28S alignment comprised 474 sequences of which 305 are
198 newly generated sequences for this study. In total this alignment was 905 bp long, of which
199 325 bp were constant, 66 bp parsimony uninformative and 514 bp parsimony informative. Both
200 alignments from this study are freely available at OpenDataLMU doi.:XXXXXX. Phylogenetic
201 tree reconstructions for both datasets were performed on a parallel version of MrBayes v3.2.4
202 (Ronquist et al., 2012) on a Linux cluster. The most generalized GTR+G+I evolutionary model,
203 indicated as the most suitable by jModelTest v.2.1.7 (Darriba et al., 2012), was used. Analyses
204 were run in two concurrent runs of four Metropolis-coupled Markov-chains (MCMCMC) for
205 100,000,000 generations and stopped when the average standard deviation of split frequencies
206 dropped below 0.01. The first 20% of the sampled trees were removed as Burn-in from further
207 analyses.

208 **Inclusive molecular phylodiversity and abundance analyses**

209 The Inclusive Phylogenetic Diversity (PD_I) is the sum of all branch lengths of a gene tree
210 connecting a set of taxa from the root of the tree to the tips of all phylogenetic branches spanned
211 by this set of taxa (see e.g. Lewis and Lewis, 2005). To evaluate the PD_I , a Maximum Likelihood
212 (ML) tree was first calculated from the most comprehensive dataset (28S, C1-D2 partition) using
213 RAxML 7.2.8 (Stamatakis, 2014). The GTRGAMMA nucleotide evolutionary model selected by
214 jModelTest v.2.1.7 (Darriba et al., 2012) was taken with 1000 fast pseudo-replicated bootstraps.
215 The resulting tree topology was used to calculate the PDI for several areas in the TWA using
216 a modified python script from Vargas et al. (2015). All non-TWA genera and all TWA genera
217 less than five were excluded from this analysis. In total, the PD_I of Bonaire, Curaçao, Florida,

218 Honduras, Jamaica, Puerto Rico and Turks and Caicos was calculated. In order to compensate
219 for different sampling efforts across the seven regions, rarefaction curves (Sanders, 1968) were
220 used for each location. The rarefaction curves were generated in RStudio (RStudio Team, 2014).
221 Both scripts are available at <https://bitbucket.org/molpalmuc/>.

222 The relative abundance of eight 'lithistid' families from five depth zones (0–60 m; 61–150
223 m; 151–300 m; 301–600 m; 601–914 m) from the TWA was plotted and illustrated using ggplot2
224 (Wickham, 2009) as implemented in RStudio. These depth zonations follow Reed and Pomponi
225 (1997) and Pomponi et al. (2001), which are based on the geomorphological observations of the
226 sites sampled.

227 RESULTS AND DISCUSSION

228 Integrative morphological and molecular systematics of 'lithistid' demosponges 229 with focus on TWA species

230 *Higher-taxa relationships of desma-bearing tetractinellids*

231 The 296 lithistid sequences of at least 88 species from 27 genera (35 known) constitute the largest
232 and most comprehensive taxon set on desma-bearing tetractinellids to date. Our phylogenies (Fig.
233 2) corroborate the monophyly of Tetractinellida, currently including the suborders Astrophorina
234 and Spirophorina (Morrow and Cárdenas, 2015) (Fig. 2C). In addition, the affinity of eight
235 desma-bearing families to the suborder Astrophorina (Cárdenas et al., 2011; Morrow and
236 Cárdenas, 2015; Schuster et al., 2015) is confirmed (Fig. 2A-C). The 28S phylogeny (Fig. 2A)
237 indicates a sister relationship of Astrophorina and Spirophorina. In both gene trees (Fig. 2A,
238 B) desma-bearing tetractinellids do not group with the Spirophorina (only represented by the
239 Tetillidae in our sampling). In both gene trees the rhizomorine-bearing families Scleritodermidae,
240 Siphonidiidae and Azoricidae form a clade (Fig. 2). However, *Gastrophanella* (Siphonidiidae) is
241 distinct and sister (1.0 Posterior Probability (PP)) to Scleritodermidae/Siphonidiidae/Azoricidae
242 in the 28S phylogeny (Fig. 2A). This sister-group relationship could not be corroborated by *cox1*
243 analysis as no sequence of *Gastrophanella* could be generated. We suspected an intron insertion
244 within *cox1* due to the discovery of these in closely related rhizomorine-bearing genera (*Setidium*
245 Schmidt, 1879, *Microscleroderma* Kirkpatrick, 1903, *Aciculites* Schmidt, 1879, *Scleritoderma*
246 Sollas, 1888) (Schuster et al., 2017). Based on this, various primer sets suggested by Schuster
247 et al. (2017) were tested, however, without success. We suspect that *Gastrophanella* has one
248 or several intron insertions in the *cox1* gene in a yet unknown position. By including several
249 additional rhizomorine-bearing genera such as *Gastrophanella*, *Leiodermatium*, *Siphonidium* and
250 *Amphibleptula* in our datasets, the family Thrombidae could not be recovered within Astrophorina
251 as hypothesized by the Systema Porifera (Hooper and Van Soest, 2002). The 28S gene tree
252 recovers Thrombidae as sister to all rhizomorine-bearing tetractinellids, but this relationship is
253 not supported (0.72 PP) (Fig. 2 and Fig. 3) and needs further investigation, including also 28S for
254 Stupendidae Kelly and Cárdenas 2016, a recently established new family (Kelly and Cárdenas,
255 2016). In the *cox1* phylogeny (Fig. 2B) Stupendidae is included and a highly supported sister
256 taxon to Scleritodermidae/Siphonidiidae/Azoricidae. It should be noted that Thrombidae and
257 *Gastrophanella* are missing in the *cox1* phylogeny (Fig. 2B).

258 *Intra-subordinal relationships of astrophorine 'lithistids'*

259 The majority (15 out of 23) of the currently known tetractinellid families are located within the
260 Astrophorina (Morrow and Cárdenas, 2015). This includes eight desma-bearing families (Coral-
261 listidae, Isoraphiniidae Schrammen, 1924, Macandrewiidae Schrammen, 1924, Neopeltidae,
262 Pleromidae, Phymaraphiniidae Schrammen, 1924, Phymatellidae and Theonellidae) and seven
263 non-desma bearing families (Cárdenas et al., 2011; Morrow and Cárdenas, 2015; Schuster et
264 al., 2015) (see also Fig. 2A-C). Thus, the present study supports earlier findings, which were

265 based on lower taxon sampling and additionally provides deeper insights into the intraspecific
266 relationship of desma-bearing astrophorids.

267 The family **Theonellidae** consists of the genera *Discodermia* du Bocage, 1869, *Manihinea*
268 Pulitzer, Finali, 1993, *Racodiscula* Zittel, 1878, *Siliquariaspongia* Hoshino, 1981 and *Theonella*
269 Gray, 1868. Theonellidae possesses tetracone desmas and phyllostriaenes to discotriaenes as
270 characteristic megascleres. Typical microscleres are acanthorhabds, spirasters and amphisters
271 (Pisera and Lévi, 2002a). Until now, only *Theonella* and *Discodermia* species as well as one
272 *Manihinea* sp. were sequenced in different phylogenetic studies using 18S, 28S and *cox1*
273 (see e.g. Redmond et al., 2013; Hall, Ekins and Hooper, 2014; Schuster et al., 2015). By
274 providing sequences for all known genera, our 28S phylogeny (Fig. 3) recovers Theonellidae
275 as monophyletic (PP=1.0), thus conclusively support earlier findings of Schuster et al. (2015),
276 while the *cox1* phylogeny (Fig. 4) lacks support in this respect. The 28S phylogeny indicates
277 the monophyly of the genera *Discodermia*, *Manihinea*, *Racodiscula* and a potential new taxon,
278 here denoted as Theonellidae sp., a potential new genus mainly distinct by the layered network
279 of tetracone desma with smooth rays and strongly tuberculated tips and the less abundant
280 microscleres on the ectosome (SBD2102–2106). The sister relationship of *Manihinea conferta*
281 to *Theonella* sp. 1 is highly supported (PP=0.99) by 28S (Fig. 3), whereas it is not supported by
282 *cox1* (Fig. 4). A close relationship of *Theonella* and *Manihinea* was observed in an earlier study
283 by Redmond et al. (2013) using a nearly complete 18S gene fragment, but unsupported. The
284 genus *Discodermia* is sister to a clade consisting of *Manihinea*+*Theonella*+*Siliquariaspongia*,
285 which is sister to *Racodiscula*+Theonellidae sp.

286 The genus *Racodiscula* is highly supported (PP=1.0) as sister to Theonellidae sp. Although
287 the outer morphology of Theonellidae sp. (SBD2106 A–D) is very similar to that of *Racodiscula*,
288 it differs in spicule composition, desma and skeleton structure: the usually abundant spinose
289 microacanthorhabds, covering the surface of *Racodiscula* species (SBD2065) building a dense
290 crust on the surface, are rarer or even absent in Theonellidae sp. Instead of microacanthorabds,
291 phyllo- to discotriaenes are the main components of the dense surface crust. In addition,
292 Theonellidae sp. possesses desmas with smooth rays and strongly tuberculated tips (SBD2105
293 and SBD2106) building a layered network (SBD2102), which clearly differs from *Racodiscula*
294 (Schuster et al. 2018).

295 *Theonella mirabilis* (de Laubenfels, 1954) was first named within the homoscleromorphid
296 genus *Placinalopha* (Class Homoscleromorpha, Order Homosclerophorida, Family Plakinidae)
297 on the possession of what de Laubenfels described as 'lophotetractines'. The key size and shape
298 differences between the 'tetralophs' of *T. mirabilis* and other *Placinalopha* species were noted by
299 Muricy and Díaz (2002), who suggested that the species *mirabilis* had a more likely affinity with
300 species in family Theonellidae. 28S sequences (Fig. 3) unite specimens identified as *Theonella*
301 *mirabilis* in a single clade with a specimen identified as *T. conica* (Kieschnick, 1896) which
302 also has tetraloph-like desmas, suggesting that species with non-articulated 'tetraloph' desmas
303 may be monophyletic and separate from other *Theonella* spp. However, *cox1* sequences (Fig. 4)
304 separate *T. mirabilis* into two groups, nesting them within diverse species of *Theonella*. *Theonella*
305 *mirabilis* is very similar in spicule complement to the type species of the genus *Siliquariaspongia*,
306 *S. japonica* Hoshino, 1981 (family Theonellidae), although the latter lacks the strongyles and
307 possesses frilly discotriaenes, the latter occasionally recorded in *T. mirabilis*. Our phylogenies
308 clearly place all of the sequenced *Theonella mirabilis* species within the *Theonella*+*Manihinea*
309 clade (Fig. 3), confirming that this species belongs to the family Theonellidae. This result is
310 supported by the discovery of potent new depsipeptides mirabamides A–D, that inhibit HIV-1
311 infection, adding to a small class first exemplified by the papuamides from various *Theonella*
312 spp. (Plaza et al. 2007).

313 The family **Macandrewiidae** is monogeneric with currently seven valid species (Van Soest et

314 al. 2018a). Until now, only *Macandrewia rigida* Lévi and Lévi, 1989 from the Solomon Islands
315 has been sequenced (28S C1-D2 region, LN624160, G317931) (Schuster et al., 2015). The
316 present study includes a further sequence of an undescribed *Macandrewia* sp. from the Bahamas
317 (909 m depth), which clearly differs from *M. rigida* (Fig. 3). Morphological differences in
318 desmas (SBD2004) corroborate the genetic difference to *M. rigida* and provide further evidence
319 of a possible new species, which would be the first record in the TWA. Nevertheless, further
320 morphological observations and comparison with the type material of *M. rigida* as well as its
321 sequences are needed to conclusively describe and distinguish this potential new species. Both
322 *Macandrewia* species group within the Geodiidae, close to the Erylinae Sollas, 1888, within
323 a clade of non-desma bearing astrophorins (*Calthropella* Sollas, 1888, *Caminella* Lendenfeld,
324 1894) (Fig. 3). This relationship is currently not supported by morphology (Cárdenas et
325 al., 2018) and in any case suggests a distinct evolutionary history of *Macandrewia* to other
326 'lithistid' families Corallistidae and Neopeltidae (Schuster et al., 2015), where *Macandrewia* was
327 previously allocated (Kelly, 2000; Pomponi et al., 2001).

328 The family **Phymatellidae** currently includes three genera: *Neoaulaxinia*, *Neosiphonia* and
329 *Reidispongia*. The present comprehensive study does not recover Phymatellidae as monophyletic
330 and is therefore in contrast to Schuster et al. (2015). Instead, a highly supported sister group rela-
331 tionship of *Neoaulaxinia* Pisera and Lévi, 2002 to the neopeltid genus *Daedalopelta* Sollas, 1888
332 is observed and *Reidispongia coerulea* Lévi and Lévi, 1988 is sister to this clade (Fig. 3). This
333 relationship is in conflict with morphological hypotheses as Phymatellidae is characterized by
334 ectosomal dichotriaenes, while Neopeltidae has ectosomal pseudophyllotriaenes or pseudodisco-
335 triaenes (Pisera, 2002). Until now only one species of *Daedalopelta* is known (*D. nodosa* Sollas,
336 1888 from Florida, Gulf of Mexico and Southern Caribbean), which clearly differs from our
337 *Daedalopelta* specimens. Therefore, morphological characters of both sequenced *Daedalopelta*
338 species were further investigated and illustrated (SBD1894). Both species are potentially new
339 to science. *Daedalopelta* sp. 1 (SBD1894) possesses the characteristic pseudophyllotriaenes
340 (SBD1894) known from the Neopeltidae, while *Daedalopelta* sp. 2 (SBD1895) possesses di-
341 chotriaenes characteristic for the Phymatellidae. These dichotriaenes, however, have a unique
342 shape with indented cladomes (SBD1895). A spicule drawing of *Corallistes tubulatus* Van Soest
343 and Stentoft, 1988 from Barbados, now *Neophrissospongia tubulata*, resembles those unique
344 dichotriaenes implying that *N. tubulata* may need to be reallocated to *Daedalopelta*. Interestingly,
345 dichotriaenes of *Daedalopelta* sp. 2 resemble those of the fossil *Gignouxia niciensis* Moret, 1926
346 (Corallistidae) from the Late Cretaceous (Pl. XVIII, Fig. 2, 2' fig-txt 37). We suggest to allocate
347 *Gignouxia* Moret, 1926 to the family Phymatellidae. *Gignouxia* will include *Daedalopelta* sp. 2
348 as well as *Daedalopelta tubulata* comb. nov.

349 **Neopeltidae** polyphyly is given by the highly supported (PP=1.0) sister relationship of the
350 newly sequenced species *Neopelta* sp. to the non-desma bearing astrophorid *Neamphius huxley*
351 de Laubenfels, 1953 (Fig. 3). Morphologically, these two species only share choanosomal
352 amphiasters with spiny rays and microxeas. Thus, monocrepid desmas and pseudodiscotriaenes
353 characterizing *Neopelta* were lost in *Neamphius*. Spicule losses and gains are not uncommon
354 within tetractinellids and have frequently been shown (Chombard, Boury-Esnault and Tillier,
355 1998; Cárdenas et al., 2011; Schuster et al., 2015). Nevertheless, these two genera form a robust
356 sister clade to a non-desma bearing Ancorinidae clade consisting of *Stelletta* Schmidt, 1862,
357 *Ancorina* Schmidt, 1862, *Asteropus* Sollas, 1888 and *Stryphnus* Sollas, 1886.

