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4 Phylogenetic relationships of the conoidean snails  
5 (Gastropoda: Caenogastropoda) based on  
6 mitochondrial genomes

7

8 Juan E. Uribe<sup>1,2,3</sup>; Rafael Zardoya<sup>1</sup>; Nicolas Puillandre<sup>4\*</sup>

9 <sup>1</sup> Dept. Biodiversity and Evolutionary Biology, Museo Nacional de Ciencias Naturales  
10 (MNCN-CSIC), José Gutiérrez Abascal 2, 28006, Madrid, Spain.

11 <sup>2</sup> Smithsonian Institution, National Museum of Natural History, Department of  
12 Invertebrate Zoology, 10th St. & Constitution Ave. NW, 20560 -0163, Washington,  
13 D.C., USA.

14 <sup>3</sup> Grupo de Evolucion, Sistemática y Ecología Molecular, Universidad del Magdalena,  
15 Cl. 32 #22-08, Santa Marta, Colombia.

16 <sup>4</sup> Institut Systématique Evolution Biodiversité (ISYEB), Muséum national d'Histoire  
17 naturelle, CNRS, Sorbonne Université, EPHE, 57 rue Cuvier, CP 26, 75005 Paris,  
18 France.

19 \*Corresponding author ([nicolaspuillandre@gmail.com](mailto:nicolaspuillandre@gmail.com))

20 **Abstract**

21 With more than 5,000 species, Conoidea is one of the most diversified superfamilies of  
22 Gastropoda. Recently, the family-level classification of these venomous predator snails  
23 has undergone substantial changes, on the basis of a phylogenetic tree reconstructed  
24 combining partial mitochondrial and nuclear gene sequences, and up to 16 families are  
25 now recognized. However, phylogenetic relationships among these families remain  
26 largely unresolved. Here, we sequenced 20 complete or nearly complete mitochondrial  
27 (mt) genomes, which were combined with mt genomes available in GenBank to  
28 construct a dataset that included representatives of 80% of the known families, although  
29 for some we had only one species or genus as representative. Most of the sequenced  
30 conoidean mt genomes shared a constant genome organization, and observed  
31 rearrangements were limited exclusively to tRNA genes in a few lineages. Phylogenetic  
32 trees were reconstructed using probabilistic methods. Two main monophyletic groups,  
33 termed “Clade A” and “Clade B”, were recovered with strong support within a  
34 monophyletic Conoidea. Clade A (including families Clavatulidae, Horaiclavidae,  
35 Turridae *s.s.*, Terebridae, Drilliidae, Pseudomelatomidae, and Cochlespiridae) was  
36 composed of four main lineages, one of which was additionally supported by a  
37 rearrangement in the gene order. Clade B (including families Conidae, Borsoniidae,  
38 Clathurellidae, Mangeliidae, Raphitomidae, and Mitromorphidae) was composed of five  
39 main lineages. The reconstructed phylogeny rejected the monophyly of Clavatulidae,  
40 Horaiclavidae, Turridae, Pseudomelatomidae, and Conidae, indicating that several of  
41 the currently accepted families may be ill-defined. The reconstructed tree also revealed  
42 new phylogenetic positions for genera characterized as tentative (*Gemmuloborsonia*,  
43 *Lucerapex*, and *Leucosyrinx*), enigmatic (*Marshallena*) or challenging to place  
44 (*Fusiturris*), which will potentially impact the classification of the Conoidea.

## 46 1. Introduction

47 The Conoidea is the most diverse of the seven superfamilies included in the order  
48 Neogastropoda (Cunha et al., 2009; Osca et al., 2015; Bouchet et al., 2017). The  
49 conoidean snails are characterized by a venom gland, which allow their species to  
50 actively capture preys or deter predators, usually with the aid of a specialized radular  
51 system (Dutertre et al., 2014). These evolutionary novelties are hypothesized to have  
52 favored the extreme diversification of the group, which has successfully colonized the  
53 marine realm from polar regions to tropical latitudes, and from the shore to the very  
54 deep sea (Kantor et al., 2016). Although still debated, the origin of the group could be  
55 dated in the Early Cretaceous, Berriasian age, about 139.8-145.0 million years ago  
56 (Murphy and Rodda, 1960; Kotetishvili, 1989), and they diversified since into 16 extant  
57 recognized families, 382 accepted genera and more than 5,000 extant recognized  
58 species (WoRMS; Bouchet and Gofas, 2015). Shell collectors count the Conoidea, and  
59 more precisely the family Conidae (cone snails) among their favorites for their beautiful  
60 and colored shells whereas toxicologists study their venom since the late 1970's for  
61 their potential therapeutic applications (Prashanth et al., 2014).

62 The past century classifications of Conoidea were based solely on shell, radula and  
63 anatomical characters (Powell, 1966; McLean, 1971; Taylor et al., 1993; see Puillandre  
64 et al. 2008 for a historical review). More recently, molecular data have helped clarifying  
65 the phylogenetic relationships within Conoidea, although most of the work focused  
66 primarily on cone snails (Puillandre et al., 2011). Puillandre et al. (2008) performed the  
67 first thorough molecular study on Conoidea based on partial mitochondrial (mt) and  
68 nuclear gene sequences and including a fair representation of the main clades at the  
69 family-level, later completed by Puillandre et al. (2011); see a summary of the resulting  
70 phylogenetic hypotheses in Fig. 1. The conclusions of the two studies emphasized the

71 high diversity of deep lineages, recognized at the family level, and lead to the current  
72 classification in 16 families (Bouchet et al., 2011): Borsoniidae, Bouchetispiridae,  
73 Clathurellidae, Clavatulidae, Cochlespiridae, Conidae, Conorbidae, Drilliidae,  
74 Horaiclavidae, Mangeliidae, Mitromorphidae, Pseudomelatomidae, Raphitomidae,  
75 Strictispiridae, Terebridae, and Turridae. However, despite these seminal works,  
76 phylogenetic relationships among these families remain largely unresolved, and the  
77 monophyly of some of them is controversial.

78 Mitochondrial genomes have been used with success to reconstruct phylogenetic  
79 relationships in different molluscan groups, including Polyplacophora (Irisarri et al.,  
80 2014), Cephalopoda (Kawashima et al., 2013; Strugnell et al., 2017; Uribe and Zardoya,  
81 2017), and Bivalvia (Glöckner et al., 2013; Williams et al., 2017). Within Gastropoda,  
82 mt genomes have been used to reconstruct the phylogenetic relationships within the  
83 main clades: Neritimorpha (Uribe et al., 2016a), Vetigastropoda (Lee et al., 2016; Uribe  
84 et al., 2016b; Uribe et al., 2017b), Heterobranchia (White et al., 2011; Sevigny et al.,  
85 2015), and Caenogastropoda (Cunha et al., 2009; Osca et al., 2015).

86 Within Caenogastropoda, phylogenetic inference based on mitogenomes has proven  
87 to be particularly effective at the subgeneric (Abalde et al., 2017a; Abalde et al., 2017b)  
88 and the generic (Uribe et al., 2017a; Wang et al., 2017) levels, showing less efficiency  
89 at more inclusive taxonomic levels (Cunha et al., 2009; Osca et al., 2015) mostly due to  
90 saturation and long branch attraction biases, but also in some instances associated to  
91 limited taxon sampling. As of January 2018, the mt genomes available in GenBank  
92 (<https://www.ncbi.nlm.nih.gov>) represented seven conoidean families: Conidae,  
93 Borsoniidae, Mangeliidae, Clathurellidae, Clavatulidae, Terebridae, and Turridae. These  
94 sequence data covered less than half of the currently recognized families within  
95 Conoidea, and therefore, our primary goal was to sequence additional mitogenomes in

96 order to increase the family coverage and better represent the diversity of the group. The  
97 new taxon sampling was aimed at improving resolution of phylogenetic relationships,  
98 and thus, providing a robust framework for further evolutionary studies of the group.

99

## 100 **2. Materials and methods**

### 101 *2.1. Samples and DNA extraction*

102 The list of samples analyzed in this study is provided in Table 1. All newly sequenced  
103 samples were collected during two expeditions of the Muséum National d'Histoire  
104 Naturelle (Paris), namely Atimo Vatae (Madagascar, 2011) and Papua Niugini (Papua  
105 New Guinea, 2012) (expeditions.mnhn.fr). Specimens out of the shell (Galindo et al.,  
106 2014) were stored in 99% ethanol. DNA was isolated from 30–60 mg of muscle from  
107 the foot following a standard phenol-chloroform extraction (Sambrook et al., 1989).

### 108 *2.2. PCR amplification and sequencing*

109 Fragments of the mt *cox1* gene were amplified by standard PCR (reaction conditions  
110 described in Uribe et al. 2017a) using universal primers (Folmer et al., 1994) and  
111 sequenced by the Sanger method. The new sequences were used to design specific  
112 primers (see the complete list in Suppl. Mat 1), which were combined with previously  
113 published *cox3* (forward), *rrnL* (forward and reverse), and *trnF* (reverse) primers (Uribe  
114 et al., 2017a) to amplify by long-PCR reactions the complete or nearly complete  
115 (without control region) mt genomes in several overlapping fragments (Table 1). The  
116 long-PCR reaction protocol and profiles are described by Uribe et al. (2017a).

117 The long-PCR products were purified by ethanol precipitation. The overlapping

118 fragments from the same mt genome were pooled together in equimolar concentrations  
119 and subjected to massive parallel sequencing. For each mt genome, a separate indexed  
120 library was constructed using the NEXTERA XT DNA library prep kit (Illumina, San  
121 Diego, CA, USA) and run in an Illumina MiSeq platform (v.2 chemistry; 2 x 150  
122 paired-end) at Sistemas Genómicos (Valencia, Spain). Only in one case (sample  
123 MNHN-IM-2013-9848, *Otitoma* sp), the Ion-Torrent platform at Service de  
124 Systématique Moléculaire (UMS 2700 CNRS-MNHN, Paris, France) was used to  
125 complete the corresponding mt genome.

### 126 2.3. Genome assembly and annotation

127 The reads corresponding to the different PCR-amplified mt genomes were sorted using  
128 the library indices. Assembly of the mt genomes was performed using the TRUFA  
129 webserver (Kornobis et al., 2015). Briefly, removal of adapters, read trimming, and  
130 quality check were performed using SeqPrep (John, 2011), FastQC v. 0.10.1 (Andrews,  
131 2010), and PRINSEQ v. 0.20.3 (Schmieder and Edwards, 2011) programs, respectively,  
132 with default parameters. The *de novo* assemblies were carried out using Trinity r2012–  
133 06–08 (Grabherr et al., 2011), and searching for contigs with a minimum length of 3 kb.  
134 To overlap the assembled contigs and measure the mean depth of coverage of each mt  
135 genome, we used the methods described in Uribe et al. (2017a).

136 The new mt genomes were annotated using the MITOS (Bernt et al., 2013)  
137 webserver. The annotated 13 mt protein-coding genes were further corroborated by  
138 identifying the corresponding open reading frames using the invertebrate mt genetic  
139 code. The two ribosomal RNA (rRNA) genes were identified by sequence comparison  
140 with other reported gastropod mt genomes, and assumed to extend to the boundaries of  
141 adjacent genes (Boore et al., 2005). The transfer RNA (tRNA) genes were further

142 identified with tRNAscan-SE 1.21 (Schattner et al., 2005), which infers cloverleaf  
143 secondary structures (with a few exceptions that were determined manually).

#### 144 2.4. Sequence alignment

145 The 13 protein coding and two rRNA genes of the complete or nearly complete mt  
146 genomes were aligned with orthologous genes of conoidean mt genomes available in  
147 GenBank (Table 1). Mitogenomes from closely related neogastropod groups (Cunha et  
148 al., 2009; Osca et al., 2015) were downloaded from GenBank and used as outgroups:  
149 *Amalda northlandica* (Olivoidea), *Babylonia areolata* (Muricoidea: Babyloniidae),  
150 *Rapana venosa* (Muricoidea: Muricidae), *Columbella adansoni* (Buccinoidea:  
151 Columbellidae), *Nassarius reticulatus* (Buccinoidea: Nassariidae), and *Galeodea*  
152 *echinophora* (Tonnoidea). Two concatenated matrices were constructed, one with  
153 protein coding plus rRNA genes at the nucleotide level (NT) and the other with protein  
154 coding genes at the amino acid level (AA). In order to construct these datasets, the  
155 nucleotide sequences of each of the protein coding and rRNA genes were aligned  
156 separately. The alignment of the nucleotide sequences of the protein coding genes was  
157 guided by the alignment of the deduced amino acid sequences in Translator X (Abascal  
158 et al., 2010) using MAFFT v5 (Katoh et al., 2005). The nucleotide sequences of each of  
159 the rRNA genes were aligned using MAFFT v7 server (Katoh et al., 2017) with default  
160 parameters. All poorly aligned sites were removed using GBlocks, v.0.91b (Castresana,  
161 2000) with the following settings: minimum sequence for flanking positions: 85%;  
162 maximum contiguous non-conserved positions: 8; minimum block length: 10; gaps in  
163 final blocks: no.