358 **Corallistidae** is another major family dominating the HBOI collection and subsequently our
359 phylogenies (Fig. 3 and 4). These taxa were the focus of biomedical investigations (e.g. Haar et
360 al., 1996; Wright, 2010), thus targeted during the HBOI expeditions. Therefore, whether the
361 genera *Discoderma* and *Corallistes* Schmidt, 1870 are over-represented in this study due to their
362 increased sampling, or whether they actually dominate the sponge fauna in the TWA regions

363 remain obscure and awaits further investigations. Even though *Corallistes* were frequently
364 sampled in the past and 15 species are described to date (Van Soest et al. 2018b), only five
365 sequences are published (Kelly Borges and Pomponi, 1994; Chombard, Boury-Esnault and
366 Tillier, 1998; McInerney, Adams and Kelly, 1999). With 52 *Corallistes* specimens sequenced,
367 this study presents the largest data set to date and reveals the monophyly of this genus (28S,
368 PP= 1.0, Fig. 3). *Corallistes typus* Schmidt, 1870 specimens, type species of the genus, were
369 examined (SBD1888, 1889, 1892) and sequenced (Fig. 3 and 4). In addition, a *Corallistes*
370 *isabela* Desqueyroux-Faúndez and Van Soest, 1997 sample from Honduras was sequenced.
371 Until this study *Corallistes isabela* was only known from the Eastern Pacific (Galápagos) and
372 discussed as endemic to the Galápagos (Desqueyroux-Faúndez and Van Soest, 1997 and Schuster
373 et al., 2018). In addition, six *Corallistes* (*C. sp. 2* to *C. sp. 7*, see Fig. 3) differ by 1-3 bp in the
374 28S fragment, while no differences were found in *cox1*. Morphological differences are observed
375 between *C. sp. 2* (SBD1872) and *C. sp. 4* (SBD1879). For example, *C. sp. 2* has long (700
376 μm) thin ectosomal oxeads (SBD1872 A), while *C. sp. 4* has ectosomal styles (SBD1879 D) and
377 subectosomal microxea with spined surfaces (SBD1879 C). Morphological identifications are in
378 progress and necessary to discriminate the remaining *Corallistes* species.

379 The polyphyletic corallistid genus *Herengeria* Lévi and Lévi, 1983, only known from the
380 Pacific Norfolk Ridge, New Caledonia, and New Zealand (Schlacher-Hoenlinger, Pisera and
381 Hooper, 2005; Kelly et al., 2009), was sequenced (Fig. 3) and morphologically illustrated
382 (SBD1949) in the present study for the first time from the Bahamas and Honduras, representing
383 a new genus for the Atlantic. Only two species of *Herengeria* are described (*H. auriculata* Lévi
384 and Lévi 1988 and *H. vasiformis* Schlacher-Hoenlinger, Pisera and Hooper, 2005). The morpho-
385 logical observations delimit the new TWA species from *H. auriculata* (Schlacher-Hoenlinger
386 and Hooper, 2005) due to a lack of subectosomal rhabd-like spirasters. With respect to molecular
387 markers, *Herengeria* spp. from the TWA are distinct from *H. vasiformis/Herengeria* sp. from
388 the Pacific (Fig. 3). Our 28S (Fig. 3) and *cox1* (Fig. 4) phylogenies strongly support *Neoschram-*
389 *meniella* Pisera and Lévi, 2002 as sister to the *Herengeria/Isabella* clade. Currently, seven valid
390 species of *Neophrissospongia* Pisera and Lévi, 2002 are described (Van Soest et al. 2018c). Only
391 a few *Neophrissospongia* sequences (two 28S and one 18S) from the Pacific Ocean are currently
392 published. However, in order to gain a better understanding of their geographical distribution
393 and genetic differences, additional material from the Caribbean were sequenced in this study:
394 Their resulting 28S phylogeny clearly separates *Neophrissospongia* from the Pacific and the
395 Caribbean Islands. *Neophrissospongia* sp. 1 from different Caribbean Islands is sister (PP=1.0)
396 to *N. microstylifera* and *Neophrissospongia* sp. 3, from the Pacific (Fig. 3). A further Caribbean
397 *Neophrissospongia* species (sp. 2) forms a robust sister clade to *Neophrissospongia* from the
398 Eastern Pacific (Galápagos, Panama) (Fig. 3).

399 A clade of six as yet unidentified specimens from the HBOI collection (SBD1814) is sister
400 to the monophyletic *Neophrissospongia* (PP=1.0, Fig. 3). We assume that this clade consists
401 of species from the as yet unsequenced genus *Awhiowhio* Kelly, 2007 from the Pacific based
402 on morphological evidence. These show similar mega- and microsclere types to *Awhiowhio*
403 such as dicranoclone desmas and smooth dichotriaenes in *Awhiowhio* sp. 1 (SBD1815), most
404 similar to the *Awhiowhio osheai* from New Zealand (Kelly, 2007), but slightly different in terms
405 of desma ornamentation. Streptaster microscleres and acanthose microrhabds in *Awhiowhio*
406 sp. 1 (SBD1814, 1815) differ from those in *Awhiowhio osheai* in sizes and shapes (SBD1814).
407 The *cox1* phylogeny (Fig. 4) indicates the sister group relationship of *Awhiowhio osheai* Kelly,
408 2007 to *Neophrissospongia*. A close relationship of *Awhiowhio* to *Herengeria* as suggested
409 by Kelly (2007) based on morphological features is not supported by any of our phylogenies.
410 Instead, both markers independently suggest a close relationship (strongly supported by PP=1.0)
411 to *Neophrissospongia*. The genus *Pleroma* Sollas, 1888 (family Pleromidae) is recovered as

412 paraphyletic in both phylogenies (Fig. 3 and 4). *Pleroma menoui* Sollas, 1888 is distant to other
413 *Pleroma* spp. (including the type species *P. turbinatum*) in a close relationship to Corallistidae
414 (Fig. 3 and 4).

415 ***Intra-subordinal relationships of Spirophorina ‘lithistids’***

416 The suborder Spirophorina is characterized by sigmaspire microscleres and its members share
417 triaene spicules with Astrophorina. Currently, three families are known: Samidae Sollas, 1888,
418 Spirasigmidae Hallmann, 1912 and Tetillidae Sollas, 1886, whereas the latter is the largest in
419 terms of genera and species (e.g. Van Soest and Hooper, 2002). The relationships of major
420 clades within our *cox1* and 28S phylogenies (Fig. 3 and 4) were in concordance with the findings
421 of Carella et al. (2016) and Schuster et al. (2017). The latest revised classification of Morrow
422 and Cárdenas (2015) included the desma-bearing families Azoricidae, Scleritodermidae and
423 Siphonidiidae within Spirophorina. Since then, several studies (Schuster et al., 2015, 2017; Kelly
424 and Cárdenas, 2016) using *cox1*, 18S and 28S markers showed the separation of all rhizomorine-
425 bearing sponges from Spirophorina (=Tetillidae) The present enlarged dataset corroborates again
426 the absence of desma-bearing sponges in Spirophorina and their grouping in a well supported
427 clade along with the Stupendidae and the Thrombidae (Fig.2). In order to establish this clade as
428 a new taxa, we await further molecular data from the latter two families (work in progress, MK
429 and PC).

430 ***Subordinal structure of Tetractinellida***

431 Kelly and Cárdenas (2016) provided strong support for families Azoricidae, Scleritodermidae
432 and Siphonidiidae within a new suborder, supported in part by the common possession of
433 rhizomorine desmas.

434 Regarding **Azoricidae**, Maldonado et al. (2015) discovered a dense and large aggrega-
435 tion of *Leiodermatium pfeifferae* Carter, 1873 on seamounts in the Mediterranean building
436 complex reef-forming structures. Even though *Leiodermatium* Schmidt, 1870 has very few
437 diagnostic characters (no microscleres) to discriminate between species (Pisera, 2002; Pis-
438 era and Lévi, 2002b), 11 species are valid to date (WPD access Aug. 2017). In the present
439 study we sequenced the 28S C1-D2 fragment for 52 *Leiodermatium* specimens from several
440 regions in the TWA (Fig. 3) representing at least 8 species and the largest sequenced dataset
441 for this genus to date. The monophyly of *Leiodermatium* is highly supported by our 28S
442 phylogeny (PP=1.0; Fig. 3). The amplification of *cox1* unfortunately failed, most likely due
443 to the presence of introns similar to other rhizomorine-bearing genera like e.g. *Microsclero-*
444 *derma* and *Scleritoderma* (Schuster et al., 2017). Preliminary morphological investigations
445 (SBD1966,1967,1959,1965,1956,1955,1975,1977,1976,1994,2000,2001,2003) adumbrate de-
446 tailed differences of *Leiodermatium* spp., in particular their surfaces (oscles and ostia sizes),
447 diactines and desma morphology. For instance *Leiodermatium* sp. 1 (SBD1955) has large and
448 marginate oscules, while *Leiodermatium* sp. 6 (SBD1994) and *Leiodermatium* sp. 8 (SBD2003)
449 have large but elevated oscules on exterior margins, in contrast to *Leiodermatium* sp. 7, whose
450 oscules are small and closely distributed. Based on molecular and morphological data we propose
451 eight different species of *Leiodermatium* (Fig. 3) in the TWA, however further morphological in-
452 vestigations are needed to corroborate this assumption. *Leiodermatium* is unsupported (PP=0.65)
453 sister to a clade of *Siphonidium* spp. (Siphonidiidae); the same relationship was revealed with
454 small fragment of the 18S gene (482 bp) for *Leiodermatium* sp. (Kelly-Borges and Pomponi,
455 1994, Kelly and Cárdenas, 2016). Further investigation and a review of all extant and fossil
456 *Leiodermatium* species is suggested to better understand the geographical distribution and recent
457 diversification of this paleontological important group.

458 Within the polyphyletic rhizomorine family **Scleritodermidae**, its genera *Aciculites* is poly-
459 and *Scleritoderma* is paraphyletic, while *Microscleroderma*, *Amphibleptula* Schmidt, 1879 and

460 *Setidium* Schmidt, 1879 are monophyletic (Fig. 3). The genus *Amphibleptula* is currently
461 monospecific with *A. madrepora* Schmidt, 1879 from the Caribbean (Pisera and Lévi, 2002c).
462 Morphologically, *A. madrepora* is very similar and easy to confuse with *Microscleroderma*
463 *spirophora* Lévi, 1960 as discussed in Van Soest and Stentoft (1988). *Amphibleptula* is here
464 sequenced for the first time and our 28S phylogeny shows *Microscleroderma* and *Amphibleptula*
465 sp.1 as sister groups, although unsupported in the 28S phylogeny (PP=0.63). Morphological
466 observations (SBD1802,1803) provide conclusive evidence that our three samples are *Amphiblep-*
467 *tula* species, due to their dense tuberculated/blunt spinose rhizoclonal, the protruding bundles of
468 oxeas in the oscula area (SBD1802,1803) as well as the presence of sigmaspires (SBD1802).
469 Differences to *A. madrepora* are the diactine spicules present in all three *Amphibleptula* sp.1. In
470 addition, fusiform spined microxeas and acanthorhabds are found in the specimen from Jamaica
471 (HBOI 1-IX-93-1-006, SBD1802). To conclude, we sequenced two potential new species of
472 *Amphibleptula* with clear unique morphological characters, different from *A. madrepora*.

473 During this study a new suborder Thoosina was suggested by Carballo et al. 2018 including
474 the genera *Thoosa* and *Alectona* so far. However, since no desma-bearing tetractinellids are
475 grouping within this suborder, we decided to not further discuss Thoosina in the scope of this
476 study.

477 **Molecular phylodiversity of TWA desma-bearing demosponges**

478 In the present study the inclusive phylodiversity was calculated for Bonaire, Curaçao, Florida,
479 Honduras, Jamaica, Puerto Rico, Turks and Caicos and the Bahamas (Fig. 5). The PD_I
480 analyses disclosed a high variation within the TWA locations (Fig. 5). At comparable sampling
481 efforts, the highest PD_I was observed in Jamaica (Fig. 5A) indicating a high biodiversity in
482 this region, closely followed by the Bahamas (Fig. 5B). At sample size of 20, Curaçao and
483 Florida showed the lowest PD_I, followed by Turks and Caicos and Honduras. The high PD_I
484 of 'lithistid' demosponges calculated for the Bahamas is in agreement with the findings of
485 Reed and Pomponi (1997), and may be explained by the high habitat diversity observed in this
486 region (Reed and Pomponi, 1997) and their close proximity to the species-rich Atlantic (see e.g.
487 Carvalho, Pomponi and Xavier, 2015). Even though Turks and Caicos are close to the Bahamas
488 and the Atlantic, a much lower PD_I was calculated, maybe due to less habitat diversity.

489 **Bathymetric distribution and relative abundance of TWA desma-bearing families**

490 The evaluation of the relative abundance of eight 'lithistid' families within each depth zone is
491 based upon 234 specimens collected from eight localities in the TWA (Fig. 6). Theonellidae
492 and Corallistidae are the two dominant families in the present dataset, and assumed to be the
493 dominant families in the TWA (Pomponi et al., 2001). While Theonellidae dominate depth zones
494 of 0–151 m, Corallistidae are more abundant in depth zones of 151–600 m. This corroborates
495 the result of Pomponi et al. (2001) showing that *Discodermia* (Theonellidae) is the dominant
496 genus from 0–151 m, while *Corallistes* (Corallistidae) dominates the zone of 151–914 m. An
497 explanation for this might be that Corallistidae have a dense rigid skeleton of dicranoclone
498 desmas, while Theonellidae possess a less articulated skeleton of tetracclone desmas. Thus, it can
499 be hypothesized, that 'lithistids' with a hyper-silicified dense desma skeleton like Corallistidae
500 occur in deeper zones ≥ 300 m, while those with a less dense desma skeleton like most of
501 the *Theonella* species (Theonellidae) moved into more shallow water habitats, as less silica
502 is required for their skeleton construction. This trend was also observed in the South West
503 Pacific (Kelly et al., 2007; Hall, Ekins and Hooper, 2014). As Corallistidae and Theonellidae are
504 considered to be polymorphic (Pisera and Lévi, 2002a,d), it is difficult, to draw any conclusion
505 of different depth zones or habitats influencing growth form patterns in these two families.

506 However, further 'lithistid' families with a similar bathymetric trend are observed and growth

507 forms are suggested to play a role in the bathymetric distributions of ‘lithistids’. For instance
508 *Leiodermatium* spp. (Azoricidae) are abundant (27 specimens) in depth zones 301–1000 m.
509 Similar to Corallistidae *Leiodermatium* possess a dense heavily articulated skeleton, but of
510 strongly spinose rhizoclone desmas. The growth form of *Leiodermatium* species are described as
511 being foliated or vase to ear-shaped (Pisera and Lévi, 2002b). Such growth forms are suggested
512 to improve the water circulation in sponges, in particular of those in the deep-sea habitats, and to
513 be more resistant to higher water viscosity and scarcity of particles (Levinton, 1982; Gage and
514 Tyler, 1991). Many vase to cup or ear-shaped sponges have their inhalant pores facing the outer
515 side and exhalant openings on the upper side separating incoming and processed water (Sará and
516 Vacelet, 1973), which may reduce any negative effect on filtering due to a sedimentation. This is
517 in contrast to Siphonidiidae, a family represented in this analysis by the genera *Gastrophanella*
518 and *Siphonidium*, which are rather encrusting or irregular cylindrical, thus more abundant in the
519 depth zone of 61–150 m.

520 **Scleritodermidae** occurred more often on vertical walls in depth 301–600 m, but was also
521 not observed to be a major component of the ‘lithistid’ fauna in the TWA. The greatest number
522 of desma-bearing demosponges were found in depth zone 301–600 m (87 specimens), with
523 Corallistidae as the dominant family (34 specimens) followed by Azoricidae with 27 specimens.
524 Diverse habitats from fine mud and sand slopes to rock pinnacles, boulders and vertical walls
525 in this depth zone (Fig. 6) could be a possible explanation. The families Neopeltidae and
526 Macandrewiidae are rare in our study with only one species discovered at 909 m depth on a
527 vertical wall in the Bahamas (*Macandrewia* sp.), and two *Daedalopelta* sp. species collected
528 from the Bahamas at 301–600 m. This corroborates the findings of Pomponi et al. (2001),
529 because they found one species of *Daedalopelta nodosa* at 452 m in the Bahamas, one *Neopelta*
530 *perfecta* in 116 m depth from Grenada and one *Macandrewia clavatella* in the southwest coast of
531 Florida. These families and species are also found to be rare in the Southwest Pacific (Lévi, 1991;
532 Kelly, 2000). Besides the tetractinellid ‘lithistid’ sponges, we noted that other desma-bearing
533 sponge lineages, such as family Vetulinidae (Order Sphaerocladina) constitute only a minor
534 component in any depth-zone in the TWA.

535 Further testing is required to assess whether geomorphological conditions resulting of a
536 variety of complex tectonic interactions (e.g., strike-slip faults, thrust fault, subduction and
537 seafloor spreading in Cayman Trough, see Fig. 1), directly affect diversity and bathymetric
538 distribution of ‘lithistids’ in the TWA (Fig. 6).

539 CONCLUSION

540 In summary, this is the first integrative approach using molecular and morphological data on TWA
541 ‘lithistid’ demosponges, thus contributing to a better understanding of their phylogenetic affinities,
542 diversity and bathymetric distribution patterns. The present study points to specimens/groups
543 in need of deeper taxonomic investigations and revision, however, additional morphological
544 as well as other independent markers are needed. With recent evidence (Pomponi et al. 2001)
545 that ‘lithistids’ are dominant components among all investigated TWA regions, we suggest a
546 comparable diversity to the Pacific ‘lithistids’ as well as to the Mesozoic fauna. Furthermore,
547 there is a clear shift of lithistids with a rigid and heavily articulated desma towards deeper
548 habitats (Corallistidae and Azoricidae), whereas ‘lithistids’ with a less articulated skeleton tend
549 to occur in more shallow habitats (Theonellidae and Siphoniidae). A major effect causing this
550 shift is the availability of silica in the ocean throughout time. Our robust phylogeny enables
551 relaxed molecular clock analyses in conjunction with the rich fossil record of lithistids to better
552 correlate such shifts to geological/geochemical events in the past.

553 ACKNOWLEDGMENTS

554 We acknowledge the Government of the Bahamas, Curaçao, Jamaica, Turks and Caicos, Bonaire
555 and St. Vincent Islands, Martinique, Guadeloupe, Puerto Rico, Cuba, Jamaica, Honduras, Gulf
556 of Mexico, and the Philippines, for granting permission to conduct research in their territorial
557 waters. Thirty-two new specimens and associated data were supplied by the NIWA Invertebrate
558 Collection (NIC) for sequencing; we are particularly grateful to Sadie Mills for her diligent
559 assistance with loans. A further 31 specimens and associated images and data were supplied
560 by Lori J. Bell and the Coral Reef Research Foundation (CRRF) for sequencing; these were
561 collected under contract to the U.S. National Cancer Institute. We thank colleagues Amy Wright,
562 John Reed and Megan Conkling (HBOI-FAU) for their assistance with the HBOI collection
563 of samples and associated data. AS thanks Sergio Vargas (Dept. of Earth- and Environmental
564 Sciences, LMU Munich, Germany) for his help with the modification of the phylodiversity script.
565 Nicole Enghuber is thanked for her help in spicule preparations and Simone Schätzle is thanked
566 for sequencing assistance (both Dept. of Earth- and Environmental Sciences, LMU Munich,
567 Germany).

568 ADDITIONAL INFORMATION AND DECLARATIONS

569 This document reflects only the authors' view and the Executive Agency for Small and Medium-
570 sized Enterprises (EASME) is not responsible for any use that may be made of the information it
571 contains.

572 FUNDING

573 Financial support for this study was provided by the German Science Foundation to DE and
574 GW (DFG ER 611/3-1, DFG Wo869/15-1, respectively). The LMU Mentoring and the HELGE
575 AX:Son JOHNSON STIFTELSE provided funding for AS to visit HBOI (Florida, USA) and
576 NIWA (National Institute of Water and Atmospheric Research, Auckland and Wellington in New
577 Zealand). Financial support for the R/V Seward Johnson/Johnson Sea Link I+II expedition was
578 provided by HBOI. MK's participation was funded by NIWA under Coasts and Oceans Research
579 Programme 2 Marine Biological Resources: Discovery and definition of the marine biota of
580 New Zealand (2016/2017 and 2017/2018 SCI). PC and SP received support from the European
581 Union's Horizon 2020 research and innovation program through the SponGES project (Grant
582 agreement No. 679849).

583 COMPETING INTERESTS

584 The authors declare there are no competing interests.

585 AUTHOR CONTRIBUTIONS

586 Astrid Schuster and Dirk Erpenbeck conceived and designed the study. Dirk Erpenbeck and Gert
587 Wörheide acquired funding, contributed reagents, materials and analysis tools. Astrid Schuster,
588 Andrzej Pisera, Paco Cárdenas, Shirley A. Pomponi and Michelle Kelly identified genera/species.
589 Shirley A. Pomponi (HBOI), Michelle Kelly (NIWA) contributed to the sampling. Astrid Schuster
590 performed the laboratory experiments, did the phylogenetic analyses, bathymetric distribution
591 plot, phylodiversity analysis and SEM. Astrid Schuster wrote the manuscript, prepared figures
592 and tables. Paco Cárdenas, Dirk Erpenbeck, Michelle Kelly, Andrzej Pisera and Gert Wörheide
593 edited versions of the manuscript. All authors reviewed drafts of the paper.

594 **DATA AVAILABILITY**

595 The following information was supplied regarding data availability:

596 Novel sequences will be archived at the European Nucleotide Archive (ENA) under the
597 accession numbers: XXXX–XXXXX.

598 **REFERENCES**

- 599 Addis JS., Peterson KJ. 2005. Phylogenetic relationships of freshwater sponges (Porifera,
600 Spongillina) inferred from analyses of 18S rDNA, COI mtDNA, and ITS2 rDNA sequences.
601 *Zoologica Scripta* 34:549–557.
- 602 Bergquist PR. 1970. Sponges. Hutchinson University Library, University of California Press,
603 Berkeley and Los Angeles 1–268.
- 604 Carballo JL., Bautista-Guerrero E., Cárdenas P., Cruz-Barraza JA., Aguilar-Camacho JM.
605 2018. Molecular and morphological data from Thoosidae in favour of the creation of a new
606 suborder of Tetractinellida. *Systematics and Biodiversity* (2018):1–10.
- 607 Cárdenas P., Rapp HT., Schander C., Tendal OS. 2010. Molecular taxonomy and phy-
608 logeny of the Geodiidae (Porifera, Demospongiae, Astrophorida) – combining phylogenetic and
609 Linnaean classification. *Zoologica Scripta* 39:89–106.
- 610 Cárdenas P., Vacelet J., Chevaldonné P., Pérez T., Xavier JR. 2018. From marine caves to the
611 deep sea, a new look at *Caminella* (Demospongiae, Geodiidae) in the Atlanto-Mediterranean
612 region. *Zootaxa* 4466:174–196.
- 613 Cárdenas P., Xavier JR., Reveillaud J., Schander C., Rapp HT. 2011. Molecular phylogeny
614 of the Astrophorida (Porifera, Demospongiae) reveals an unexpected high level of spicule
615 homoplasy. *PloS ONE* 6:e18318.
- 616 Carella M., Agell G., Cárdenas P., Uriz M j. 2016. Phylogenetic reassessment of Antarctic
617 Tetillidae (Demospongiae, Tetractinellida) reveals new genera and genetic similarity among
618 morphologically distinct species. *PloS ONE* 11:e0160718.
- 619 Carvalho FC., Pomponi SA., Xavier JR. 2015. Lithistid sponges of the upper bathyal of
620 Madeira, Selvagens and Canary Islands, with description of a new species of *Isabella*. *Journal of*
621 *the Marine Biological Association of the United Kingdom* 95:1287–1296.
- 622 Chombard C., Boury-Esnault N., Tillier S. 1998. Reassessment of homology of morphologi-
623 cal characters in tetractinellid sponges based on molecular data. *Systematic Biology* 47:351–366.
- 624 Darriba D., Taboada GL., Doallo R., Posada D. 2012. jModelTest 2: more models, new
625 heuristics and parallel computing. *Nature Methods* 9:772–772.
- 626 Desqueyroux-Faúndez R., Van Soest RWM. 1997. Shallow waters Demosponges of the
627 Galápagos Islands. *Revue Suisse de Zoologie* 104:379–467.
- 628 Erpenbeck D., Sutcliffe P., Cook SDC., Dietzel A., Maldonado M., Van Soest RWM., Hooper
629 JNA., Wörheide G. 2012. Horny sponges and their affairs: On the phylogenetic relationships of
630 Keratose sponges. *Molecular Phylogenetic and Evolution* 63:809–816.
- 631 Gage JD., Tyler PA. 1991. Deep-Sea Biology: A Natural History of Organisms at the
632 Deep-Sea Floor. Cambridge: *Cambridge University Press*.
- 633 Giunta G., Orioli S. 2011. The Caribbean Plate Evolution: Trying to resolve a very com-
634 plicated tectonic puzzle. In Sharkov EV eds. *New Frontiers in Tectonic Research - General*
635 *Problems, Sedimentary Basins and Island Arcs* Chapter 10.
- 636 Haar ET., Kowalski RJ., Hamel E., Lin CM., Longley RE., Gunasekera SP., Rosenkranz HS.,
637 Day BW. 1996. Discodermolide, a cytotoxic marine agent that stabilizes microtubules more
638 potently than taxol. *Biochemistry* 35:243–250.
- 639 Hall KA., Ekins MG., Hooper J. 2014. Two new desma-less species of *Theonella* Gray,
640 1868 (Demospongiae: Astrophorida: Theonellidae), from the Great Barrier Reef, Australia, and a

- 641 re-evaluation of one species assigned previously to *Dercitus* Gray, 1867. *Zootaxa* 3814:451–477.
- 642 Hallmann EF. 1912. Report on the Sponges obtained by the F.I.S. 'Endeavour' on the Coasts
643 of New South Wales, Victoria, South Australia, Queensland, and Tasmania, 1909-10. Part I.
644 *Zoological Results of the Fishing Experiments carried out by F.I.S. 'Endeavour'*, 11909-14.
- 645 Hoshino. 1981. Shallow-Water Demosponges of Western Japan 2. *Journal of Science of the*
646 *Hiroshima University* (B) 29:207–289.
- 647 Katoh K., Standley DM. 2013. MAFFT Multiple sequence alignment software version 7:
648 Improvements in performance and usability. *Molecular Biology and Evolution* 30:772–780.
- 649 Kearse M., Moir R., Wilson A., Stones-Havas S., Cheung M., Sturrock S., Buxton S., Cooper
650 A., Markowitz S., Duran C., Thierer T., Ashton B., Meintjes P., Drummond A. 2012. Geneious
651 Basic: an integrated and extendable desktop software platform for the organization and analysis
652 of sequence data. *Bioinformatics* 28:1647–1649.
- 653 Kelly M. 2000. Description of a new lithistid sponge from northeastern New Zealand, and
654 consideration of the phylogenetic affinities of families Corallistidae and Neopeltidae. *Zoosystema*
655 22:265–284.
- 656 Kelly M. 2007. The Marine Fauna of New Zealand: Porifera : Lithistid Demospongiae (rock
657 Sponges). *NIWA Biodiversity Memoir* 121:1–100.
- 658 Kelly Borges M., Pomponi SA. 1994. Phylogeny and classification of lithistid sponges
659 (Porifera: Demospongiae): a preliminary assessment using ribosomal DNA sequence compar-
660 isons. *Molecular Marine Biology and Biotechnology* 3:87–103.
- 661 Kelly M., Cárdenas P. 2016. An unprecedented new genus and family of Tetractinellida
662 (Porifera, Demospongiae) from New Zealand's Colville Ridge, with a new type of mitochondrial
663 group I intron. *Zoological Journal of the Linnean Society* 177:335–352.
- 664 Kelly M., Edwards AR., Wilkinson MR., Alvarez B., Cook S de C., Bergquist PR., Buck-
665 eridge S., Campbell HJ., Reiswig HM., Valentine C., Vacelet J. 2009. Phylum Porifera: sponges.
666 In: Gordon DP ed. *New Zealand inventory of biodiversity: 1 Kingdom Animalia: Radiata,*
667 *Lophotrochozoa, Deuterostomia. New Zealand Inventory of Biodiversity* 1, 23–46.
- 668 Kelly M., Ellwood M., Tubbs L., Buckeridge J. 2007. The lithistid Demospongiae in
669 New Zealand waters: species composition and distribution. *Porifera Research: Biodiversity,*
670 *Innovation and Sustainability* 393–404.
- 671 Kieschnick O. 1896. Silicispongiae von Ternate nach den Sammlungen von Herrn Prof. Dr.
672 W. Kükenthal. *Zoologischer Anzeiger* 19:526–534.
- 673 Kirkpatrick R. 1903. Descriptions of South African Sponges. *Marine Investigations in South*
674 *Africa* 2:171–180.
- 675 Lê HLV., Lecointre G., Perasso R. 1993. A 28S rRNA-based phylogeny of the gnathostomes:
676 first steps in the analysis of conflict and congruence with morphologically based cladograms.
677 *Molecular Phylogenetics and Evolution* 2:31–51.
- 678 Lévi C. 1991. Lithistid sponges from the Norfolk Rise, Recent and Mesozoic genera. In:
679 Reitner J, Keupp H eds. *Fossil and Recent Sponges*. Berlin, Heidelberg: Springer-Verlag, 72–82.
- 680 Levinton JS. 1982. *Marine Ecology*. New Jersey: Prentice-Hall. Lewis LA., Lewis PO. 2005.
681 Unearthing the molecular phylodiversity of desert soil green algae (Chlorophyta). *Systematic*
682 *Biology* 54:936–947.
- 683 Maldonado M., Aguilar R., Blanco J., García S., Serrano A., Punzón A. 2015. Aggregated
684 Clumps of Lithistid Sponges: A Singular, Reef-Like Bathyal Habitat with Relevant Paleontologi-
685 cal Connections. *PLoS ONE* 10:e0125378.
- 686 Maldonado M., Young CM. 1996. Bathymetric patterns of sponge distribution on the
687 Bahamian slope. *Deep Sea Research Part I: Oceanographic Research Papers* 43:897–915.
- 688 Marshall W. 1876. Ideen über die Verwandtschaftsverhältnisse der Hexactinelliden. *Zeitschrift*
689 *für wissenschaftliche Zoologie* 21:113–136.