#### 164 2.5. Phylogenetic analyses



165 Phylogenetic relationships within superfamily Conoidea were inferred using  
166 maximum likelihood (ML; Felsenstein, 1981) and Bayesian inference (BI; Huelsenbeck  
167 and Ronquist, 2001). The phylogenetic analyses of the NT matrix were conducted using  
168 IQ-TREE v1.6.1 (Nguyen et al., 2014) for ML and MrBayes v3.1.2 (Ronquist and  
169 Huelsenbeck, 2003) for BI. The unpartitioned best-fit models of nucleotide substitution  
170 were identified using IQ-TREE Model Selection (Trifinopoulos et al., 2016) using +R  
171 option (FreeRate model) that generalizes the +G model by relaxing the assumption of  
172 Gamma-distributed rates. ML searches were run using a combination of rapid hill-  
173 climbing approaches and the stochastic perturbation method with 1,000 ultrafast  
174 bootstraps (UFB). The UFB values  $< 70\%$ , between 70-94%, and  $\geq 95\%$  were  
175 considered to indicate non-significant, moderate, and high statistical support,  
176 respectively (Minh et al., 2013). The MrBayes analysis was run with four simultaneous  
177 Markov chains for six million generations, sampling every 1,000 generations, and  
178 discarding the first 25% generations as burn-in (as judged by plots of ML scores and  
179 low SD of split frequencies) to prevent sampling before reaching stationarity. Two  
180 independent runs were performed to increase the chance of adequate mixing of the  
181 Markov chains and of detecting failure to converge. Node support in the BI analysis was  
182 assessed based on Bayesian Posterior Probabilities (BPP); values  $< 0.90$ , between 0.90–  
183 0.94, and  $\geq 0.95$  were considered to indicate non-significant, moderate, and high  
184 statistical support, respectively.

185 Additionally, a BI analysis was conducted with PhyloBayes (Lartillot et al., 2013)  
186 using the AA matrix, with two independent MCMC chains until convergence, sampling  
187 every cycle, and without constant sites (`-dc-` option) using the site-heterogeneous  
188 mixture CAT model (Lartillot and Philippe, 2004), which is helpful in ameliorating the  
189 well-known long branch attraction (LBA) bias (Felsenstein, 1978). Convergence of

190 analyses was checked *a posteriori* using the convergence tools implemented in  
191 PhyloBayes (maxdiff < 0.125, maximum discrepancy < 0.1 and effective size > 100).  
192 Node support was assessed based on BPP.

193

### 194 3. Results

195 Twenty complete or nearly complete (without control region) mt genomes were newly  
196 sequenced and assembled, representing ten conoidean families. The length, the presence  
197 of rearrangements, the GenBank accession number, the number of reads and the mean  
198 depth of coverage for each mt genome are provided in Table 1. Most mt genomes were  
199 amplified typically in two or three overlapping fragments (see primer information in  
200 Suppl. Mat. 1). The Illumina MiSeq sequencing generated a total of 1,305,206 reads.  
201 For one sample (*Otitoma* sp., MNHN-IM-2013-9848), the Illumina sequencing was  
202 complemented with IonTorrent technology, adding 12,689 reads to the final assembly  
203 for a total of 28,966 reads and a mean depth of coverage of 240x (Table 1). Of the  
204 remaining mt genomes, those of *Gemmuloborsonia moosai* and *Pinguiggemmula* sp.  
205 received the minimum (23,023 and 148x) and maximum (157,709 and 1,557x) reads  
206 and mean depth of coverage, respectively (Table 1).

#### 207 3.1. Mitogenomic organization

208 Most of the conoidean mitogenomes share the same gene order, where all genes are  
209 disposed in the major strand, with the exception of the *trnM*, *trnY*, *trnC*, *trnW* *trnQ*,  
210 *trnG*, *trnE* gene cluster (MYCWQGE) and the *trnT* gene (see Conoidea consensus order  
211 Fig. 2a). Three events of gene rearrangement were detected: (1) the mt genomes of  
212 *Clionella kraussii* and *Clavatula tripartita* (Clavatulidae), and of the two *Anguloclavus*

213 species (Horaiclavidae) showed a translocation of the *trnS* (*tca*) gene from the 3' end to  
214 the 5' end of the *cob* gene (in yellow, Fig. 2b); (2) the mt genome of *Gemmuloborsonia*  
215 *moosai* (Clavatulidae?) shows a translocation of the *trnF* gene from the 3' end of the  
216 *nad5* gene to the 5' end of the *nad4L* gene (Fig. 2c); and (3) the most conspicuous  
217 change occurred in the mt genome of *Cochlespira* sp. (Cochlespiridae) affecting the  
218 relative position and order of the *trnK*, *trnA*, *trnR*, *trnN*, and *trnI* (KARNI) gene cluster  
219 (Fig. 2d). The remaining features of each mt genome (stop and start codons, overlapping  
220 genes, intergenic non-coding regions and encoding strands) are provided in Suppl. Mat.  
221 2.

### 222 3.2. Phylogenetic relationships

223 The ML ( $-\ln L = 24.87648$ ; using GTR+R7+F model) and BI ( $-\ln L = 24.66123$  for run  
224 1;  $-\ln L = 24.66121$  for run 2; using GTR+I+G model) analyses using the NT dataset  
225 (13,014 positions; matrix available in Suppl. Mat. 3) provided almost identical  
226 topologies, which only differed in the relative position of *Fusiturris similis*  
227 (Clavatulidae) (see yellow inset in Fig. 3). The monophyly of the Conoidea was  
228 recovered with maximal support. The phylogenetic tree recognized two strongly  
229 supported main lineages, hereinafter referred to as Clade A and Clade B, respectively  
230 (Fig. 3), Clade A included the families Clavatulidae, Turridae *s.s.*, Terebridae,  
231 Horaiclavidae, Drilliidae, Pseudomelatomidae and Cochlespiridae (Fig. 3). The genera  
232 *Cochlespira* (Cochlespiridae) and *Marshallena* (tentatively assigned to Horaiclavidae in  
233 Bouchet et al., (2011)) grouped together with maximal statistical support and were sister  
234 to the rest of Clade A, which was composed of three moderately to highly supported  
235 main lineages: (1) two genera of Pseudomelatomidae (*Inquisitor* and *Otitoma*) were  
236 sister to a clade having the genus *Leucosyrinx* (tentatively assigned to

237 Pseudomelatomidae in Bouchet et al., (2011)) sister to the genus *Splendrillia*  
238 (Drilliidae). All these phylogenetic relationships received high statistical support; (2)  
239 the genera *Lucerapex* (tentatively attributed to Turridae in Bouchet et al., (2011)) and  
240 *Gemmuloborsonia* (tentatively attributed to Clavatulidae in Bouchet et al., (2011))  
241 formed a strongly supported clade, which was sister, with high BPP and moderate UFB  
242 support, to another moderately to highly supported clade having the genus *Oxymeris*  
243 (Terebridae) sister to genera *Iotyrris* and *Pinguigemmula* (Turridae *s.s.*); and (3) a clade  
244 with different topologies in the ML and BI analyses. The ML tree recovered with  
245 moderate support (73%) the genus *Anguloclavus* (Horaiclavidae) sister to a clade  
246 including *Fusiturris* (tentatively attributed to Clavatulidae in Bouchet et al. (2011)),  
247 which was sister to *Clionella* + *Clavatula* (both Clavatulidae). In contrast, the BI tree  
248 recovered with maximal support *Fusiturris* sister to *Anguloclavus* (see yellow inset in  
249 Fig. 3).

250 Clade B included the families Mangeliidae, Raphitomidae, Mitromorphidae,  
251 Conidae, Borsoniidae, and Clathurellidae (Fig. 3). Clade B could be further subdivided  
252 into four main lineages: (1) *Mitromorpha* (Mitromorphidae) was the single  
253 representative of this lineage; (2) Mangeliidae was sister to Raphitomidae with  
254 moderate to high statistical support; (3) *Glyphostoma* (Clathurellidae) was the single  
255 representative of this lineage; (4) the Borsoniidae were sister to genus *Profundiconus*  
256 (Conidae) with high statistical support; and (5) all analyzed Conidae but *Profundiconus*  
257 were grouped together with moderate to high statistical support (Fig. 3). The BI analysis  
258 supported with maximal BPP a sister group relationship between lineages 1 and 2 and  
259 between lineages 3 and 4+5 (Fig. 3).

260 The phylogeny reconstructed using the AA matrix (3,648 positions long) and the  
261 CAT-GTR model, converged at ten million of generations (maxdiff: 0.0666 and

262 meandiff: 0.0052). The reconstructed tree also recovered the monophyly of Conoidea as  
263 well as Clade A and Clade B (see Suppl. Mat. 4). Internal phylogenetic relationships  
264 within both clades were compatible with the NT-based tree but largely unresolved.

265

#### 266 4. Discussion

267 The primers anchoring in *cox3*, *rrnL*, and *trnF* genes (Uribe et al., 2017a) combined  
268 with the specific primers designed for *cox1* allowed consistent long PCR amplification  
269 of 20 mt genomes across the diversity of families within Conoidea. The number of reads  
270 and mean depth of coverage for each mt genome were high and at the same level of  
271 those previously reported for gastropod mitogenomes obtained with the same next  
272 generation sequencing technology (Abalde et al., 2017a; Abalde et al., 2017b; Uribe et  
273 al., 2017a). After adding the conoidean mitogenomes available in GenBank, our dataset  
274 included 13 out of the 16 recognized families of Conoidea (only the Bouchetispiridae,  
275 Conorbidae and Strictispiridae were missing). For the Borsoniidae, Clavatulidae,  
276 Horaiclavidae, Raphitomidae, Mangeliidae and Pseudomelatomidae, only one genus  
277 was previously available in GenBank, and our study extended the sampling to  
278 additional genera. For Terebridae, Drilliidae, Cochlespiridae, Clathurellidae, and  
279 Mitromorphidae, still only one genus is available for phylogenetic inference after the  
280 present work. Therefore, the monophyly of these families still requires further  
281 validation.

282 The gene order determined in most of the newly sequenced mt genomes conformed  
283 to the consensus genome organization of the Caenogastropoda (Osca et al., 2015),  
284 including previously reported Conoidea. Three alternative gene orders (two of them not  
285 previously reported) were found and were limited to translocations of tRNA genes, the

286 most common mobile elements in the mt genome (Boore, 1999). One rearrangement,  
287 involving the translocation of *trnS* (*tca*) to the 5' end of the *cob* gene is shared by  
288 *Fusiturris* (Cunha et al., 2009), *Clavatula*, *Clionella*, and *Anguloclavus*, suggesting that  
289 it occurred in the common ancestor of these genera and could be considered a molecular  
290 synapomorphy, which is in full agreement with the recovered (highly supported) clade  
291 in the phylogeny. The translocation of the *trnF* gene in the mt genome of  
292 *Gemmuloborsonia moosai* could be linked to the well-known instability associated to  
293 genes adjacent to control regions (Gissi et al., 2008; San Mauro et al., 2014). The  
294 KARNI cluster is generally conserved across distant classes of mollusks including  
295 Polyplacophora (Irisarri et al., 2014), Cephalopoda (Yokobori et al., 2004), and within  
296 the Gastropoda, in Neomphalina (Nakagawa et al., 2014), Vetigastropoda (Lee et al.,  
297 2016; Uribe et al., 2016b; Uribe et al., 2017b), Neritimorpha (Castro and Colgan, 2010;  
298 Arquez et al., 2014; Uribe et al., 2016a) and several Caenogastropoda (Osca et al.,  
299 2015). However, at least two gene rearrangements broke up this cluster in the mt  
300 genome order of *Cochlespira* sp.: first, either the whole cluster except the *trnI* gene or  
301 without both the *trnI* and *trnN* genes was translocated from the 3' end of the *cox3* gene  
302 to the 3' end of the *nad3* gene; then, the *trnN* gene was secondarily translocated to the  
303 5' end of the *trnK* gene. The alteration of the KARNI cluster has been also reported in  
304 several Gastropoda such as Turbinidae (*Lunella*, *Bolma*, and *Astralium*; Williams et al.,  
305 2014; Lee et al., 2016; Uribe et al., 2016b), Fissurellidae (*Diodora* and *Fissurella*; Uribe  
306 et al., 2016b), Haliotoidea (*Haliotis*; Maynard et al., 2005), and in other mollusks such  
307 as Chaetodermomorpha (*Scutopus*; Osca et al., 2014).