- 690 McInerney JO., Adams CI., Kelly M. 1999. Phylogenetic resolution potential of 18S and 28S
691 rRNA genes within the lithistid Astrophorida. *Memoirs of the Queensland Museum* 44:343–351.
- 692 Meyer CP., Geller JB., Paulay G. 2005. Fine scale endemism on coral reefs: Archipelagic
693 differentiation in turbinid gastropods. *Evolution* 59:113–125.
- 694 Miloslavich P., Díaz JM., Klein E., Alvarado JJ., Díaz C., Gobin J., Escobar-Briones E.,
695 Cruz-Motta JJ., Weil E., Cortés J., Bastidas AC., Robertson R., Zapata F., Martín A., Castillo J.,
696 Kazandjian A., Ortiz M. 2010. Marine Biodiversity in the Caribbean: regional estimates and
697 distribution patterns. *PLoS ONE* 5:e11916.
- 698 Moret L. 1926. Contribution à l'étude des spongiaires siliceux du Crétacé supérieur français.
699 *Mémoires de la Société géologique de France* 5:1–327.
- 700 Morrow C., Cárdenas P. 2015. Proposal for a revised classification of the Demospongiae
701 (Porifera). *Frontiers in Zoology* 12:1–27.
- 702 Muricy G, and Diaz MC. 2002. Order Homosclerophorida Dendy, 1905. Family Plakinidae
703 Schulze, 1880. In: Hooper JNA, and Van Soest RWM, eds. *Systema Porifera A guide to the*
704 *classification of sponges*. New York, Boston, Dordrecht, London, Moscow: Kluwer Academic/
705 Plenum Publishers, 71–82.
- 706 Nardo GD. 1833. De Spongiis. In: Isis, oder *Encyclopädische Zeitung Coll. Oken, Jena*
707 519–523.
- 708 Pallas PS. 1766. Elenchus zoophytorum sistens generum adumbrationes generaliores et
709 specierum cognitarum succintas descriptiones, cum slectis auctorum synonymis. Fransiscum
710 Varrentrapp, Hagae 451.
- 711 Pisera A. 1999. Lithistid sponge *Setidium obtectum* Schmidt, 1879, rediscovered. In: Hooper
712 JNA ed. *Memoirs of the Queensland Museum Proceedings of the 5th International Sponge*
713 *Symposium*, Brisbane, June-July 1998. 473–478.
- 714 Pisera A. 2002. Fossil “Lithistids”: An Overview. In: Hooper JNA, Van Soest RWM eds.
715 *Systema Porifera. A guide to the classification of sponges*. New York, Boston, Dordrecht, London,
716 Moscow: Kluwer Academic/ Plenum Publishers, 388–402. Pisera A. 2006. Palaeontology of
717 sponges — a review. *Canadian Journal of Zoology* 84:242–261.
- 718 Pisera A., Lévi C. 2002a. Family Theonellidae Lendenfeld, 1903. In: Hooper JNA, Van
719 Soest RWM eds. *Systema Porifera. A guide to the classification of sponges*. New York, Boston,
720 Dordrecht, London, Moscow: Kluwer Academic/ Plenum Publishers, 327–337.
- 721 Pisera A., Lévi C. 2002b. Family Azoricidae Sollas, 1888. In: Hooper JNA, Van Soest RWM
722 eds. *Systema Porifera. A guide to the classification of sponges*. New York, Boston, Dordrecht,
723 London, Moscow: Kluwer Academic/ Plenum Publishers, 352–355.
- 724 Pisera A., Lévi C. 2002c. Family Scleritodermidae Sollas, 1888. In: Hooper JNA, Van
725 Soest RWM eds. *Systema Porifera. A guide to the classification of sponges*. New York, Boston,
726 Dordrecht, London, Moscow: Kluwer Academic/ Plenum Publishers, 302–311.
- 727 Pisera A., Lévi C. 2002d. Family Corallistidae Sollas, 1888. In: Hooper JNA, Van Soest
728 RWM eds. *Systema Porifera. A guide to the classification of sponges*. New York, Boston,
729 Dordrecht, London, Moscow: Kluwer Academic/ Plenum Publishers, 312–320.
- 730 Pisera A., Pomponi SA. 2015. New data on lithistid sponges from the deep Florida shelf
731 with description of a new species of *Theonella*. *Journal of the Marine Biological Association of*
732 *the United Kingdom* 95:1297–1309.
- 733 Plaza A., Gustchina E., Baker HL., Kelly M., Bewley CA. 2007. Mirabamides A–D,
734 Depsipeptides from the Sponge *Siliquariaspongia mirabilis* that inhibit HIV-1 fusion. *Journal of*
735 *Natural Products* 70:1753–1760.
- 736 Pomponi SA., Kelly M., Reed JA., Wright EA. 2001. Diversity and bathymetric distribution
737 of lithistid sponges in the tropical western Atlantic region. *Bulletin of the Biological Society of*
738 *Washington* 10:344–353.

- 739 Redmond NE., Morrow CC., Thacker RW., Diaz MC., Boury-Esnault N., Cardenas P., Hajdu
740 E., Lobo-Hajdu G., Picton BE., Pomponi SA., Kayal E., Collins AG. 2013. Phylogeny and
741 systematics of Demospongiae in light of new small-subunit ribosomal DNA (18S) Sequences.
742 *Integrative and Comparative Biology* 53:388–415.
- 743 Reed JK., Pomponi SA. 1997. Biodiversity and distribution of deep and shallow wa-
744 ter sponges in the Bahamas. *Proceedings of the 8th International Coral Reef Symposium*
745 2:1387–1392.
- 746 Ronquist F., Teslenko M., van der Mark P., Ayres DL., Darling A., Höhna S., Larget B.,
747 Liu L., Suchard MA., Huelsenbeck JP. 2012. MrBayes 3.2: Efficient Bayesian Phylogenetic
748 Inference and Model Choice across a Large Model Space. *Systematic Biology* 61:539–542.
- 749 RStudio Team. 2014. RStudio: *Integrated Development for R*.
- 750 Ryan W., Carbotte SM., Coplan JO., O’Hara S., Melkonian A., Arko R., Weissel RA.,
751 Ferrini V., Goodwillie A., Nitsche F., Bonczkowski., Zemsky R. 2009. Global Multi-Resolution
752 Topography synthesis. *Geochemistry, Geophysics, Geosystems* 10:1–9.
- 753 Sanders HL. 1968. Marine Benthic Diversity: A Comparative Study. *The American Natural-*
754 *ist* 102:243–282.
- 755 Sará M., Vacelet J. 1973. Écologie des Démosponges. In: Grassé P-P ed. *Traité de Zoologie.*
756 *Anatomie, Systématique, Biologie*. Paris: Masson et Cie, 472–576.
- 757 Schlacher-Hoenlinger MA., Pisera A., Hooper JNA. 2005. Deep-sea “lithistid” assemblages
758 from the Norfolk Ridge (New Caledonia), with description of seven new species and a new genus
759 (Porifera, Demospongiae). *Zoosystema* 27:649–698.
- 760 Schmidt O. 1870. Grundzüge einer Spongien-Fauna des atlantischen Gebietes. Verlag von
761 Wilhelm Engelmann, Leipzig.
- 762 Schmidt O. 1879. Die Spongien des Meerbusen von Mexico. I Abt. Lithistiden. Verlag G.
763 Fischer.
- 764 Schrammen A. 1910. Neue Kieselschwämme aus der oberen Kreide von Nordwestdeutsch-
765 land. I. Teil. Tetraxonia, Monaxonia und Silicea incertae sedis. *Palaeontographica* 5:1–175.
- 766 Schrammen A. 1924. Die Kieselspongien der oberen Kreide von Nordwestdeutschland. III.
767 und letzter Teil. *Monographien zur Geologie und Paläontologie* 1:1–159.
- 768 Schuster A., Erpenbeck D., Pisera A., Hooper J., Bryce M., Fromont J., Wörheide G.
769 2015. Deceptive Desmas: Molecular phylogenetics suggests a new classification and uncovers
770 convergent evolution of lithistid demosponges. *PloS ONE* 10:e116038.
- 771 Schuster A., Lopez JV., Becking LE., Kelly M., Pomponi SA., Wörheide G., Erpenbeck D.,
772 Cárdenas P. 2017. Evolution of group I introns in Porifera: new evidence for intron mobility and
773 implications for DNA barcoding. *BMC Evolutionary Biology* 17:1–21.
- 774 Schuster A., Cárdenas, P., Pisera A., Pomponi SA., Kelly M., Wörheide G., Erpenbeck D.
775 2018. Seven new deep-water Tetractinellida (Porifera: Demospongiae) from the Galápagos
776 Islands – Morphological descriptions and DNA barcodes. *Zoological Journal of the Linnean*
777 *Society* 184:1–31.
- 778 Sollas WJ. 1887. Sponges. In Black, AC, eds. *Encyclopaedia Britannica* 412–429.
- 779 Sollas WJ. 1888. Report on the Tetractinellida collected by H.M.S. Challenger, during the
780 years 1873–1876. *Zoology* 25:1–458.
- 781 Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of
782 large phylogenies. *Bioinformatics* 30:1312–1313.
- 783 Tautz D., Renz M. 1983. An optimized freeze-squeeze method for the recovery of DNA
784 fragments from agarose gels. *Analytical Biochemistry* 132:14–19.
- 785 Topsent E. 1894. Etude monographique des spongiares de France. I. Tetractinellida. *Archives*
786 *de Zoologie Expérimentale et Générale* 3:259–400.

- 787 Van Soest RWM., Boury-Esnault N., Hooper JNA., Rützler K., de Voogd NJ., Alvarez B.,
788 Hajdu E., Pisera AB., Manconi R., Schönberg C., Klautau M., Picton B., Kelly M., Vacelet J.,
789 Dohrmann M., Díaz, MC., Cárdenas P., Carballo JL., Ríos P., Downey R. 2018b. *World Porifera*
790 *database. Corallistes* Schmidt, 1870. Accessed at: <http://www.marinespecies.org/porifera/porifera.php?p=taxd>
791 on 2018-09-20
- 792 Van Soest RWM., Boury-Esnault N., Hooper JNA., Rützler K., de Voogd NJ., Alvarez B.,
793 Hajdu E., Pisera AB., Manconi R., Schönberg C., Klautau M., Picton B., Kelly M., Vacelet J.,
794 Dohrmann M., Díaz, MC., Cárdenas P., Carballo JL., Ríos P., Downey R. 2018a. *World Porifera*
795 *database. Macandrewia* Gray, 1859. Accessed at: <http://www.marinespecies.org/porifera/porifera.php?p=taxd>
796 on 2018-09-20
- 797 Van Soest RWM., Boury-Esnault N., Hooper JNA., Rützler K., de Voogd NJ., Alvarez B.,
798 Hajdu E., Pisera AB., Manconi R., Schönberg C., Klautau M., Picton B., Kelly M., Vacelet J.,
799 Dohrmann M., Díaz, MC., Cárdenas P., Carballo JL., Ríos P., Downey R. 2018c. *World Porifera*
800 *database. Neophrissospongia* Pisera and Lévi, 2002. Accessed at: <http://www.marinespecies.org/porifera/porifera.php?p=taxd>
801 on 2018-09-20
- 802 Van Soest RWM., Hooper JNA. 2002. Order Spirophorida Bergquist and Hogg, 1969. In:
803 Hooper JNA, Van Soest RWM eds. *Systema Porifera. A guide to the classification of sponges*.
804 New York, Boston, Dordrecht, London, Moscow: Kluwer Academic/ Plenum Publishers, 83–84.
- 805 Van Soest RWM., Stentoft N. 1988. Barbados deep-water sponges. *Studies on the Fauna of*
806 *Curaçao and Other Caribbean Islands* 70:1–175.
- 807 Vargas S., Kelly M., Schnabel K., Mills S., Bowden D., Wörheide G. 2015. Diversity in
808 a cold hot-spot: DNA-barcoding reveals patterns of evolution among antarctic demosponges
809 (Class Demospongiae, Phylum Porifera). *PLoS ONE* 10:e0127573.
- 810 von Lendenfeld R. 1903. Tetraxonia. In Schulze FE eds. *Das Tierreich. Friedländer, Berlin*
811 *Publishers*, 1–168.
- 812 Wickham H. 2009. ggplot2: Elegant Graphics for Data Analysis. New York: *Springer-Verlag*.
- 813 Wright AE. 2010. The Lithistida: important sources of compounds useful in biomedical
814 research. *Current Opinion in Biotechnology* 21:801–807.
- 815 Xia X. 2013. DAMBE5: a comprehensive software package for data analysis in molecular
816 biology and evolution. *Molecular Biology and Evolution* 30:1720–1728.
- 817 Xia X., Xie Z., Salemi M., Chen L., Wang Y. 2003/1. An index of substitution saturation and
818 its application. *Molecular Phylogenetics and Evolution* 26:1–7.