308 Thus far, phylogenetic analyses based on mt genomes focused primarily either on a  
309 single family within the Conoidea, the Conidae (Abalde et al., 2017a; Abalde et al.,  
310 2017b; Uribe et al., 2017a), or, on the contrary, at a more inclusive taxonomic level, on

311 the relative position of Conoidea within the Neogastropoda (Cunha et al., 2009). Our  
312 study is the first filling the gap in between by specifically targeting the relationships at  
313 the family level within the Conoidea. For that, we focused on ensuring broad taxon  
314 coverage of the diversity of the superfamily, and sequenced 20 new mt genomes,  
315 representing 10 different families, which combined with available mt genomes from  
316 GenBank, allowed us to cover 80% of the currently accepted families of Conoidea.  
317 However, for some of the families we had only one genus as representative, which  
318 impeded us to test their monophyly. This is not trivial as the conoidean families are  
319 highly diverse, and it is challenging the definition of all their members. In fact, in our  
320 phylogenetic analyses, some of the families with more than one genus resulted non-  
321 monophyletic. Therefore, the present phylogeny needs to be treated as ongoing and will  
322 need in the future to be completed with many more genera per family.

323 The monophyly of Conoidea was previously recovered using the concatenation of  
324 partial gene sequences with moderate to strong statistical support (Puillandre et al.,  
325 2008; 2011). Here, it is further confirmed with maximal support in both the NT  
326 (UFB=100 /BPP=1) and AA (BPP=1) phylogenetic analyses. Within the Conoidea, the  
327 two main clades, designated as Clade A and Clade B following Puillandre et al. (2008),  
328 and named Turroidea and Conoidea, respectively, by Tucker and Tenorio (2009), were  
329 also recovered here with strong (UFB=98/BPP=1 with the NT matrix and BPP=0.95  
330 with the AA matrix) and maximal support, respectively. In general, and not surprisingly  
331 as both studies are based on mitochondrial data only, our analyses are congruent with  
332 the phylogenetic relationships obtained within Clade A and Clade B by Puillandre et al.  
333 (2011), but clearly improving the statistical support of many of the internal nodes, and  
334 thus increasing the resolution of the overall tree. Most contradictions between our tree  
335 and published trees (Puillandre et al., 2008, 2011) concern previously unsupported

336 relationships; only the few supported contradictions between our and previous  
337 phylogenies are discussed in detail below.

338 Within Clade A, the genus *Cochlespira* (Cochlespiridae), here grouped with the  
339 newly sequenced taxa *Marshallena* in the NT-based phylogenetic analyses, is sister to  
340 the remaining Conoidea, a relationship already found by Puillandre et al. (2011).  
341 *Marshallena* is a deep-water genus from the Indo Pacific, initially assigned to  
342 Turriculinae and Cochlespirinae in older classifications (Powell, 1966; Taylor et al.,  
343 1993; Bouchet et al., 2005), and more recently tentatively included in Horaiclavidae  
344 (Bouchet et al., 2011). Our results favor the close relationship of *Marshallena* and  
345 Cochlespiridae. However, these two lineages show relatively long branches and their  
346 sister group relationship could be a LBA artifact (Felsenstein, 1978). In fact, this sister  
347 group relationship is not recovered in the AA-based phylogenetic analysis using the  
348 CAT model (site-heterogeneous mixture), which is recognized as a better model to  
349 ameliorate LBA artifacts (Lartillot et al., 2007; Philippe et al., 2009; Irisarri et al.,  
350 2014). Discerning whether *Cochlespira* (Cochlespiridae) and *Marshallena* are sister  
351 lineages or not awaits future phylogenetic studies with a denser sampling of the related  
352 taxa. With regards to the remaining taxa within Clade A, our results confirm the  
353 presence of three main lineages as already suggested in Puillandre et al. (2011):  
354 *Splendrillia* (Drilliidae) + Pseudomelatomidae, *Oxymeris* (Terebridae) + Turridae, and  
355 *Anguloclavus* (Horaiclavidae) + Clavatulidae (here further reinforced by the sharing of  
356 a specific mt genome rearrangement and by an amino acid insertion in the ATPase 6  
357 protein after position 42; see Suppl. Mat. 5). The first two clades were also strongly  
358 supported by the AA-based phylogenetic analysis. A sister group relationships of  
359 *Oxymeris* + Turridae and *Anguloclavus* + Clavatulidae to the exclusion of *Splendrillia* +  
360 Pseudomelatomidae received moderate to high support. In Bouchet et al. (2011), several



361 taxa within Clade A were tentatively attributed to a particular family, based on the  
362 molecular tree obtained by Puillandre et al. (2011). However, our results raise serious  
363 doubts about some of these assignments. According to our results, *Gemmuloborsonia* is  
364 not closely related to Clavatulidae, but more likely to Turridae and Terebridae;  
365 *Lucerapex* does not cluster with Turridae but it is closely related to *Gemmuloborsonia*;  
366 and *Leucosyrinx* is sister to *Splendrillia* (Drilliidae) with strong support, and thus  
367 cannot be assigned to Pseudomelatomidae without making this taxon paraphyletic.  
368 Finally, the relative phylogenetic position of *Fusiturris similis* could not be confidently  
369 resolved beyond determining its close affinity to *Anguloclavus* and Clavatulidae. This  
370 species was sister to *Clavatula* and *Clionella* in the ML analysis, which would confirm  
371 its assignment to Clavatulidae by Bouchet et al. (2011), but sister to *Anguloclavus*  
372 (Horaiclavidae) in both (NT and AA) BI analyses. Given the shell variability in both  
373 Clavatulidae and Horaiclavidae, it is difficult to determine to which family *Fusiturris*  
374 would be more similar. Furthermore, the radula of *Fusiturris* is unique in Conoidea  
375 (Powell, 1966), and does not match neither the ones of the Clavatulidae nor the one of  
376 the Horaiclavidae

377 Clade B showed poor resolution in the deeper nodes, similar to previously published  
378 phylogenetic analyses based on concatenated partial gene sequences (Puillandre et al.,  
379 2008; Puillandre et al., 2011). However, this lack of resolution was rather evident in the  
380 ML and AA BI analyses but not in the NT BI analysis, which rendered maximal support  
381 for a sister relationship between *Mitromorpha* (Mitromorphidae) and clade including  
382 Raphitomidae + Mangellidae and between *Glyphostoma* (Clathurellidae) and a clade  
383 including Borsoniidae and paraphyletic Conidae. Both *Mitromorpha* and *Glyphostoma*  
384 showed relatively long branches and were the only representatives of their  
385 corresponding families, so their relative phylogenetic positions should be interpreted

386 with caution and as tentative (the families Mitromorphidae, Raphitomidae, and  
387 Mangeliidae were also found closely related in Puillandre et al., 2011). The genus  
388 *Profundiconus* did not group with other Conidae but instead was placed as sister to  
389 Borsoniidae with high support in the NT (ML and BI) analyses, and as sister to  
390 Mitromorphidae with low support in the AA phylogenetic analysis. A recent  
391 phylogenetic analysis also based on mt genomes and focusing on the Conidae (Uribe et  
392 al., 2017a), recovered this family as a monophyletic group with high support, placing  
393 *Profundiconus* as sister to all remaining Conidae. However, the sampling of other  
394 conoidean families in this study was too limited to thoroughly test the monophyly of the  
395 cone snails and set definitively the controversy. In other studies (Puillandre et al., 2011;  
396 Kantor et al., 2012) with denser taxon sampling but based on partial gene sequences, the  
397 monophyly of the Conidae was not supported, except in the Bayesian tree of Puillandre  
398 et al., (2011), in which the posterior probability was 0.97. The genus *Profundiconus*  
399 includes species that live exclusively in the deep sea and show a typical cone-shape  
400 shell. Therefore, it was considered until now a true member of the Conidae. Pending  
401 further confirmation, our results would thus suggest that the cone shell shape, distinctive  
402 of the Conidae and used until now as a synapomorphy to recognize the members of  
403 these well-known seashell group, would be present in two divergent lineages, either  
404 evolving in the ancestor of the Conidae + Borsoniidae clade, and then lost secondarily  
405 in the Borsoniidae, or appearing twice independently during the evolutionary history of  
406 Conoidea. Discerning between these alternative hypotheses requires a denser taxon  
407 sampling, especially for the Borsoniidae, whose monophyly, here highly supported, was  
408 actually not supported in Puillandre et al. (2011).

409

## 410 **5. Conclusions**

411 With mitogenomes available for 80% of the valid families of Conoidea, we proposed  
412 here the most complete and resolved phylogenetic tree for the group at the family level  
413 to date. However, several of the families were represented by a single genus and others  
414 resulted non-monophyletic. Hence, the need of completing the present phylogeny with a  
415 more thorough sampling at the genus level in the future. Most of the phylogenetic  
416 relationships recovered here are congruent with previously published hypotheses, and  
417 received stronger statistical support. However, the relative phylogenetic position of  
418 *Fusiturris* with regards to *Anguloclavus* (Horaicalvidae) and Clavatulidae awaits final  
419 resolution. Additionally, striking results further emerged such as e.g., the potential close  
420 relationship of the *Cochlespira* and *Marshallena*, *Splendrillia* and *Leucosyrinx*,  
421 *Gemmuloborsonia* and *Lucerapex*, and the non-monophyly of the cone snails due to the  
422 sister group relationship of *Profundiconus* and Borsoniidae. The sequencing of mt  
423 genomes, if not resolving the entire conoidean tree, helps providing a tentative  
424 backbone, which needs to be further confirmed and resolved using nuclear sequence  
425 data. In the past, nuclear genes have been difficult to amplify and sequence compare to  
426 mtDNA but this is drastically changing in recent years with new available technology  
427 such as exon-capture techniques (Bi et al., 2012; Hugall et al., 2015; Bragg et al., 2016),  
428 which are particularly promising for non-model systems and broad divergences. The  
429 increase in sequence data needs to be accompanied in parallel by a denser taxonomic  
430 coverage. This later issue is not the least: obtaining representatives of all the known  
431 conoidean families (and of sufficient genera to test their monophyly) in good  
432 preservation conditions for its use with new genome-scale techniques is already an  
433 important challenge, which will become cumbersome in the near future given the  
434 potential high rate of discovery of unknown lineages in the group, especially in the  
435 deep-sea, as the case of the family Bouchetispiridae tends to suggest.



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458

459

## 7. References

460

461 Abalde, S., Tenorio, M.J., Afonso, C.M., Uribe, J.E., Echeverry, A.M., Zardoya, R.,  
462 2017a. Phylogenetic relationships of cone snails endemic to Cabo Verde based on  
463 mitochondrial genomes. BMC Evol. Biol. 17, 231.

464 Abalde, S., Tenorio, M.J., Afonso, C.M., Zardoya, R., 2017b. Mitogenomic phylogeny  
465 of cone snails endemic to Senegal. Mol. Phylogenet. Evol. 112, 79-87.

466 Abascal, F., Zardoya, R., Telford, M.J., 2010. TranslatorX: multiple alignment of  
467 nucleotide sequences guided by amino acid translations. Nucleic Acids Res. 38,  
468 W7-W13.

469 Andrews, S., 2010. FastQC. [http://www.bioinformatics.babraham.ac.uk/  
470 projects/fastqc/](http://www.bioinformatics.babraham.ac.uk/projects/fastqc/).

471 Arquez, M., Colgan, D., Castro, L.R., 2014. Sequence and comparison of mitochondrial  
472 genomes in the genus *Nerita* (Gastropoda: Neritimorpha: Neritidae) and  
473 phylogenetic considerations among gastropods. Mar. Genomics 15, 45-54.

474 Bandyopadhyay, P.K., Stevenson, B.J., Cady, M.T., Olivera, B.M., Wolstenholme,  
475 D.R., 2006. Complete mitochondrial DNA sequence of a Conoidean gastropod,  
476 *Lophiotoma (Xenuroturris) cerithiformis*: gene order and gastropod phylogeny.  
477 Toxicon 48, 29-43.