819 FIGURES

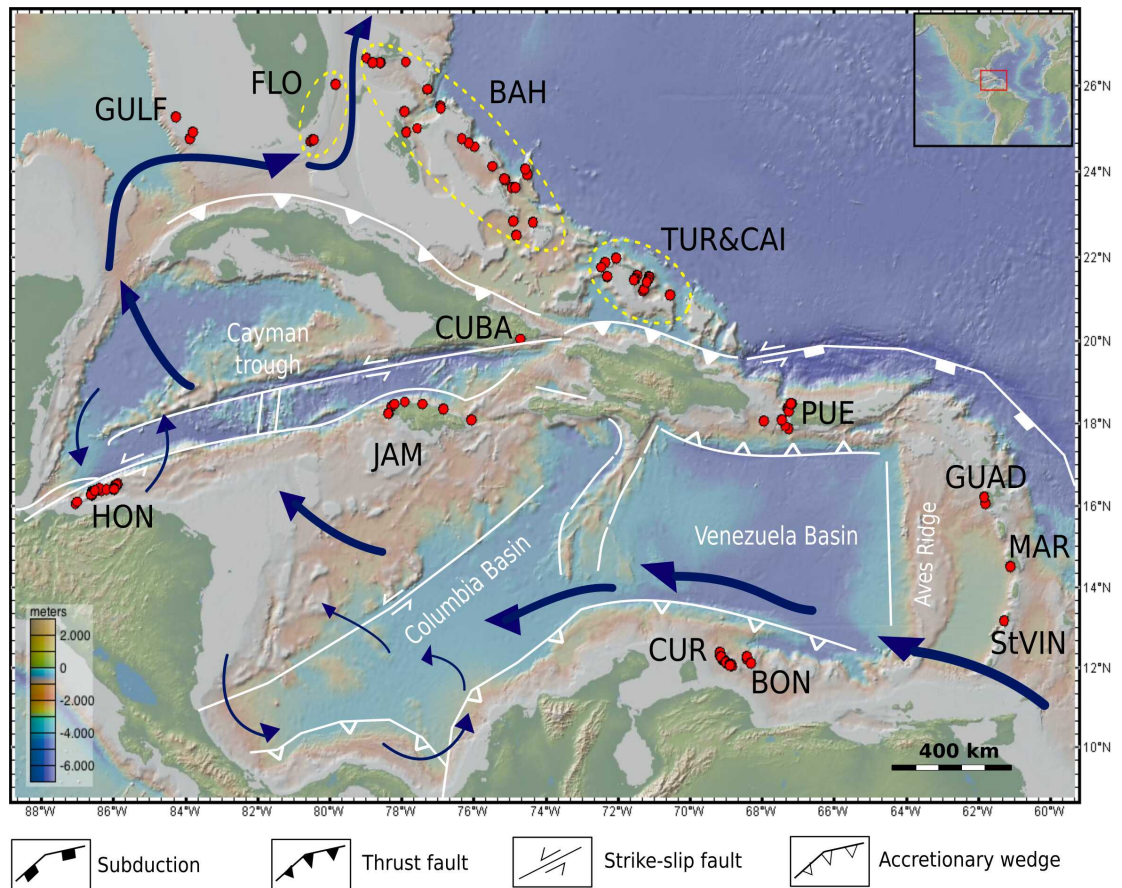


Figure 1. Distribution map of investigated HBOI and other desma-bearing tetractinellids and Vetulinidae from the TWA. Abbreviations correspond to the different locations (CUR=Curaçao, BON=Bonaire, StVIN=St. Vincent, MAR=Martinique, GUAD=Guadaloupe, PUE=Puerto Rico, JAM=Jamaica, HON=Honduras, TUR and CAI=Turks and Caicos, BAH=Bahamas, FLO=Florida). Tectonic settings are schematically indicated (white lines) (Giunta 2011). Main water currents (dark blue arrows) follow Miloslavich et al. (2010). Map generated with GeoMapApp 3.6.3 (<http://www.geomapapp.org>, Ryan et al., 2009).

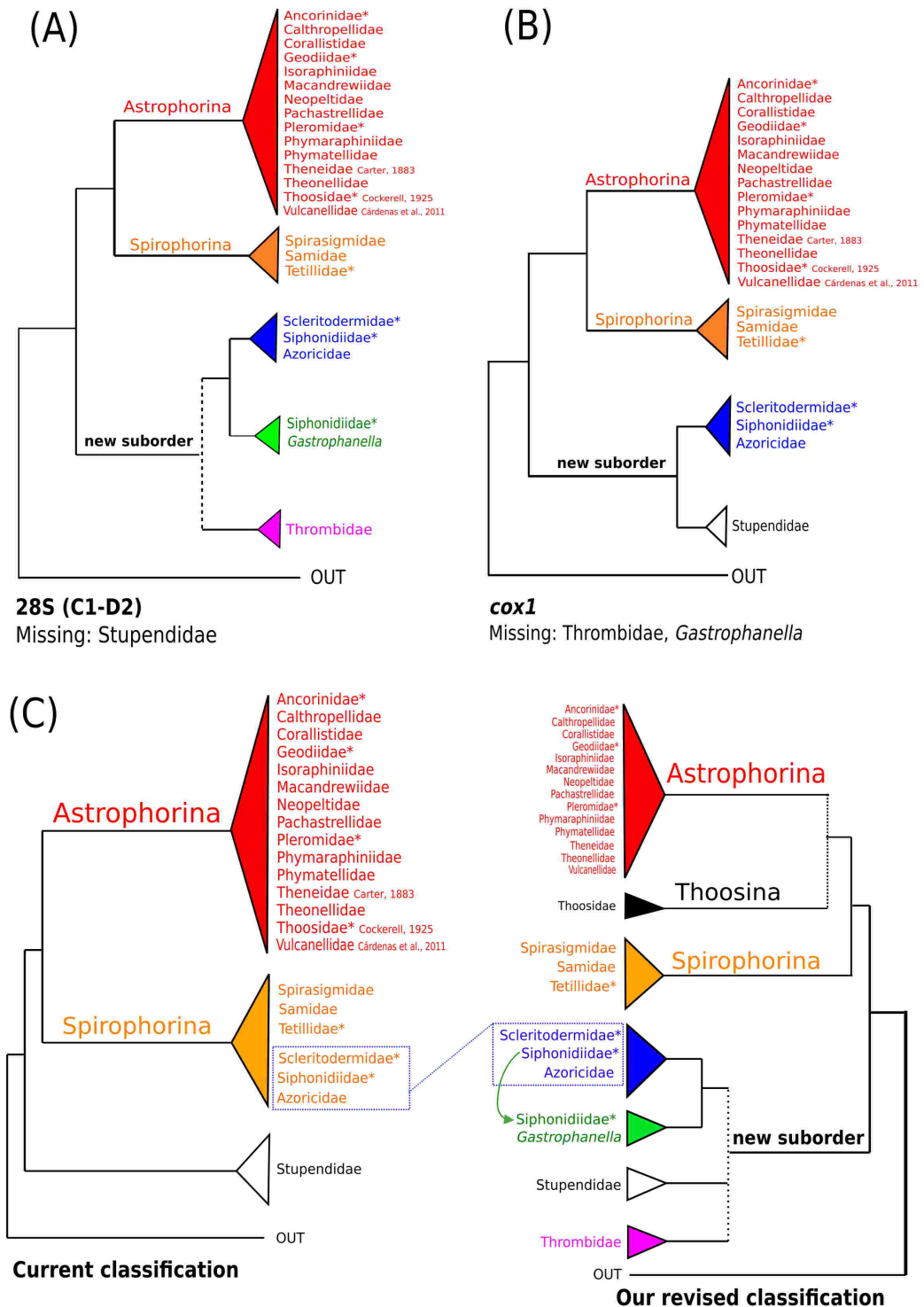
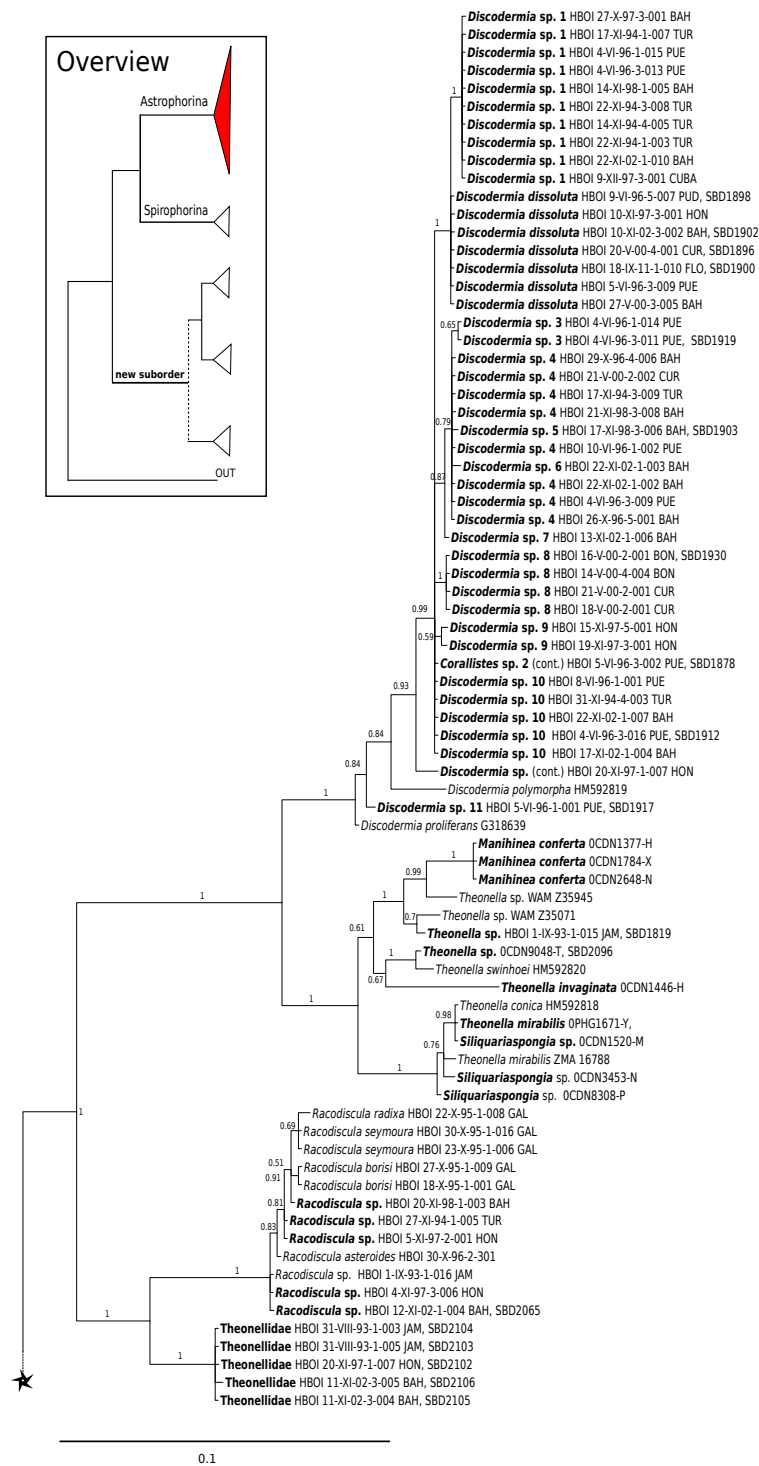
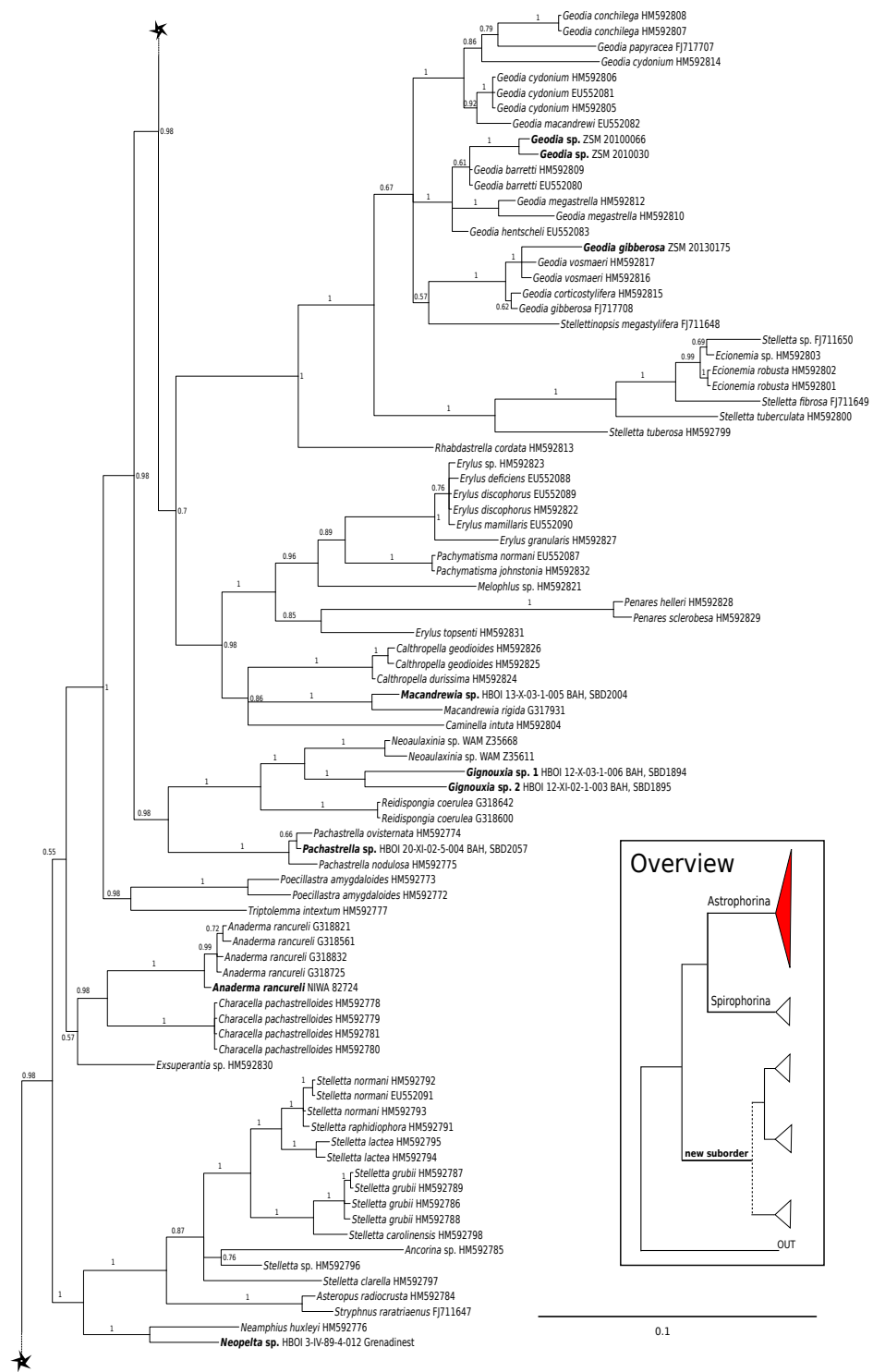
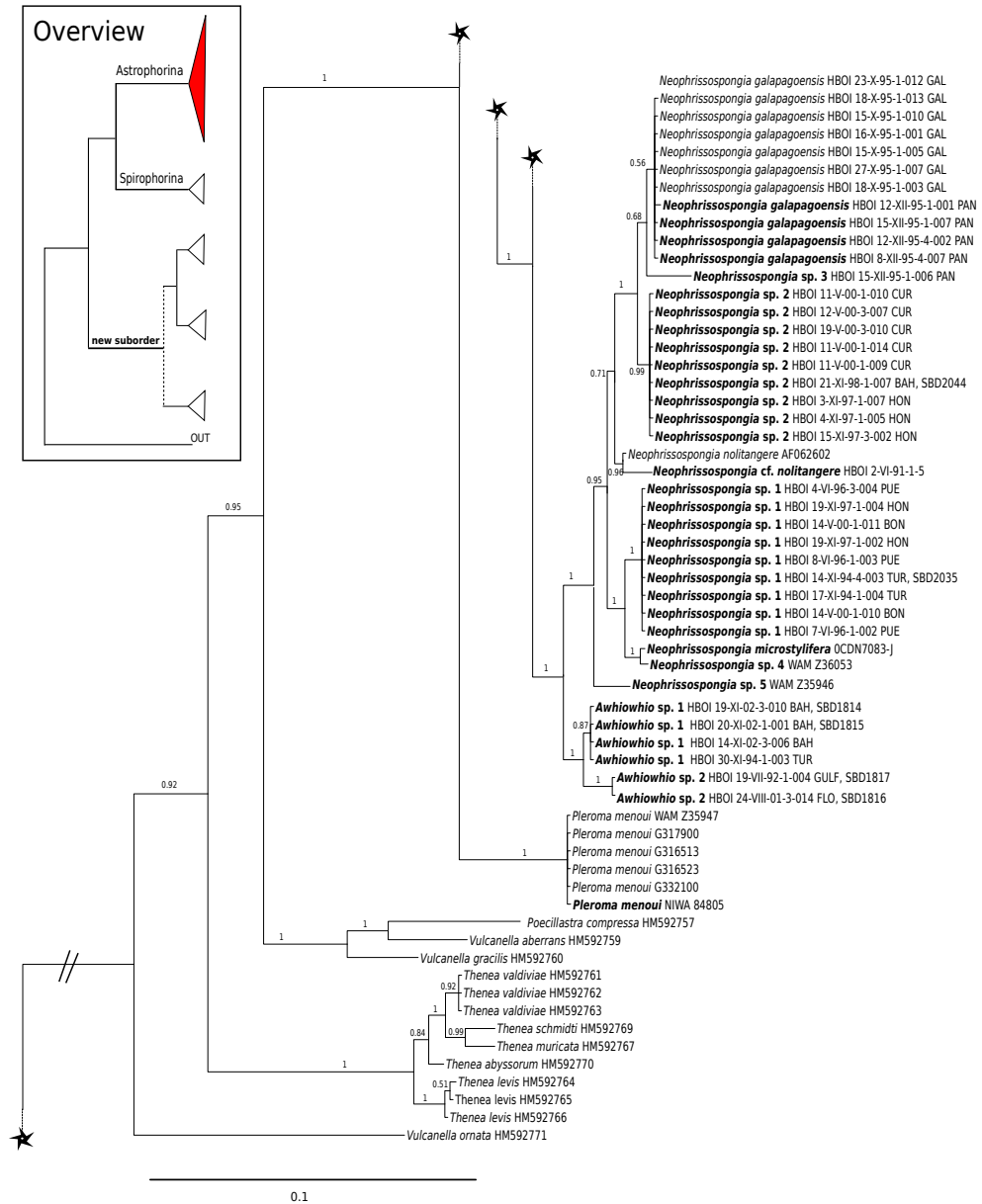
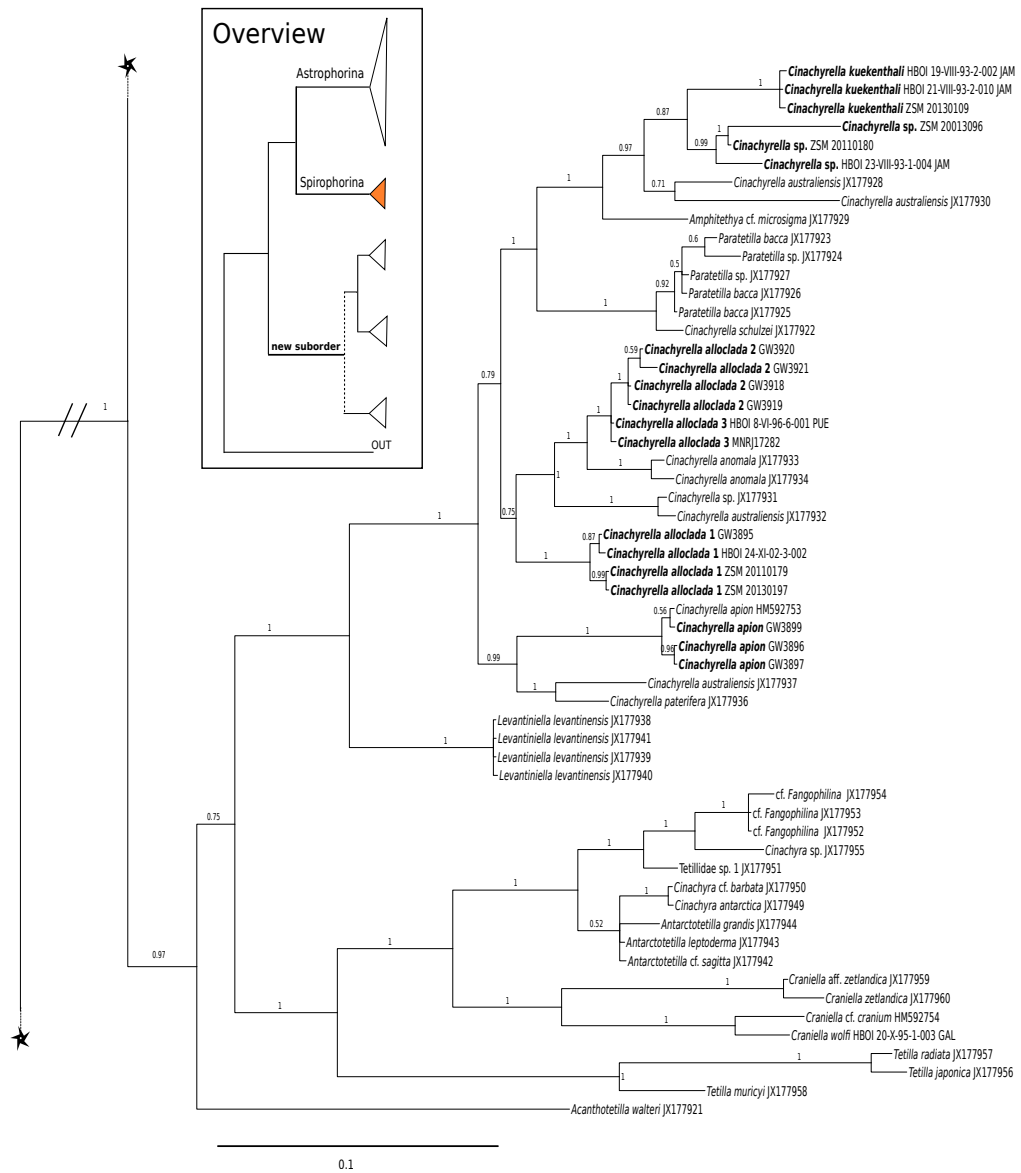