478 Bernt, M., Donath, A., Jühling, F., Externbrink, F., Florentz, C., Fritzschn, G., Pütz, J.,  
479 Middendorf, M., Stadler, P.F., 2013. MITOS: improved *de novo* metazoan  
480 mitochondrial genome annotation. Mol. Phylogenet. Evol. 69, 313-319.

481 Bi, K., Vanderpool, D., Singhal, S., Linderoth, T., Moritz, C., Good, J.M., 2012.  
482 Transcriptome-based exon capture enables highly cost-effective comparative  
483 genomic data collection at moderate evolutionary scales. BMC Genomics 13, 403.

484 Boore, J.L., 1999. Animal mitochondrial genomes. *Nucleic Acids Res.* 27, 1767-1780.

485 Boore, J.L., Macey, J.R., Medina, M., 2005. Sequencing and comparing whole  
486 mitochondrial genomes of animals. *Methods Enzymol.* 395, 311-348.

487 Bouchet, P., Gofas, S., 2015. Conoidea Fleming, 1822. In: *MolluscaBase* (2018).  
488 Accessed through: World Register of Marine Species at:  
489 <http://www.marinespecies.org/aphia.php?p=taxdetails&id=15140> on 2018-01-24.

490 Bouchet, P., Kantor, Y.I., Sysoev, A., Puillandre, N., 2011. A new operational  
491 classification of the Conoidea (Gastropoda). *J. Mollus. Stud.* 77, 273-308.

492 Bouchet, P., Rocroi, J.-P., Frýda, J., Hausdorf, B., Ponder, W., Valdés, Á., Warén, A.,  
493 2005. Classification and nomenclator of gastropod families. *Malacologia* 47(1-2):  
494 1-397.

495 Bouchet, P., Rocroi, J.-P., Hausdorf, B., Kaim, A., Kano, Y., Nützel, A., Parkhaev, P.,  
496 Schrödl, M., Strong, E.E., 2017. Revised classification, nomenclator and  
497 typification of gastropod and monoplacophoran families. *Malacologia* 61, 1-526.

498 Bragg, J.G., Potter, S., Bi, K., Moritz, C., 2016. Exon capture phylogenomics: efficacy  
499 across scales of divergence. *Mol. Ecol. Resour.* 16, 1059-1068.

500 Castresana, J., 2000. Selection of conserved blocks from multiple alignments for their  
501 use in phylogenetic analysis. *Mol. Biol. Evol.* 17, 540-552.

502 Castro, L.R., Colgan, D., 2010. The phylogenetic position of Neritimorpha based on the  
503 mitochondrial genome of *Nerita melanotragus* (Mollusca: Gastropoda). *Mol.*  
504 *Phylogenet. Evol.* 57, 918-923.

505 Cunha, R.L., Grande, C., Zardoya, R., 2009. Neogastropod phylogenetic relationships  
506 based on entire mitochondrial genomes. *BMC Evol. Biol.* 9, 210.

507 Dutertre, S., Jin, A.-H., Vetter, I., Hamilton, B., Sunagar, K., Lavergne, V., Dutertre, V.,  
508 Fry, B.G., Antunes, A., Venter, D.J., 2014. Evolution of separate predation-and  
509 defence-evoked venoms in carnivorous cone snails. *Nat. Commun.* 5.

510 Felsenstein, J., 1978. Cases in which parsimony or compatibility methods will be  
511 positively misleading. *Syst. Zool.* 27, 401-410.

512 Felsenstein, J., 1981. Evolutionary trees from DNA sequences: a maximum likelihood  
513 approach. *J. Mol. Evol.* 17, 368-376.

514 Folmer, O., Black, M., Hoeh, W., Lutz, R., Vrijenhoek, R., 1994. DNA primers for  
515 amplification of mitochondrial cytochrome *c* oxidase subunit I from diverse  
516 metazoan invertebrates. *Mol. Mar. Biol. Biotechnol.* 3, 294-299.

517 Galindo, L., Puillandre, N., Strong, E.E., Bouchet, P., 2014. Using microwaves to  
518 prepare gastropods for DNA barcoding. *Mol. Ecol. Resour.* 14, 700-705.

519 Gissi, C., Iannelli, F., Pesole, G., 2008. Evolution of the mitochondrial genome of  
520 Metazoa as exemplified by comparison of congeneric species. *Heredity* 101, 301-  
521 320.

522 Glöckner, G., Heinze, I., Platzer, M., Held, C., Abele, D., 2013. The mitochondrial  
523 genome of *Arctica islandica*; phylogeny and variation. *PLoS one* 8, e82857.

524 Grabherr, M.G., Haas, B.J., Yassour, M., Levin, J.Z., Thompson, D.A., Amit, I.,  
525 Adiconis, X., Fan, L., Raychowdhury, R., Zeng, Q., 2011. Trinity: reconstructing  
526 a full-length transcriptome without a genome from RNA-Seq data. *Nat.*  
527 *Biotechnol.* 29, 644.

528 Huelsenbeck, J.P., Ronquist, F., 2001. MRBAYES: Bayesian inference of phylogenetic  
529 trees. *Bioinformatics* 17, 754-755.

530 Hugall, A.F., O'Hara, T.D., Hunjan, S., Nilsen, R., Moussalli, A., 2015. An exon-  
531 capture system for the entire class Ophiuroidea. *Mol. Biol. Evol.* 33, 281-294.



532 Irisarri, I., Eernisse, D.J., Zardoya, R., 2014. Molecular phylogeny of Acanthochitonina  
533 (Mollusca: Polyplacophora: Chitonida): three new mitochondrial genomes,  
534 rearranged gene orders and systematics. *J. Nat. Hist.* 48, 2825-2853.

535 John, S., J, 2011. SeqPrep <https://github.com/jstjohn/SeqPrep>.

536 Kantor, Y.I., Harasewych, M.G., Puillandre, N., 2016. A critical review of Antarctic  
537 Conoidea (Neogastropoda). *Molluscan Res.* 36, 153-206.

538 Kantor, Y.I., Strong, E.E., Puillandre, N., 2012. A new lineage of Conoidea  
539 (Gastropoda: Neogastropoda) revealed by morphological and molecular data. *J.*  
540 *Mollus. Stud.* 78, 246-255.

541 Katoh, K., Kuma, K.-i., Toh, H., Miyata, T., 2005. MAFFT version 5: improvement in  
542 accuracy of multiple sequence alignment. *Nucleic Acids Res.* 33, 511-518.

543 Katoh, K., Rozewicki, J., Yamada, K.D., 2017. MAFFT online service: multiple  
544 sequence alignment, interactive sequence choice and visualization. *Brief.*  
545 *Bioinform.* bbx108.

546 Kawashima, Y., Nishihara, H., Akasaki, T., Nikaido, M., Tsuchiya, K., Segawa, S.,  
547 Okada, N., 2013. The complete mitochondrial genomes of deep-sea squid  
548 (*Bathyteuthis abyssicola*), bob-tail squid (*Semirossia patagonica*) and four giant  
549 cuttlefish (*Sepia apama*, *S. latimanus*, *S. lycidas* and *S. pharaonis*), and their  
550 application to the phylogenetic analysis of Decapodiformes. *Mol. Phylogenet.*  
551 *Evol.* 69, 980-993.

552 Kornobis, E., Cabellos, L., Aguilar, F., Frías-López, C., Rozas, J., Marco, J., Zardoya,  
553 R., 2015. TRUFA: a user-friendly web server for de novo RNA-seq analysis using  
554 cluster computing. *Evol. Bioinform.* 11, 97.

555 Kotetishvili, E., 1989. Biofacies characteristics of Lower Cretaceous deposits of  
556 Georgia. Cretaceous of the western Tethys. Proceedings 3rd International  
557 Cretaceous Symposium, pp. 543-549.

558 Lartillot, N., Brinkmann, H., Philippe, H., 2007. Suppression of long-branch attraction  
559 artefacts in the animal phylogeny using a site-heterogeneous model. BMC Evol.  
560 Biol. 7, S4.

561 Lartillot, N., Philippe, H., 2004. A Bayesian mixture model for across-site  
562 heterogeneities in the amino-acid replacement process. Mol. Biol. Evol. 21, 1095-  
563 1109.

564 Lartillot, N., Rodrigue, N., Stubbs, D., Richer, J., 2013. PhyloBayes MPI: phylogenetic  
565 reconstruction with infinite mixtures of profiles in a parallel environment. Syst.  
566 Biol. 62, 611-615.

567 Lee, H., Samadi, S., Puillandre, N., Tsai, M.-H., Dai, C.-F., Chen, W.-J., 2016. Eight  
568 new mitogenomes for exploring the phylogeny and classification of  
569 Vetigastropoda. J. Mollus. Stud. 82, 534-541.

570 Maynard, B.T., Kerr, L.J., McKiernan, J.M., Jansen, E.S., Hanna, P.J., 2005.  
571 Mitochondrial DNA sequence and gene organization in the Australian blacklip  
572 abalone *Haliotis rubra* (Leach). Mar. Biotechnol. 7, 645-658.

573 McComish, B.J., Hills, S.F., Biggs, P.J., Penny, D., 2010. Index-free *de novo* assembly  
574 and deconvolution of mixed mitochondrial genomes. Genome Biol. Evol. 2, 410-  
575 424.

576 McLean, J., 1971. A revised classification of the family Turridae, with the proposal of  
577 new subfamilies, genera, and subgenera from the eastern Pacific. The Veliger 14,  
578 114-130.

579 Minh, B.Q., Nguyen, L.T., and von Haeseler, A., 2013. Ultrafast approximation for  
580 phylogenetic bootstrap. *Mol. Biol. Evol.* 30.5: 1188-1195.

581 Murphy, M.A., Rodda, P.U., 1960. Mollusca of the Cretaceous Bald Hills Formation of  
582 California: Part I. *J. Paleontol.* 835-858.

583 Nakagawa, S., Shimamura, S., Takaki, Y., Suzuki, Y., Murakami, S.-i., Watanabe, T.,  
584 Fujiyoshi, S., Mino, S., Sawabe, T., Maeda, T., 2014. Allying with armored  
585 snails: the complete genome of gammaproteobacterial endosymbiont. *ISME J.* 8,  
586 40.

587 Nguyen, L.T., Schmidt, H.A., von Haeseler, A., Minh, B.Q., 2014. IQ-TREE: a fast and  
588 effective stochastic algorithm for estimating maximum-likelihood phylogenies.  
589 *Mol. Biol. Evol.* 32, 268-274.

590 Osca, D., Irisarri, I., Todt, C., Grande, C., Zardoya, R., 2014. The complete  
591 mitochondrial genome of *Scutopus ventrolineatus* (Mollusca:  
592 Chaetodermomorpha) supports the Aculifera hypothesis. *BMC Evol. Biol.* 14,  
593 197.

594 Osca, D., Templado, J., Zardoya, R., 2015. Caenogastropod mitogenomics. *Mol.*  
595 *Phylogenet. Evol.* 93, 118-128.

596 Philippe, H., Derelle, R., Lopez, P., Pick, K., Borchiellini, C., Boury-Esnault, N.,  
597 Vacelet, J., Renard, E., Houliston, E., Quéinnec, E., 2009. Phylogenomics revives  
598 traditional views on deep animal relationships. *Curr. Biol.* 19, 706-712.

599 Powell AWB. 1966. The molluscan families Speightiidae and Turridae. an evaluation of  
600 the valid taxa, both Recent and fossil, with lists of characteristics species. *Bull.*  
601 *Auckl. Inst. Mus.* 5:5-184.

602 Prashanth, J.R., Brust, A., Jin, A.-H., Alewood, P.F., Dutertre, S., Lewis, R.J., 2014.  
603 Cone snail venomics: from novel biology to novel therapeutics. *Future Med.*  
604 *Chem.* 6, 1659-1675.

605 Puillandre, N., Kantor, Y.I., Sysoev, A., Couloux, A., Meyer, C., Rawlings, T., Todd, J.,  
606 Bouchet, P., 2011. The dragon tamed? A molecular phylogeny of the Conoidea  
607 (Gastropoda). *J. Mollus. Stud.* 77, 259-272.

608 Puillandre, N., Samadi, S., Boisselier, M.-C., Sysoev, A., Kantor, Y.I., Cruaud, C.,  
609 Couloux, A., Bouchet, P., 2008. Starting to unravel the toxoglossan knot:  
610 molecular phylogeny of the “turrids” (Neogastropoda: Conoidea). *Mol.*  
611 *Phylogenet. Evol.* 47, 1122-1134.

612 Ronquist, F., Huelsenbeck, J.P., 2003. MrBayes 3: Bayesian phylogenetic inference  
613 under mixed models. *Bioinformatics* 19, 1572-1574.