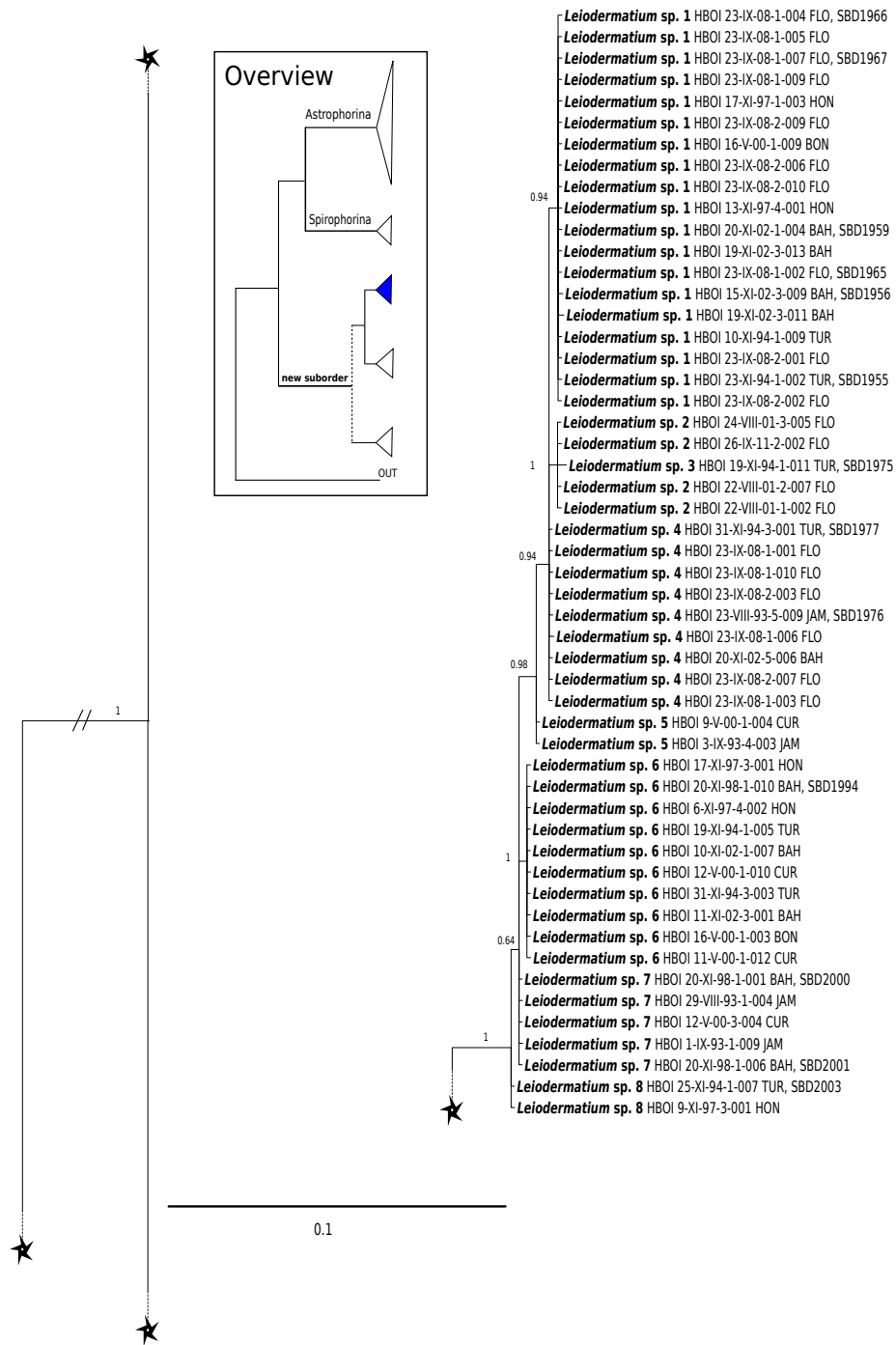
Figure 2. Schematic summary cladograms obtained from the 28S and *cox1* phylogenies indicating the higher-taxa relationships within the order Tetractinellida. (A) 28S (B) *cox1* summary tree with the suborders Astrophorina (red), Spirophorina (orange) and a new suborder (blue, green, pink and light gray) including all rhizoclone desma-bearing families and the family Thrombidae and Stupendidae. Stars behind family names indicate their proposed polyphyly. Dashed lines indicate the uncertainties of not supported topologies. (C) Comparison of current and revised classification including the proposed new suborder Thoosina from Carballo et al.