614 Sambrook, J., Fritsch, E.F., Maniatis, T., 1989. *Molecular cloning: a laboratory manual.*  
615 Cold spring harbor laboratory press.

616 San Mauro, D., Gower, D.J., Müller, H., Loader, S.P., Zardoya, R., Nussbaum, R.A.,  
617 Wilkinson, M., 2014. Life-history evolution and mitogenomic phylogeny of  
618 caecilian amphibians. *Mol. Phylogenet. Evol.* 73, 177-189.

619 Schattner, P., Brooks, A.N., Lowe, T.M., 2005. The tRNAscan-SE, snoscan and  
620 snoGPS web servers for the detection of tRNAs and snoRNAs. *Nucleic Acids*  
621 *Res.* 33, W686-W689.

622 Schmieder, R., Edwards, R., 2011. Quality control and preprocessing of metagenomic  
623 datasets. *Bioinformatics* 27, 863-864.

624 Sevigny, J.L., Kirouac, L.E., Thomas, W.K., Ramsdell, J.S., Lawlor, K.E., Sharifi, O.,  
625 Grewal, S., Baysdorfer, C., Curr, K., Naimie, A.A., 2015. The mitochondrial

626 genomes of the Nudibranch Mollusks, *Melibe leonina* and *Tritonia diomedea*, and  
627 their impact on Gastropod phylogeny. PloS one 10, e0127519.

628 Strugnell, J.M., Hall, N.E., Vecchione, M., Fuchs, D., Allcock, A.L., 2017. Whole  
629 mitochondrial genome of the Ram's Horn Squid shines light on the phylogenetic  
630 position of the monotypic order Spirulida (Haeckel, 1896). Mol. Phylogenet.  
631 Evol. 109, 296-301.

632 Taylor, J., Kantor, Y.I., Sysoev, A., 1993. Foregut anatomy, feeding mechanisms,  
633 relationships and classification of the Conoidea (= Toxoglossa)(Gastropoda).  
634 Bull. Nat. Hist. Mus. Lond. Zool. 59, 125-170.

635 Trifinopoulos, J., Nguyen, L.-T., von Haeseler, A., Minh, B.Q., 2016. W-IQ-TREE: a  
636 fast online phylogenetic tool for maximum likelihood analysis. Nucleic Acids  
637 Res. 44, W232-W235.

638 Tucker, J.K., Tenorio, M.J., 2009. Systematic classification of recent and fossil  
639 conoidean gastropods: with keys to the genera of cone shells. Conchbooks.

640 Uribe, J.E., Colgan, D., Castro, L.R., Kano, Y., Zardoya, R., 2016a. Phylogenetic  
641 relationships among superfamilies of Neritimorpha (Mollusca: Gastropoda). Mol.  
642 Phylogenet. Evol. 104, 21-31.

643 Uribe, J.E., Kano, Y., Templado, J., Zardoya, R., 2016b. Mitogenomics of  
644 Vetigastropoda: insights into the evolution of pallial symmetry. Zool. Scr. 45,  
645 145-159.

646 Uribe, J.E., Puillandre, N., Zardoya, R., 2017a. Beyond *Conus*: phylogenetic  
647 relationships of Conidae based on complete mitochondrial genomes. Mol.  
648 Phylogenet. Evol. 107, 142-151.

649 Uribe, J.E., Williams, S.T., Templado, J., Abalde, S., Zardoya, R., 2017b. Denser  
650 mitogenomic sampling improves resolution of the phylogeny of the superfamily  
651 Trochoidea (Gastropoda: Vetigastropoda). *J. Mollus. Stud.* 83, 111-118.

652 Uribe, J.E., Zardoya, R., 2017. Revisiting the phylogeny of Cephalopoda using  
653 complete mitochondrial genomes. *J. Mollus. Stud.* 83, 133-144.

654 Wang, J.-G., Zhang, D., Jakovlić, I., Wang, W.-M., 2017. Sequencing of the complete  
655 mitochondrial genomes of eight freshwater snail species exposes pervasive  
656 paraphyly within the Viviparidae family (Caenogastropoda). *PloS one* 12,  
657 e0181699.

658 White, T.R., Conrad, M.M., Tseng, R., Balayan, S., Golding, R., de Frias Martins,  
659 A.M., Dayrat, B.A., 2011. Ten new complete mitochondrial genomes of  
660 pulmonates (Mollusca: Gastropoda) and their impact on phylogenetic  
661 relationships. *BMC Evol. Biol.* 11, 295.

662 Williams, S., Foster, P., Hughes, C., Harper, E., Taylor, J., Littlewood, D., Dyal, P.,  
663 Hopkins, K., Briscoe, A., 2017. Curious bivalves: Systematic utility and unusual  
664 properties of anomalodesmatan mitochondrial genomes. *Mol. Phylogenet. Evol.*  
665 110, 60-72.

666 Williams, S., Foster, P., Littlewood, D., 2014. The complete mitochondrial genome of a  
667 turbinid vetigastropod from MiSeq Illumina sequencing of genomic DNA and  
668 steps towards a resolved gastropod phylogeny. *Gene* 533, 38-47.

669 Yokobori, S.-i., Fukuda, N., Nakamura, M., Aoyama, T., Oshima, T., 2004. Long-term  
670 conservation of six duplicated structural genes in cephalopod mitochondrial  
671 genomes. *Mol. Biol. Evol.* 21, 2034-2046.

672

673 **Legends to figures**

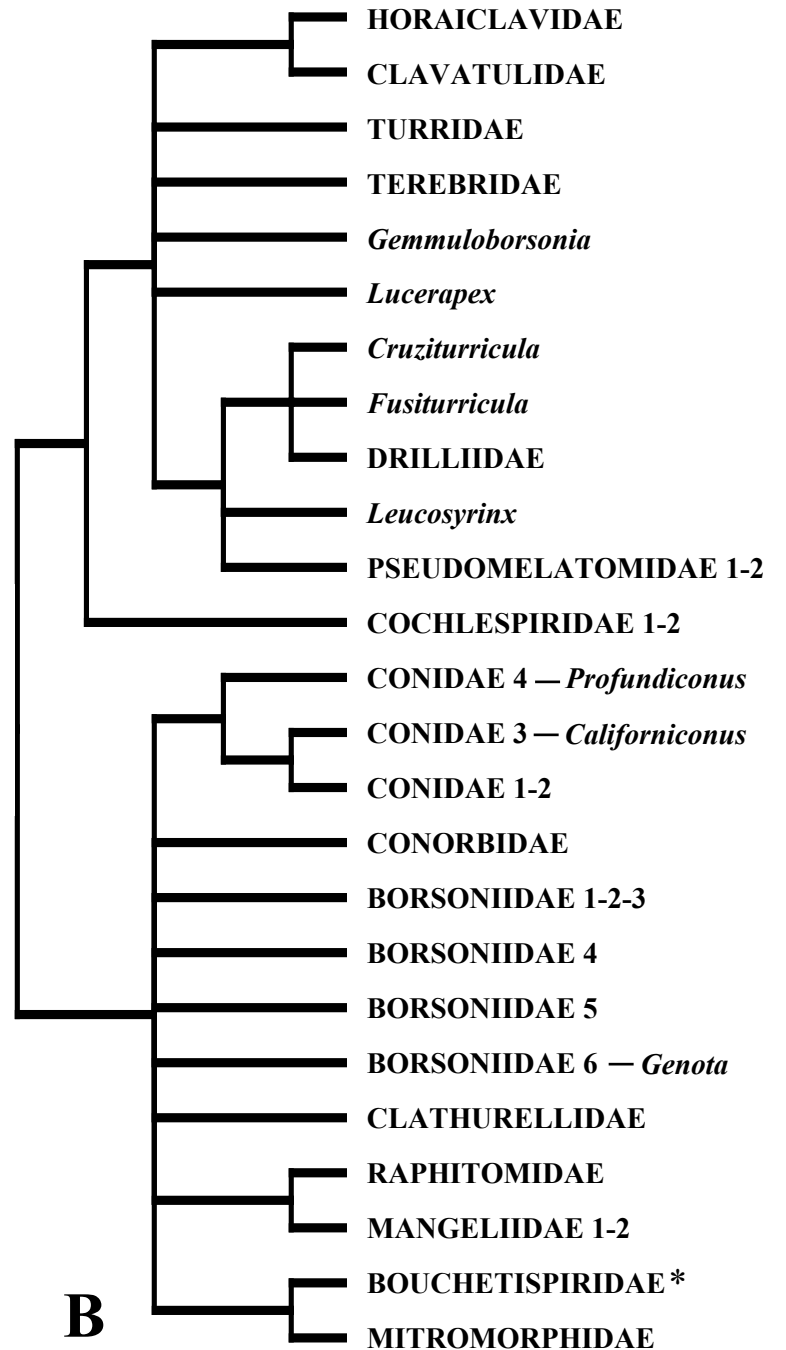
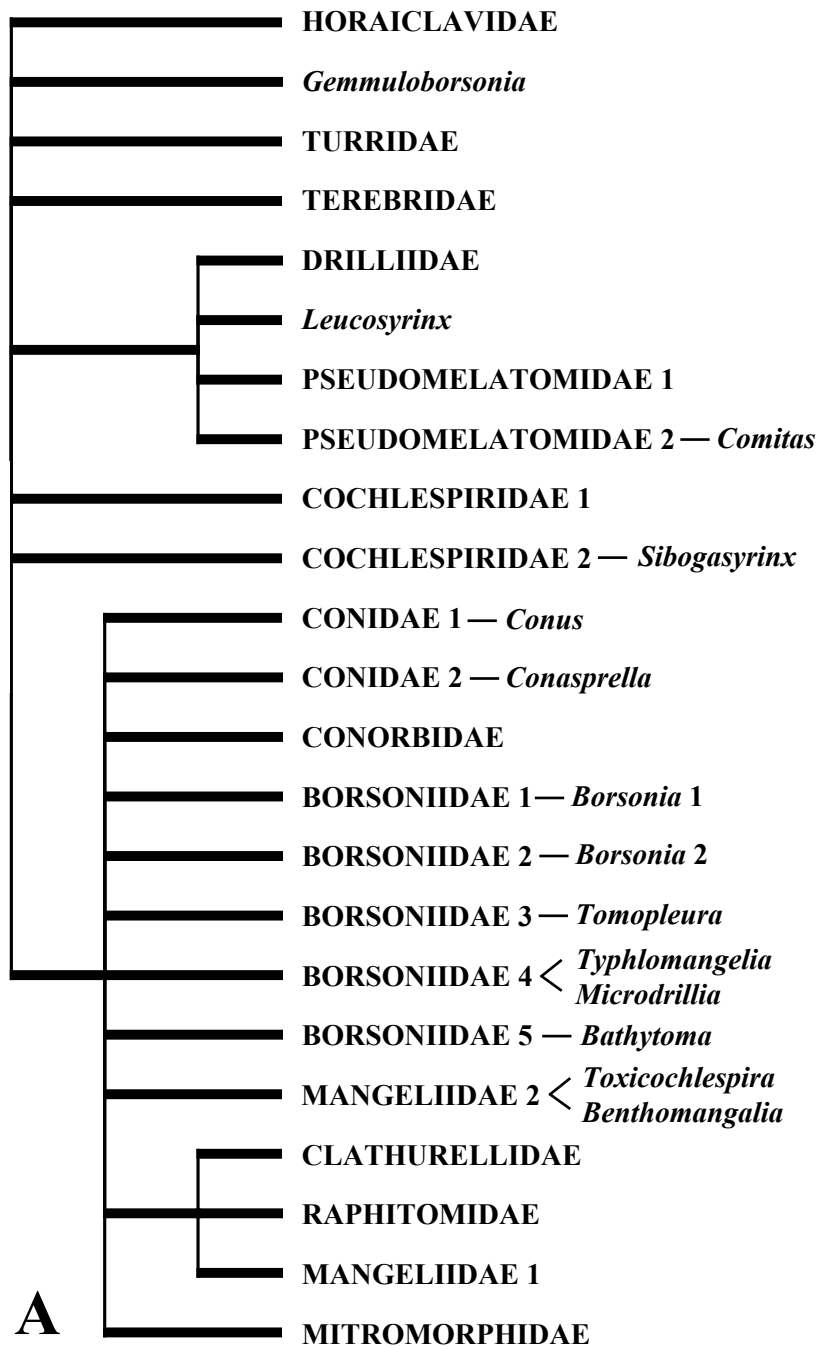
674 Figure 1. Summary of the two published phylogenetic trees of the conoidean snails. A:  
675 Puillandre et al., (2008); B: Puillandre et al., (2011). All nodes with Posterior  
676 Probability  $< 0.95$  were collapsed. The asterisk highlights a family described  
677 by Kantor et al., (2012) closely related with Mitromorphidae, not included in  
678 Puillandre et al., (2011).

679 Figure 2. Gene orders of conoidean mt genomes. The protein-coding genes are in blue,  
680 the rRNAs in red, the tRNAs in black, and the control region (CR) in grey. The  
681 genes encoded in the major and minor strands are in top and bottom positions,  
682 respectively. The translocations are indicated in yellow, each arrow  
683 corresponding to an independent event. The numbers 1 and 2, below the *trnL*  
684 genes, correspond to the anticodons (cta) and (tta) respectively. The numbers 1  
685 and 2, over the *trnS* genes, correspond to the anticodons (tca) and (agc)  
686 respectively.

687 Figure 3. Phylogenetic relationships of the Conoidea based on complete mt genomes  
688 based on protein coding genes and rRNAs. The reconstructed ML phylogram is  
689 shown. The yellow inset indicates the alternative topology found in BI  
690 analyses. The red inset indicates a tRNA gene order rearrangement, which is a  
691 synapomorphy of the corresponding clade. The red and blue asterisks represent  
692 the relative position in the tree of tRNA gene rearrangements C and D of Fig.  
693 2, respectively. Numbers at nodes are support values for ML (UFB  $> 70$ )/BI  
694 (BPP  $> 0.90$ ). The grey color in the tree applies to outgroup taxa. Scale bar  
695 indicates the number of substitutions/site. Shells A–S correspond to the  
696 samples included in the analyses (vouchers in Table 1), only the B and E shells

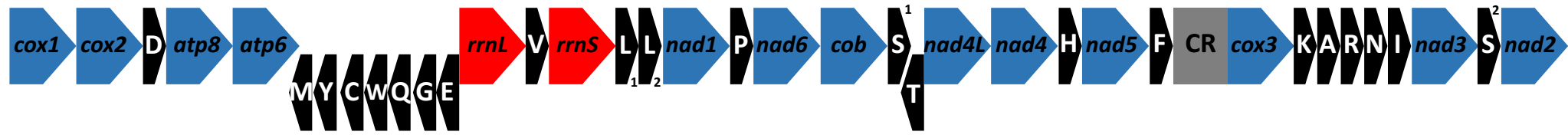
697 do not correspond to a sequenced sample but to a conspecific specimen. A.  
698 *Clionella kraussii*, B. *Fusiturris similis*, C. *Anguloclavus* sp. 1, D.  
699 *Pinguiggemmula* sp., E. *Oxymeris dimidiata*, F. *Gemmuloborsonia moosai*, G.  
700 *Lucerapex* sp., H. *Splendrillia* sp. 1, I. *Leucosyrinx* sp.. J. *Inquisitor* sp., K.  
701 *Cochlespira* sp., L. *Marshallena* sp., M. *Conasprella wakayamaensis*, N.  
702 *Bathytoma punicea*, O. *Profundiconus teramachii*, P. *Glyphostoma* sp., Q.  
703 *Benthomangelia* sp. 1, R. *Typhlosyrinx* sp., and S. *Mitromorpha fischeri*.





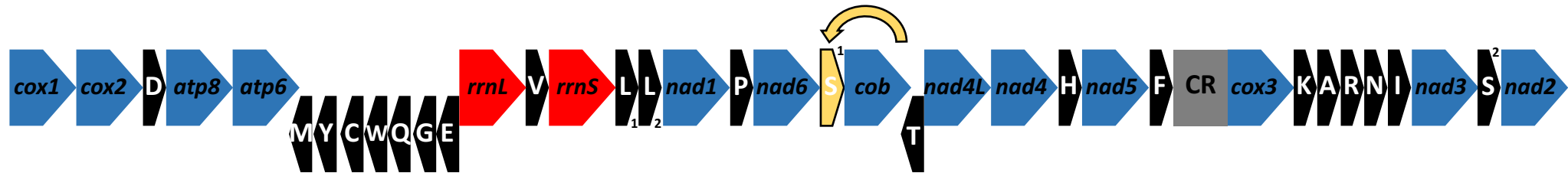
# Conoidea consensus order

A



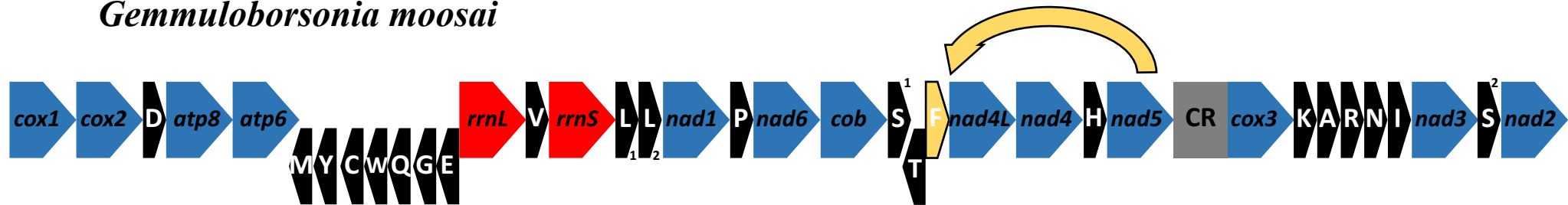
# Horaiclavidae and Clavatulidae

B



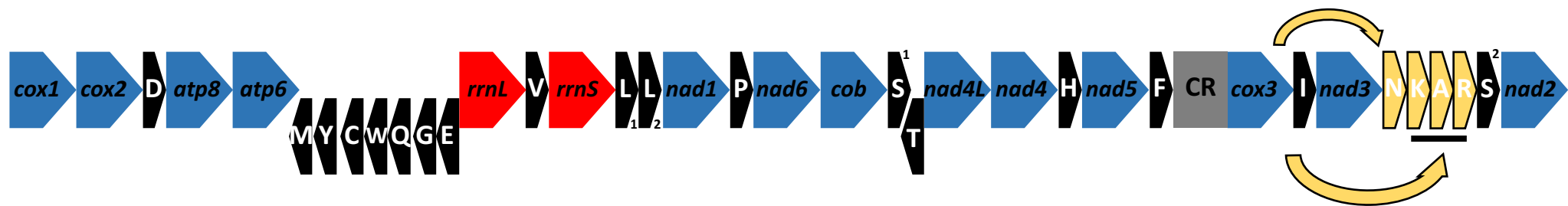
# Gemmuloborsonia moosai

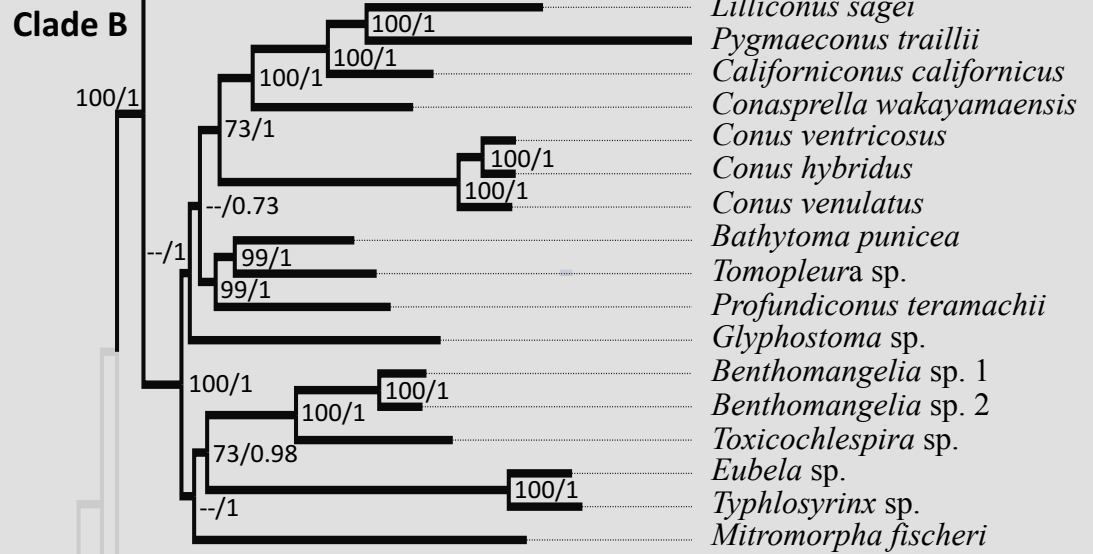
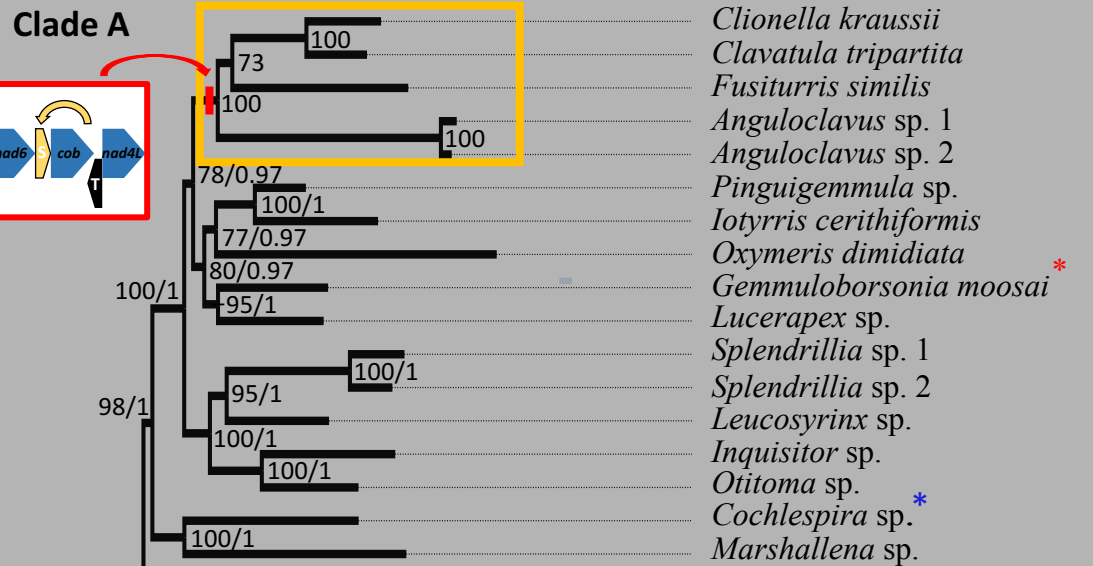
C



# Cochlespira sp.

D





- Clavatulidae**
- Horaiclavidae**
- Turridae s.s.**
- Terebridae**
- Clavatulidae?
- Turridae?
- Drilliidae**
- Pseudomelatomidae?
- Pseudomelatomidae**
- Cochlespiridae**
- Horaiclavidae?
- Conidae**
- Borsoniidae**
- Conidae?
- Clathurellidae**
- Mangeliidae**
- Raphitomidae**
- Mitromorphidae**

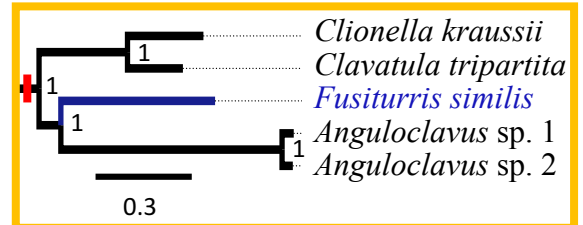
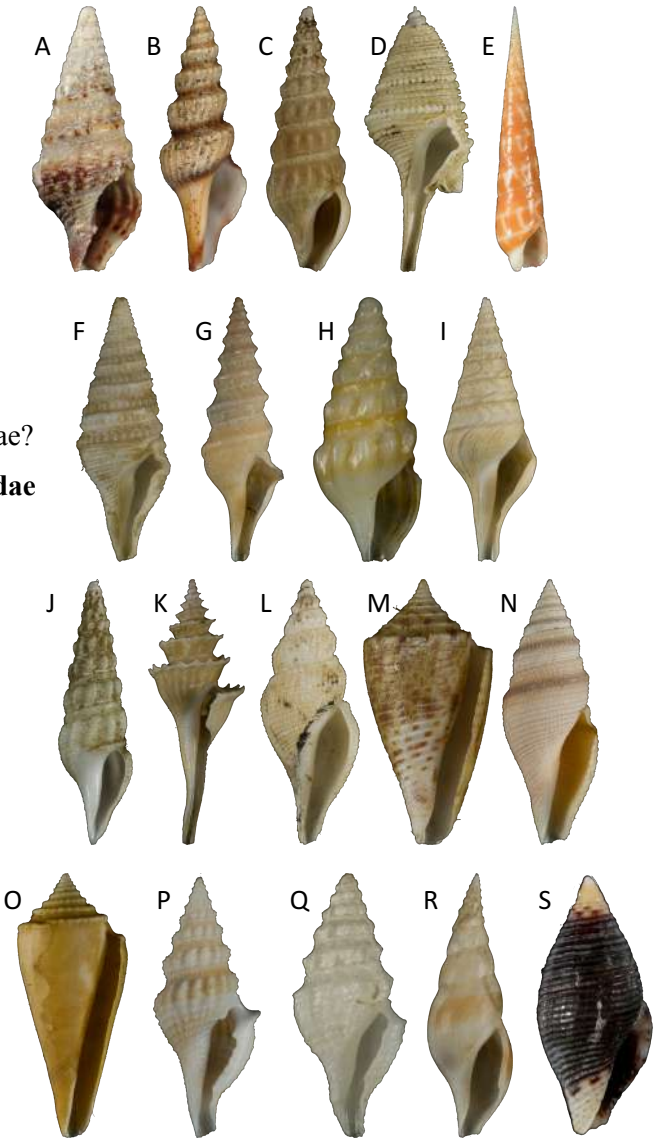


Table 1. Mitogenomes analyzed in this study. Complete mt genomes are indicated with an asterisk (\*). The length of each mt genome is indicated in base pairs (bp). The NCBI accession number of each mt genome, as well as the number of total reads (No. Reads) with its corresponding mean depth of coverage (X) are also indicated. In parenthesis the number of the reads from IonTorrent technology are shown. The crosses (†) indicate samples with shell picture (either the actual specimen used for sequencing or, when a voucher number is not indicated, a conspecific one) in Fig. 2.