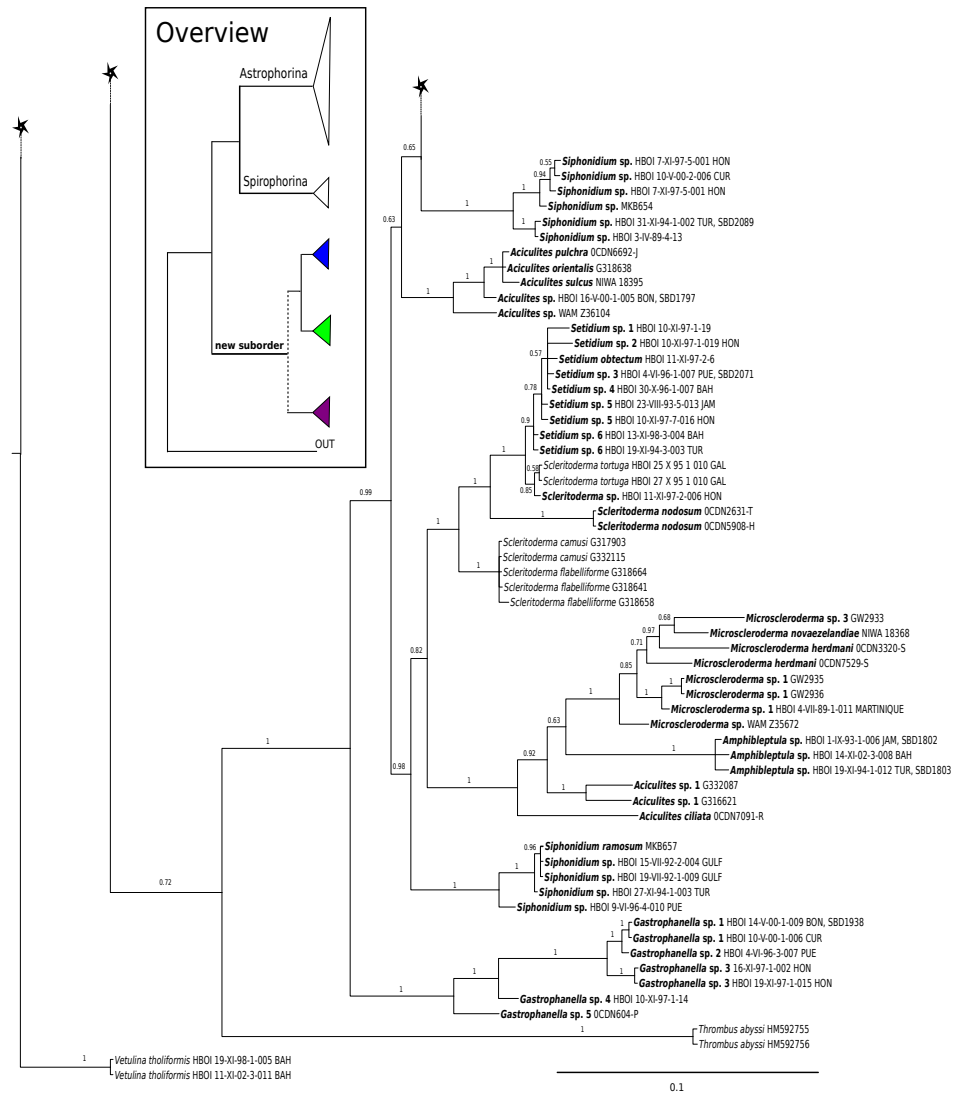
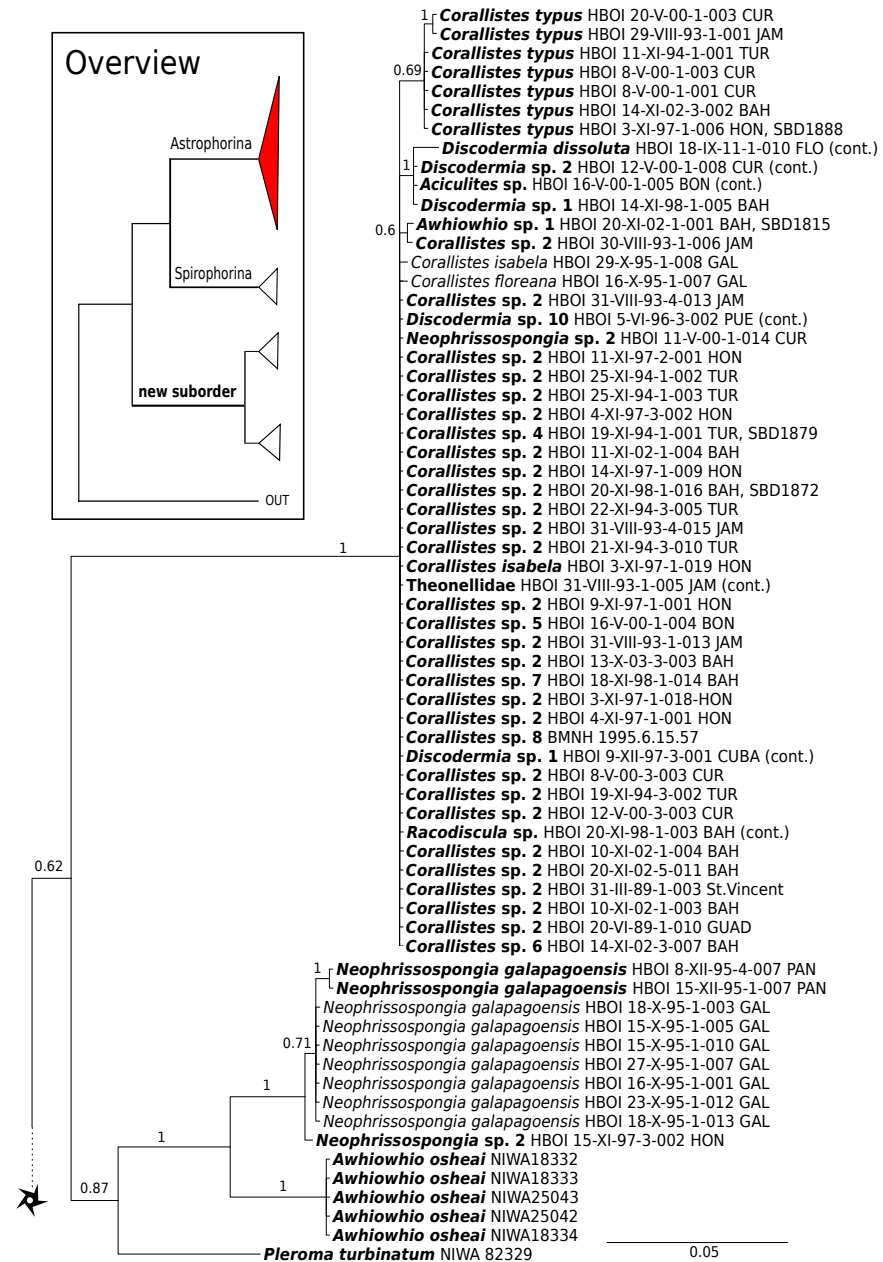
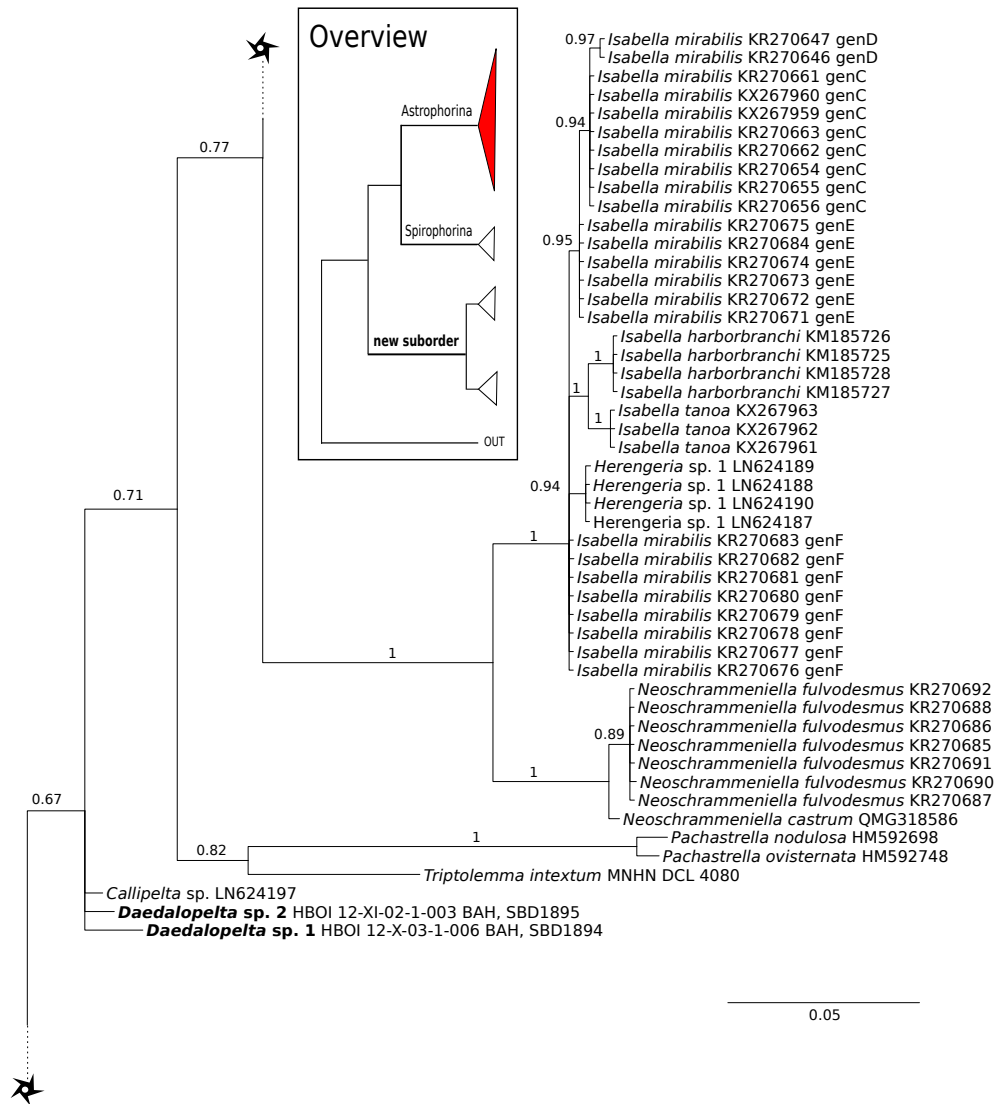
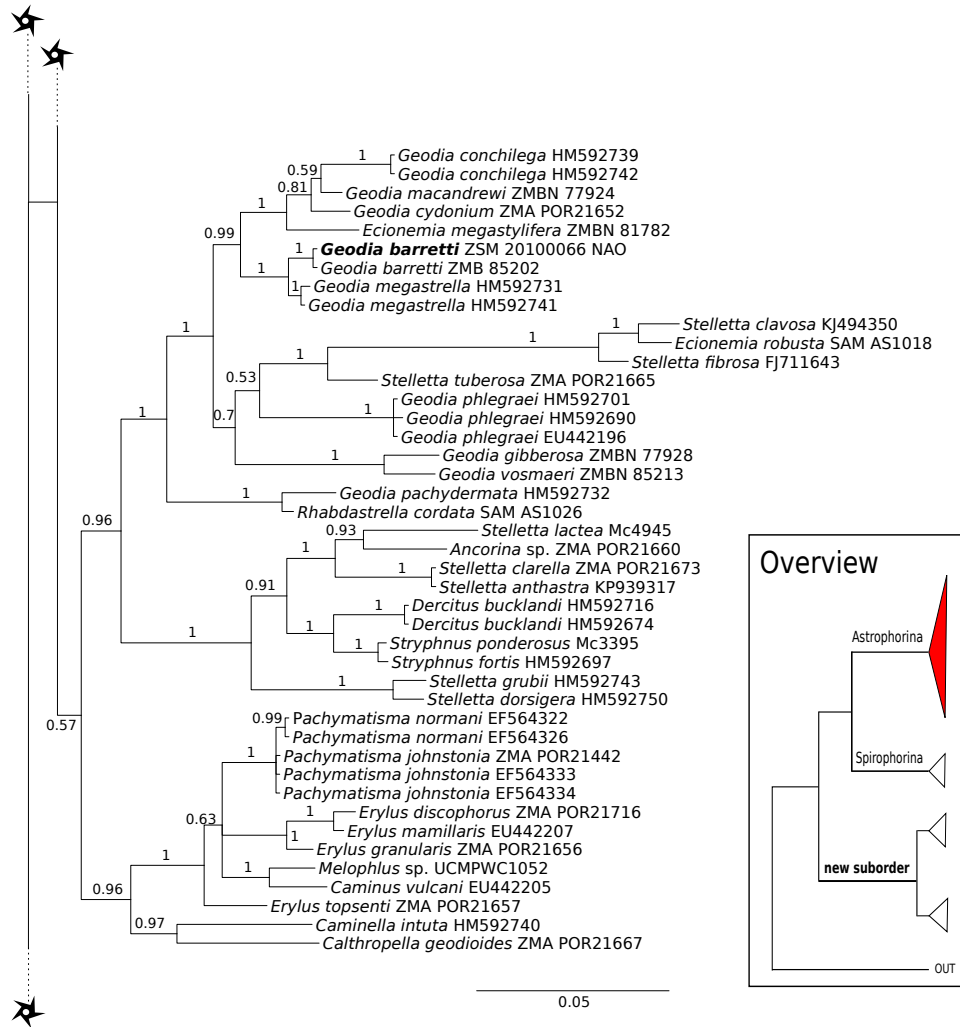
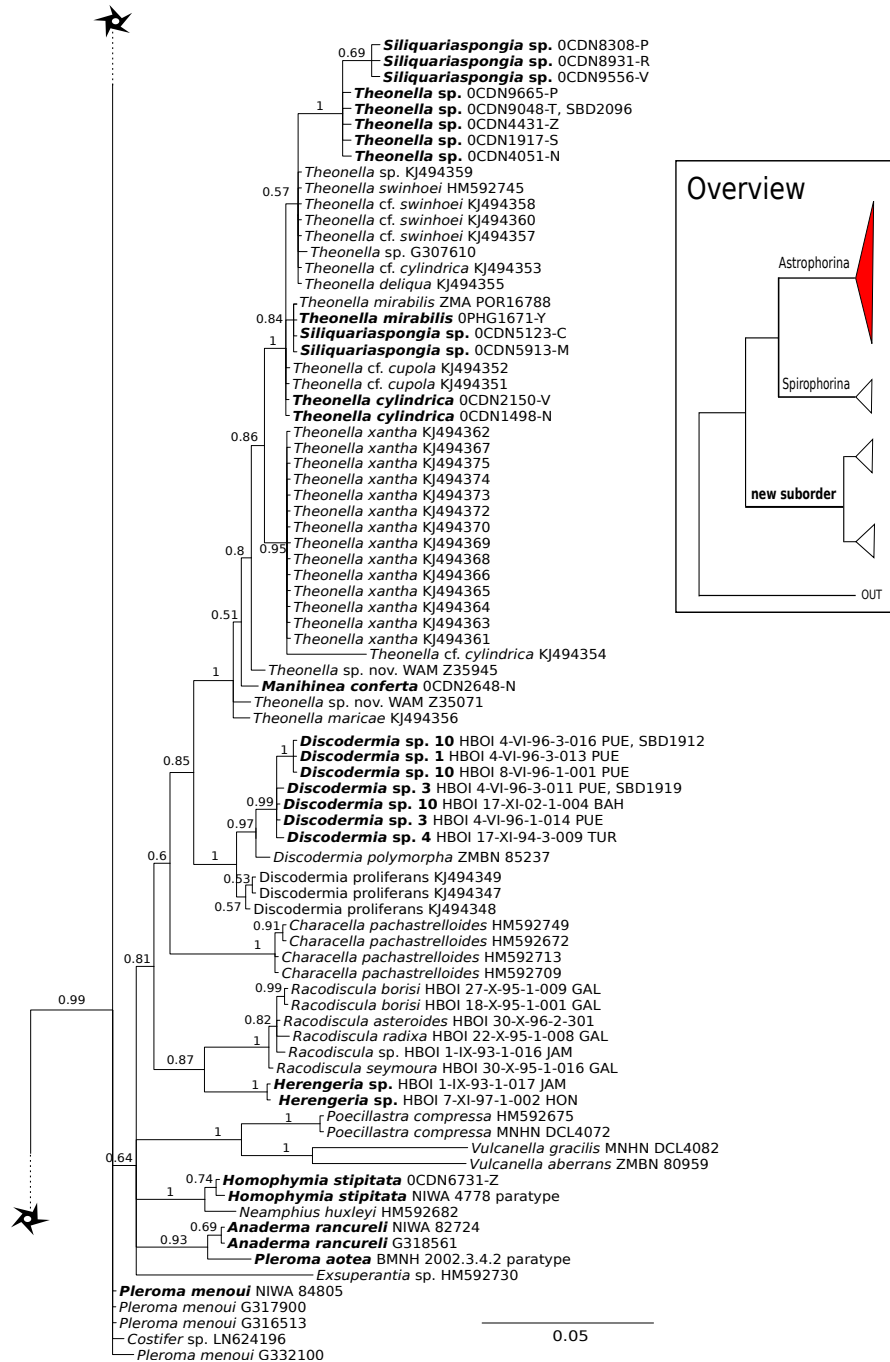


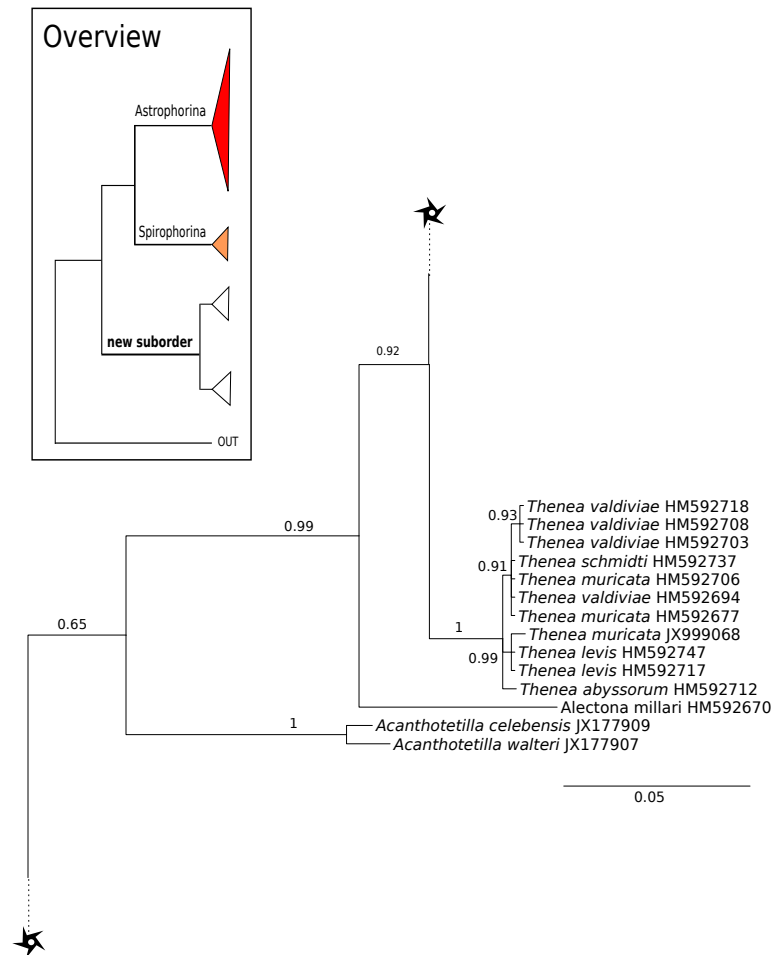
Figure 3. Bayesian Inference phylogeny of Tetractinellida based on 28S (C1-D2). Posterior probability (PP) values are provided above or below branches. Self-generated sequences are in bold. Numbers behind taxon names are either voucher numbers or GenBank/ENA accession numbers. Three letter code behind voucher numbers corresponds to the different locations (CUR=Curaçao, BON=Bonaire, StVIN=St. Vincent, MAR=Martinique, GUAD=Guadaloupe, PUE=Puerto Rico, JAM=Jamaica, HON=Honduras, TUR & CAI=Turks & Caicos, BAH=Bahamas, FLO=Florida). Taxa where the morphology was investigated are indicated with