New sequences								
Family	Taxa	bp	Rearrangement	NCBI	Voucher	Sampling locality	No. Reads	X
1	Borsoniidae	<i>Bathytoma punicea</i> *	16037	no	MH308389	MNHN-IM-2013-19279†	Papua Niugini expedition, Papua New Guinea, 03°11'S, 143°06'E; 360-380m.	95577 902
2	Clavatulidae	<i>Clionella kraussii</i>	15760	yes	MH308390	MNHN-IM-2009-17893†	Atimo Vatae expedition, Madagascar, 25°23.4'S, 44°51.7'E; 20-22m.	58509 553
3	Clavatulidae	<i>Clavatula tripartita</i>	15743	yes	MH308391	MNHN-IM-2009-14826	Atimo Vatae expedition, Madagascar, 25°46.3'S, 45°22.9'E; 52m.	140988 1345
4	Clavatulidae?	<i>Gemmuloborsonia moosai</i> *	15541	yes	MH308392	MNHN-IM-2013-19263†	Papua Niugini expedition, Papua New Guinea, 03°11'S, 143°06'E; 360-380m.	23023 148
5	Turridae?	<i>Lucerapex</i> sp.	15338	no	MH308393	MNHN-IM-2013-19988†	Papua Niugini expedition, Papua New Guinea, 05°36'S, 148°13'E; 500-640m.	41779 271
6	Cochlespiridae	<i>Cochlespira</i> sp.	15581	yes	MH308394	MNHN-IM-2013-19079†	Papua Niugini expedition, Papua New Guinea, 02°38'S, 141°18'E; 335m.	68443 437
7	Drilliidae	<i>Splendrillia</i> sp. 1*	15358	no	MH308395	MNHN-IM-2013-9619†	Papua Niugini expedition, Papua New Guinea, 04°34'S, 146°17'E; 411-430m.	124746 814
8	Drilliidae	<i>Splendrillia</i> sp. 2	15231	no	MH308396	MNHN-IM-2013-9750	Papua Niugini expedition, Papua New Guinea, 05°36'S, 148°13'E; 500-640m.	31493 310
9	Horaiclavidae	<i>Anguloclavus</i> sp. 1	15078	yes	MH308397	MNHN-IM-2013-19732†	Papua Niugini expedition, Papua New Guinea, 05°11'S, 147°03'E; 688m.	75403 747
10	Horaiclavidae?	<i>Marshallena</i> sp.	15210	no	MH308398	MNHN-IM-2013-9821†	Papua Niugini expedition, Papua New Guinea, 05°21'S, 145°49'E; 520-575m.	54953 359
11	Horaiclavidae	<i>Anguloclavus</i> sp. 2	15103	yes	MH308399	MNHN-IM-2013-9661	Papua Niugini expedition, Papua New Guinea, 05°35'S, 146°24'E; 497-657m.	32251 212
12	Mangeliidae	<i>Benthomangelia</i> sp. 2	15037	no	MH308400	MNHN-IM-2013-9652	Papua Niugini expedition, Papua New Guinea, 05°12'S, 146°59'E; 470-508m.	27274 273
13	Mangeliidae	<i>Toxicochlespira</i> sp.	15076	no	MH308401	MNHN-IM-2013-9841	Papua Niugini expedition, Papua New Guinea, 05°22'S, 145°51'E; 620-677m.	54151 538
14	Mitromorphidae	<i>Mitromorpha fischeri</i>	15243	no	MH308402	MNHN-IM-2013-5649†	Papua Niugini expedition, Papua New Guinea, 05°07'S, 145°49.4'E; 12m.	31183 306
15	Pseudomelatomidae	<i>Inquisitor</i> sp.*	15248	no	MH308403	MNHN-IM-2013-18505†	Papua Niugini expedition, Papua New Guinea, 04°30'S, 145°34'E; 600-660m.	59205 388
16	Pseudomelatomidae?	<i>Leucosyrinx</i> sp.*	15358	no	MH308404	MNHN-IM-2013-19304†	Papua Niugini expedition, Papua New Guinea, 03°11'S, 143°04'E; 510-560m.	58163 571
17	Pseudomelatomidae	<i>Otitoma</i> sp.*	15584	no	MH308405	MNHN-IM-2013-9848	Papua Niugini expedition, Papua New Guinea, 05°22'S, 145°48'E; 340-385m.	16277 (12689) 240
18	Raphitomidae	<i>Eubela</i> sp.	15153	no	MH308406	MNHN-IM-2013-9671	Papua Niugini expedition, Papua New Guinea, 06°00'S, 147°35'E; 648-652m.	98651 978
19	Raphitomidae	<i>Typhlosyrinx</i> sp.*	15804	no	MH308407	MNHN-IM-2013-18371†	Papua Niugini expedition, Papua New Guinea, 04°53'S, 145°51'E; 680-689m.	101854 642
20	Turridae	<i>Pinguigemma</i> sp.	15097	no	MH308408	MNHN-IM-2013-18391†	Papua Niugini expedition, Papua New Guinea, 04°52'S, 145°50'E; 610-620m.	157709 1557
Previous published sequences								
Family	Taxa	bp	Rearrangement	NCBI	Voucher	Author		
21	Conidae	<i>Conasprella wakayamaensis</i>	15927	no	KX263254	MNHN-IM-2013-19091†	Uribe et al., (2017)	
22	Conidae	<i>Conus ventricosus</i> *	15534	no	KX263251	MNCN-ADN-86742	Uribe et al., (2017)	
23	Conidae	<i>Conus venulatus</i> *	15524	no	KX263250	MNCN-ADN-86741	Uribe et al., (2017)	
24	Conidae	<i>Conus hybridus</i>	15304	no	KX263252	MNHN-IM-2009-18301	Uribe et al., (2017)	
25	Conidae	<i>Californiconus californicus</i> *	15444	no	NC_032377	MNCN-ADN-86740	Uribe et al., (2017)	
26	Conidae	<i>Lilliconus sagei</i>	15665	yes	KX263255	MNHN-IM-2009-31328	Uribe et al., (2017)	
27	Conidae	<i>Pygmaeconus trailii</i>	15279	no	KX263256	MNHN-IM-2013-19686	Uribe et al., (2017)	
28	Conidae	<i>Profundiconus teramachii</i>	15279	no	KX263256	MNHN-IM-2013-19686†	Uribe et al., (2017)	
29	Borsoniidae	<i>Tomopleura</i> sp.	15182	yes	KX263259	MNHN-IM-2013-9849	Uribe et al., (2017)	
30	Mangeliidae	<i>Benthomangelia</i> sp. 1	15034	no	KX263258	MNHN-IM-2013-9858†	Uribe et al., (2017)	
31	Clathurellidae	<i>Glyphostoma</i> sp.	13370	no	KX263260	MNHN-IM-2013-19173†	Uribe et al., (2017)	
32	Clavatulidae?	<i>Fusiturris similis</i> *	15595	yes	NC_013242	—†	Cunha et al., (2009)	
33	Terebridae	<i>Oxymeris dimidiata</i> *	16513	no	NC_013239	—†	Cunha et al., (2009)	
34	Turridae	<i>Iotyrriis cerithiformis</i> *	15380	no	NC_008098	—	Bandyopadhyay et al., (2006)	
Outgroups								
35	Ancillariidae	<i>Amalda northlandica</i> *	15354	—	NC_014403	—	McComish et al., (2010)	
36	Babyloniidae	<i>Babylonia areolata</i> *	15445	—	NC_023080	—	Chen and Ke, (unpublished)	
37	Muricidae	<i>Rapana venosa</i> *	15272	—	NC_011193	—	Chandler et al., (unpublished)	
38	Columbellidae	<i>Columbella adansoni</i>	15110	—	KP716637	MNCN-ADN-85224	Osca et al., (2015)	
39	Nassariidae	<i>Nassarius reticulatus</i> *	15271	—	NC_013248	—	Cunha et al., (2009)	
40	Cassidae	<i>Galeodea echinophora</i> *	15388	—	NC_028003	MNCN-ADN-65235	Osca et al., (2015)	

**Supplementary Material 1.** Long and short PCR primers used to amplify all mitochondrial genomes. The primers named Cdeacox3F, CdeaPheR, Cdea16sF, and Cdea16sR were taken from Uribe *et al.* (2017a)

1 *Bathytoma punicea*

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTRGTTGA	<i>cox3 – cox1</i> (3265)
Bor_COIR	GATATAARATAGGATCWCCRCCTCCTGC	
Bathcox1F	TACTAGGAGCTCCTGATATGGTTTTCCC	<i>cox1 – rrnL</i> (5309)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL – trnF</i> (6952)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	
Bathcox3R	AATCCTGTGGCTACAAAGAACCTAGAG	Control Region (1585)
Bathnad5F	CTCATCTCAACCTCTACTAAGTTTTCC	
<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (374)
16S_ending	AAAGATAATGCTGTTATCCCTRCGG	

2 *Clionella kraussii*

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTRGTTGA	<i>cox3 – cox1</i> (3064)
Clava_COIR	CTGCHCCTAAAATAGAAGARGCCCC	
Clava_COIF	GAGCTCCHGATATRGCTTTTCTCG	<i>cox1 – rrnL</i> (5296)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTRGTTGA	<i>cox3 – rrnL</i> (8533)
16S_kbR	TTCTGCATCTTTAGGATATTCTGGTCC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL – trnF</i> (7580)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	

3 *Clavatula tripartita*

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTRGTTGA	<i>cox3 – cox1</i> (3100)
Clava_COIR	CTGCHCCTAAAATAGAAGARGCCCC	
Clava_COIF	GAGCTCCHGATATRGCTTTTCTCG	<i>cox1 – rrnL</i> (5279)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTRGTTGA	<i>cox3 – rrnL</i> (8567)
16S_kbR	TTCTGCATCTTTAGGATATTCTGGTCC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL – trnF</i> (7544)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	

4 *Gemmuloborsonia moosai*

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Gemm_COIF	GCTTCTGGTGTAAGTGTACTTGGG	<i>cox1 – rrnL</i> (5210)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL – cox1</i> (10439)
Clava_COIR	CTGCHCCTAAAATAGAAGARGCCCC	
<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (371)
16S_ending	AAAGATAATGCTGTTATCCCTRCGG	

5 *Lucerapex* sp.

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTTRGTTGA	<i>cox3</i> – <i>cox1</i> (3044)
Turri_COIR	AACTGCYCCTAAAATAGAAGATGCCCC	
Turri_COIF	AAGTCTTCTTATTCGDGCGYAATTAGG	<i>cox1</i> – <i>rrnL</i> (5358)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL</i> – <i>trnF</i> (7206)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	
<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (372)
16S_ending	AAAGATAATGCTGTTATCCCTRCGG	

6 *Cochlespira* sp.