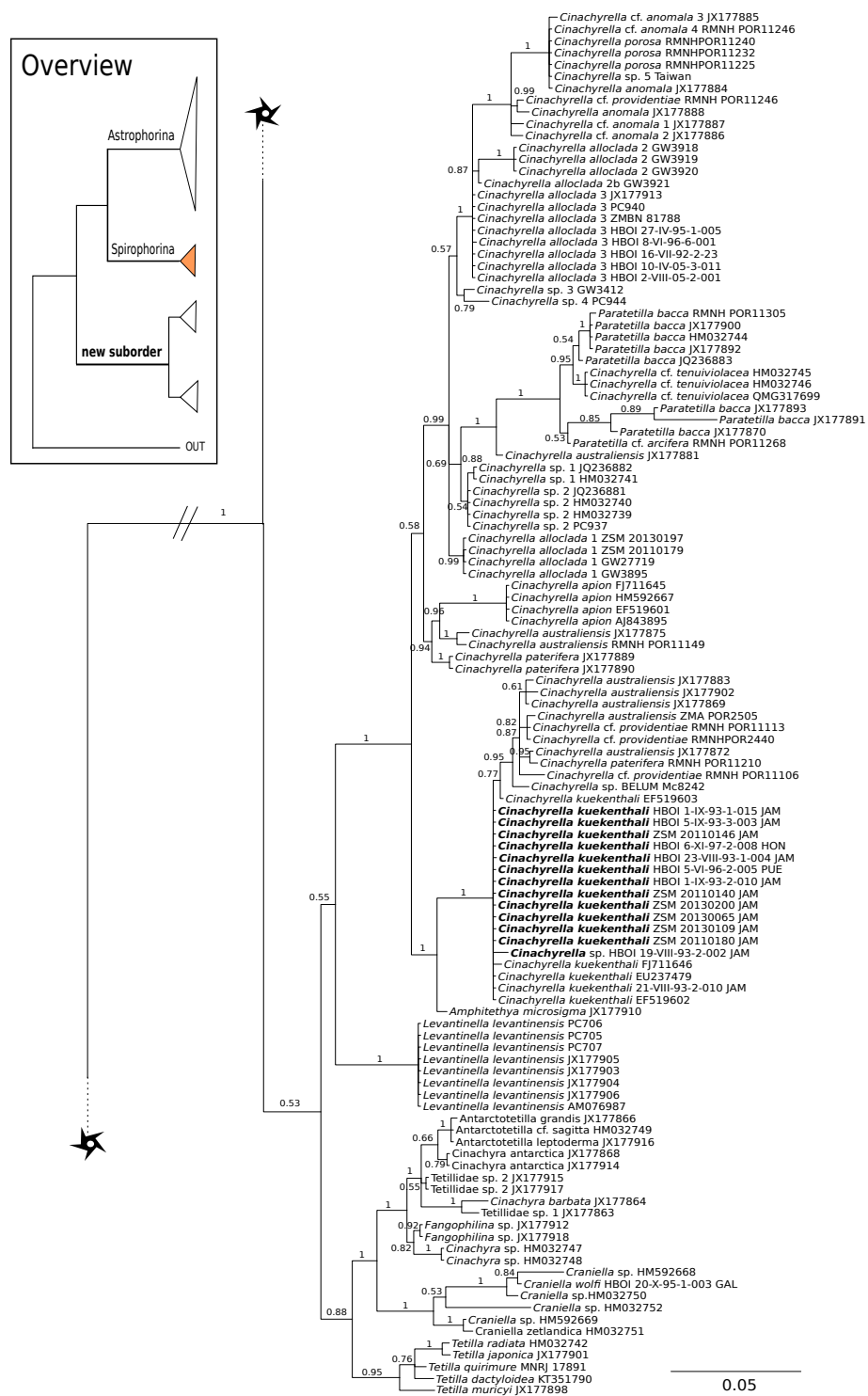












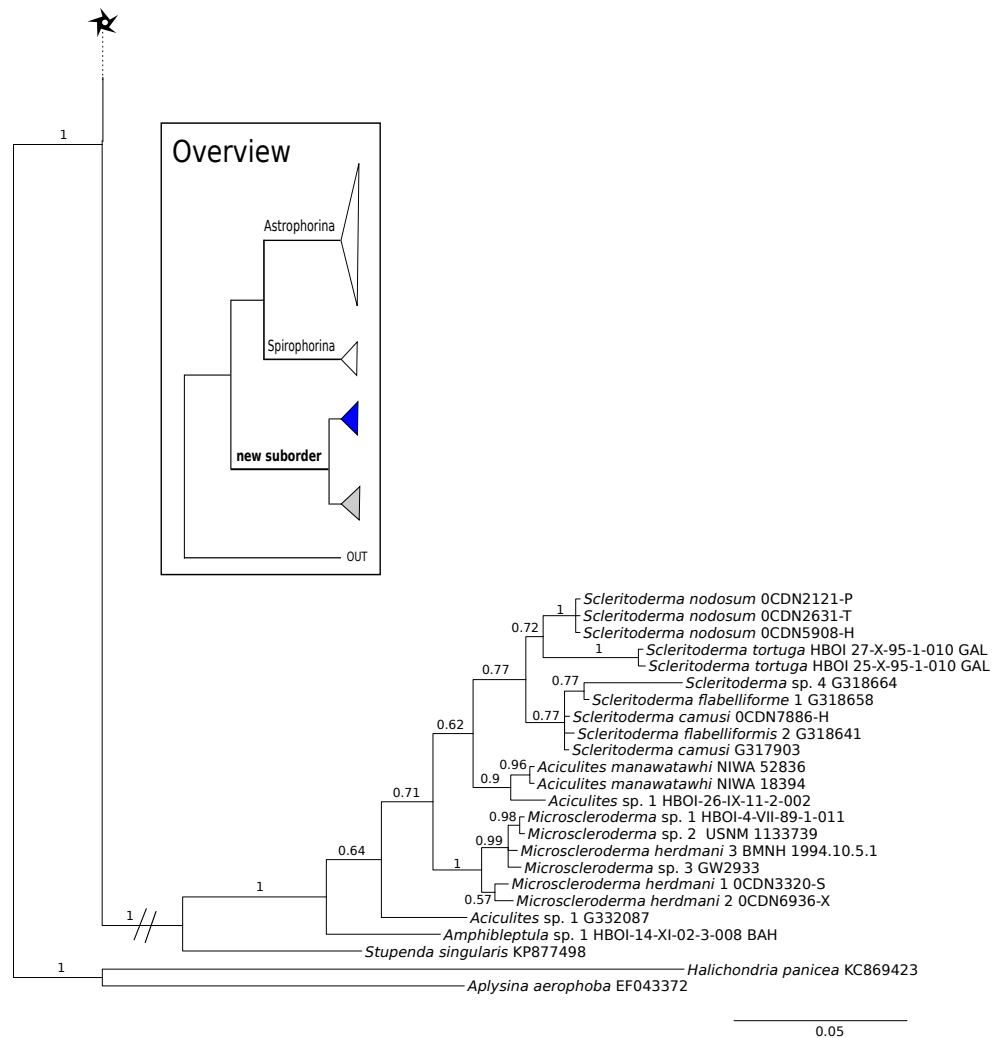


Figure 4. Bayesian Inference phylogeny of Tetractinellida based on *cox1*. Posterior probability (PP) values are provided above or below branches. Self-generated sequences are in bold. Numbers behind taxon names are either voucher numbers or GenBank/ENA accession numbers. Three letter code behind voucher numbers corresponds to the different locations (CUR=Curaçao, BON=Bonaire, StVIN=St. Vincent, MAR=Martinique, GUAD=Guadaloupe, PUE=Puerto Rico, JAM=Jamaica, HON=Honduras, TUR & CAI=Turks & Caicos, BAH=Bahamas, FLO=Florida). Taxa where the morphology was investigated are indicated with their corresponding SBD.

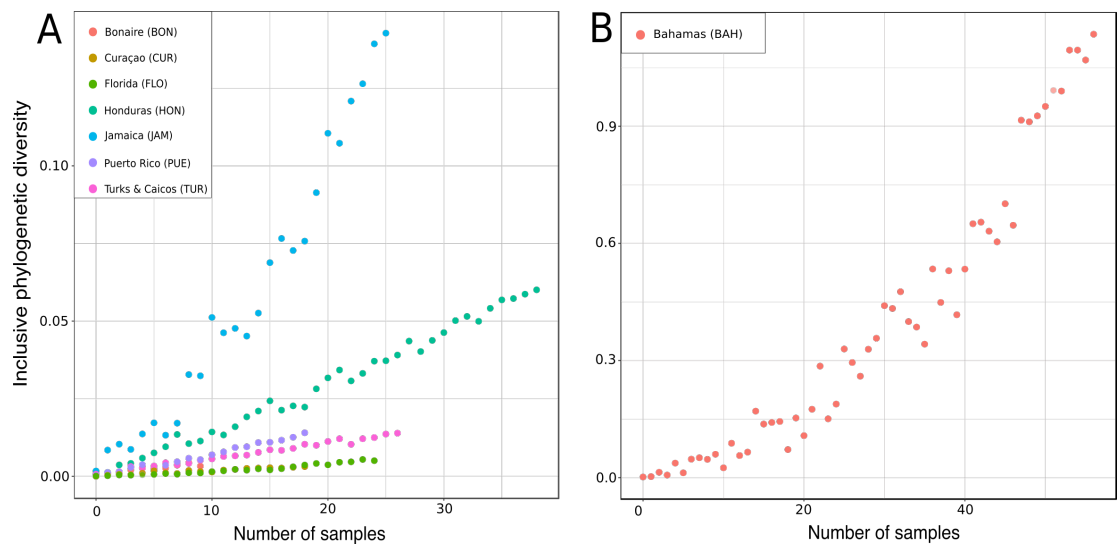


Figure 5. Rarified inclusive phylogenetic diversity (PD_I) curves per marine regions analyzed. For a better visualization the PDI for the Bahamas are illustrated separately (B) due to their larger number of samples.

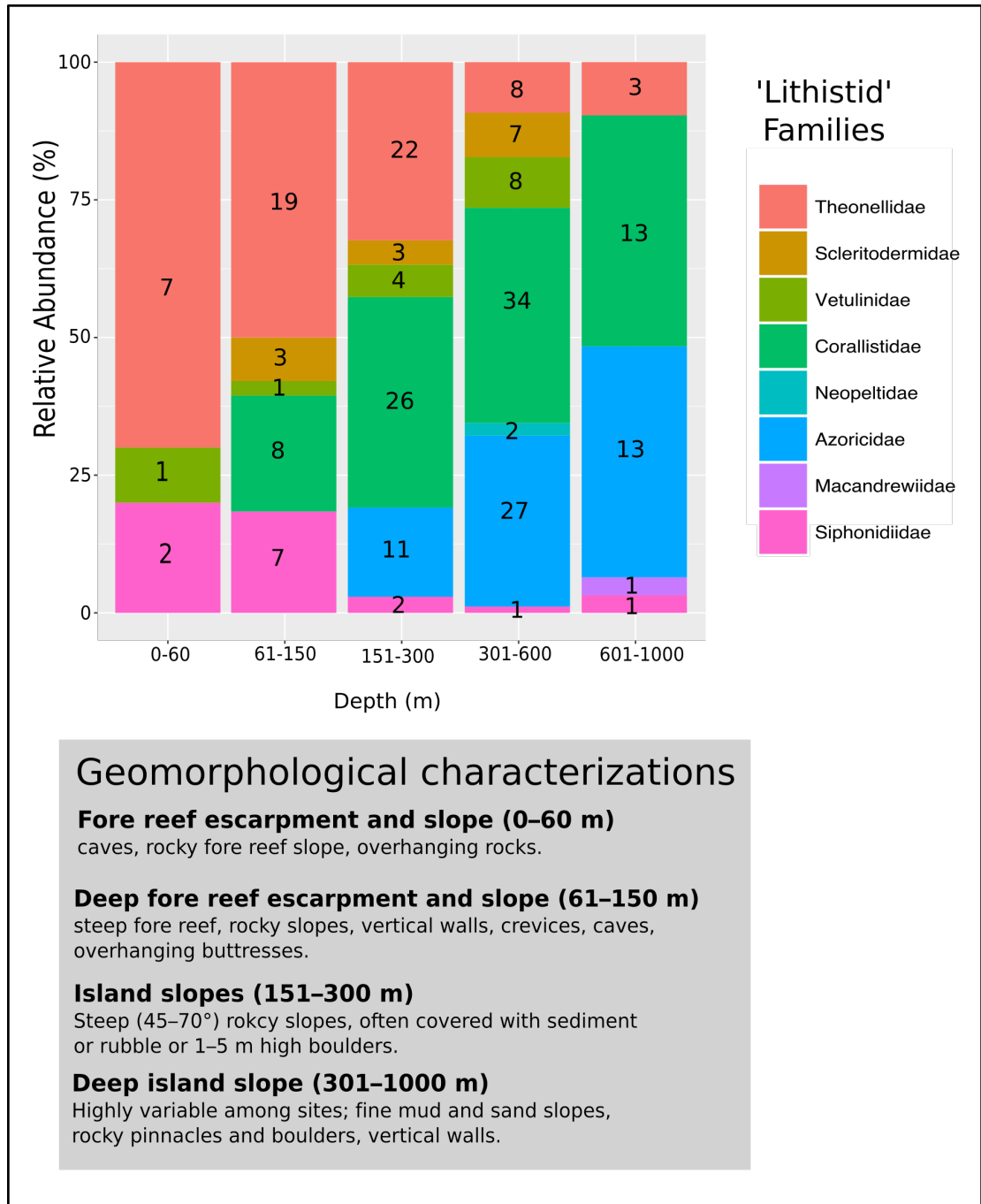


Figure 6. Bathymetric distribution and relative abundance of TWA desma-bearing demosponges based on 234 samples of eight families. Numbers in each bar represent the number of samples investigated. The following genera for each family were included: *Leiodermatium* (Azoricidae); *Corallistes*, *Herengeria*, *Neophrissospongia* and *Awhiowhio* (Corallistidae); *Macandrewia* (Macandrewiidae); *Daedalopelta* and *Neopelta* (Neopeltidae); *Aciculites*, *Amphibleptula*, *Microscleroderma*, *Scleritoderma* and *Setidium* (Scleritodermidae); *Gastrophanella* and *Siphonidium* (Siphonidiidae); *Discodermia*, *Racodiscula* and *Theonella* (Theonellidae); *Vetulina* (Vetulinidae). Geomorphological characterizations of depth zones are given below the graph and follows Pomponi et al. 2001 and Reed and Pomponi (1997; 2001).