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTTRGTTGA	<i>cox3</i> – <i>cox1</i> (3772)
CochCOIR	TGTTGGTAYAAGATSGGGTCTCCAC	
CochCOIF	CTACTAGGAGACGATCAGCTTTACAACG	<i>cox1</i> – <i>rrnL</i> (5324)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL</i> – <i>trnF</i> (6928)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	
<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (371)
16S_ending	AAAGATAATGCTGTTATCCCTRCGG	

7 *Splendrillia* sp. 1

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTTRGTTGA	<i>cox3</i> – <i>cox1</i> (3320)
Dril_COIR	AATWGGATCTCCACCTCCTGCDGG	
Dril_COIF	TRGGAGCTCCTGATATRGCTTTTCC	<i>cox1</i> – <i>rrnL</i> (5252)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL</i> – <i>trnF</i> (6971)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	
<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (377)
16S_ending	AAAGATAATGCTGTTATCCCTRCGG	
Driicox3R	GTAGTCTCTCGAATTACATCYCGTCATC	Control Region (425)
Driinad5F	ATAAAATCWATTGACATAGGTTGACTCG	

8 *Splendrillia* sp. 2

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTTRGTTGA	<i>cox3</i> – <i>cox1</i> (3301)
Dril_COIR	AATWGGATCTCCACCTCCTGCDGG	
Dril_COIF	TRGGAGCTCCTGATATRGCTTTTCC	<i>cox1</i> – <i>rrnL</i> (5263)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL</i> – <i>trnF</i> (6982)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	
<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (374)
16S_ending	AAAGATAATGCTGTTATCCCTRCGG	

9 *Anguloclavus* sp. 1

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTTRGTTGA	<i>cox3</i> – <i>cox1</i> (3046)
Hora_COIR	CCTARAATGGADGADGCACCTGC	
Hora_COIF	TTCGWGCAGAATTAGGWCAACCNGG	<i>cox1</i> – <i>rrnL</i> (5374)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL</i> – <i>trnF</i> (6916)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	
<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (371)
16S_ending	AAAGATAATGCTGTTATCCTRCGG	

10 *Marshallena* sp.

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTTRGTTGA	<i>cox3</i> – <i>cox1</i> (3076)
Hora_COIR	CCTARAATGGADGADGCACCTGC	
Hora_COIF	TTCGWGCAGAATTAGGWCAACCNGG	<i>cox1</i> – <i>rrnL</i> (5442)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL</i> – <i>trnF</i> (6930)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	
<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (373)
16S_ending	AAAGATAATGCTGTTATCCTRCGG	

11 *Anguloclavus* sp. 2

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTTRGTTGA	<i>cox3</i> – <i>cox1</i> (3030)
Hora_COIR	CCTARAATGGADGADGCACCTGC	
Hora_COIF	TTCGWGCAGAATTAGGWCAACCNGG	<i>cox1</i> – <i>rrnL</i> (5381)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL</i> – <i>trnF</i> (6938)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	
<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (371)
16S_ending	AAAGATAATGCTGTTATCCTRCGG	

12 *Benthomangelia* sp. 2

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTTRGTTGA	<i>cox3</i> – <i>cox1</i> (3041)
Mang_COIF	GGAGCTCCHGATATAGTWTTTCCTCG	
Mang_COIR	ACAGCHCCTAAAATAGAAGAAACACC	<i>cox1</i> – <i>rrnL</i> (5223)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL</i> – <i>trnF</i> (6892)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	
<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining2	TCCTTTTGGATATAAGCTTGAAAATAGC	<i>rrnL</i> (689)
16S_ending2	AAACCTTTTTTCGATAAGAGCTCTC	

13 *Toxicochlespira* sp.

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTRGTTGA	<i>cox3</i> – <i>cox1</i> (3053)
Mang_COIF	GGAGCTCCHGATATAGTWTTTCCTCG	
Mang_COIR	ACAGCHCCTAAAATAGAAGAAACACC	<i>cox1</i> – <i>rrnL</i> (5213)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL</i> – <i>trnF</i> (6918)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	
<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (376)
16S_ending	AAAGATAATGCTGTTATCCCTRCGG	

14 *Mitromorpha fischeri*

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTRGTTGA	<i>cox3</i> – <i>rrnL</i> (8239)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL</i> – <i>trnF</i> (6940)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	
<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (375)
16S_ending	AAAGATAATGCTGTTATCCCTRCGG	

15 *Inquisitor* sp.

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTRGTTGA	<i>cox3</i> – <i>cox1</i> (3048)
Pseu_COIR	GCTCCTAAAATHGAWGAAGCACCCWGC	
Pseu_COIF	TAGGAGCTCCAGATATRGCTTTYCC	<i>cox1</i> – <i>rrnL</i> (5193)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL</i> – <i>trnF</i> (6982)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	
<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (371)
16S_ending	AAAGATAATGCTGTTATCCCTRCGG	
5199-nad5F	TTACGACTTTCTCTCTGTTCCCTGTG	Control Region (843)
cox3R	GTAAGCCTTTAGATACTGAATAGTGTG	

16 *Leucosyrinx* sp.

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTRGTTGA	<i>cox3</i> – <i>rrnL</i> (8096)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL</i> – <i>trnF</i> (7067)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	
5069-nad4F	TAGCCAATTAAGGCTCCGGGATTACC	Control Region (2661)
5069-cox3R	AGCAGCTTCAAACCCAAAGTGATGC	
<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (374)
16S_ending	AAAGATAATGCTGTTATCCCTRCGG	



17 *Otitoma* sp.

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTTRGTTGA	<i>cox3</i> – <i>cox1</i> (2850)
Pseu_COIR	GCTCCTAAAATHGAWGAAAGCACCCWGC	
Pseu_COIF	TAGGAGCTCCAGATATRGCTTTYCC	<i>cox1</i> – <i>rrnL</i> (5226)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL</i> – <i>trnF</i> (7010)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	
5123-nad4F	GCTATCCAACACGGAGGAAGTCC	Control Region (2978)
5123-cox3R	CAGCAGCCTCAAAGCCAAAGTGATG	

<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (372)
16S_ending	AAAGATAATGCTGTTATCCCTRCGG	

18 *Eubela* sp.

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTTRGTTGA	<i>cox3</i> – <i>rrnL</i> (8187)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL</i> – <i>trnF</i> (6902)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	

<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (367)
16S_ending	AAAGATAATGCTGTTATCCCTRCGG	

19 *Typhlosyrinx* sp.

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTTRGTTGA	<i>cox3</i> – <i>cox1</i> (3059)
Raphi_COIR	ACAGCYCCTAAAATWGAAGAWACACCAGC	
Raphi_COIF	GGTGCTCCAGATATRGTWTTTCCTCG	<i>cox1</i> – <i>rrnL</i> (5297)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL</i> – <i>trnF</i> (6902)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	
nad4F	GTGTAATAAACATAGCGGCTCCTCC	Control Region (3385)
cox3R	CAGCTGCTTCAAACCAAATGATGC	

<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (367)
16S_ending	AAAGATAATGCTGTTATCCCTRCGG	

20 *Pinguigemmula* sp.

<b>Long PCR</b>		
Primer name	Sequence 5'-3'	Fragment (bp)
Cdeacox3F	ATGGCACGAAATCCATTTTCATTTTRGTTGA	<i>cox3</i> – <i>rrnL</i> (8081)
Cdea16sR	CTACCTTTGCACGGTCAGAGTACC	
Cdea16sF	GCCTTATAATTGAAGGCTRGWATGAATGG	<i>rrnL</i> – <i>trnF</i> (6952)
CdeaPheR	TACYTTAGCATCTTCAGCGCTAYGCTCT	

<b>Short-PCR</b>		
Primer name	Sequence 5'-3'	
16S_begining	TTCTGCCTGTTTATYAAAAACATGGCT	<i>rrnL</i> (375)
16S_ending	AAAGATAATGCTGTTATCCCTRCGG	

**Supplementary Material 2.** Main features of each mitochondrial genome. Beginning and end of each gene, length of each gene, intergenic non-coding regions, coding strand ("+" major and "-" minor), and start and stop codon of each protein-coding gene.

<i>Bathytoma punicea</i> (Borsoniidae)								
Product (gene)	Type	Start	Stop	Length	Intergenic	Strand	Start Codon	Stop Codon
COX1	CDS	1	1548	1548	129	+	ATG	TAA
COX2	CDS	1678	2362	685	0	+	ATG	T—
tRNA-Asp	tRNA	2363	2430	68	0	+		
ATP8	CDS	2431	2589	159	4	+	ATG	TAA
ATP6	CDS	2594	3289	696	38	+	ATG	TAA
tRNA-Met	tRNA	3328	3394	67	5	-		
tRNA-Tyr	tRNA	3400	3465	66	1	-		
tRNA-Cys	tRNA	3467	3532	66	0	-		
tRNA-Trp	tRNA	3533	3598	66	0	-		
tRNA-Gln	tRNA	3599	3661	63	6	-		
tRNA-Gly	tRNA	3668	3734	67	0	-		
tRNA-Glu	tRNA	3735	3801	67	0	-		
s-rRNA	rRNA	3802	4750	949	0	+		
tRNA-Val	tRNA	4751	4816	66	0	+		
l-rRNA	rRNA	4817	6165	1349	5	+		
tRNA-Leu (cta)	tRNA	6171	6239	69	4	+		
tRNA-Leu (tta)	tRNA	6244	6312	69	0	+		
ND1	CDS	6313	7254	942	6	+	ATG	TAA
tRNA-Pro	tRNA	7261	7327	67	1	+		
ND6	CDS	7329	7829	501	7	+	ATG	TAA
CYTB	CDS	7837	8976	1140	7	+	ATG	TAA
tRNA-Ser (tca)	tRNA	8984	9048	65	1	+		
tRNA-Thr	tRNA	9050	9114	65	21	-		
ND4L	CDS	9136	9432	297	-7	+	ATG	TAG
ND4	CDS	9426	10797	1372	0	+	ATG	T—
tRNA-His	tRNA	10798	10862	65	1	+		
ND5	CDS	10864	12581	1718	0	+	ATG	TA—
tRNA-Phe	tRNA	12582	12648	67	752	+		
COX3	CDS	13401	14180	780	14	+	ATG	TAA
tRNA-Lys	tRNA	14195	14262	68	10	+		
tRNA-Ala	tRNA	14273	14339	67	3	+		
tRNA-Arg	tRNA	14343	14410	68	8	+		
tRNA-Asn	tRNA	14419	14486	68	3	+		
tRNA-Ile	tRNA	14490	14556	67	3	+		
ND3	CDS	14560	14913	354	0	+	ATG	TAG
tRNA-Ser (agc)	tRNA	14914	14981	68	0	+		
ND2	CDS	14982	16037	1056	0	+	ATG	TAA

***Clionella kraussii* (Clavatulidae)**

Product (gene)	Type	Start	Stop	Length	Intergenic	Strand	Start Codon	Stop Codon
COX1	CDS	2615	4153	1539	61	+	ATG	TAA
COX2	CDS	4215	4899	685	0	+	ATG	T—
tRNA-Asp	tRNA	4900	4967	68	0	+		
ATP8	CDS	4968	5123	156	3	+	ATG	TAA
ATP6	CDS	5127	5825	699	37	+	ATG	TAA
tRNA-Met	tRNA	5863	5930	68	9	-		
tRNA-Tyr	tRNA	5940	6006	67	1	-		
tRNA-Cys	tRNA	6008	6071	64	4	-		
tRNA-Trp	tRNA	6076	6141	66	0	-		
tRNA-Gln	tRNA	6142	6205	64	1	-		
tRNA-Gly	tRNA	6207	6273	67	0	-		
tRNA-Glu	tRNA	6274	6343	70	0	-		
s-rRNA	rRNA	6344	7311	968	0	+		
tRNA-Val	tRNA	7312	7380	69	0	+		
l-rRNA	rRNA	7381	8753	1373	0	+		
tRNA-Leu (cta)	tRNA	8754	8822	69	2	+		
tRNA-Leu (tta)	tRNA	8825	8894	70	0	+		
ND1	CDS	8895	9836	942	7	+	ATG	TAA
tRNA-Pro	tRNA	9844	9911	68	1	+		
ND6	CDS	9913	10413	501	148	+	ATG	TAA
tRNA-Ser (tca)	tRNA	10562	10627	66	244	+		
CYTb	CDS	10872	12011	114	225	+	ATG	TAG
tRNA-Thr	tRNA	12237	12305	69	6	-		
ND4L	CDS	12312	12608	297	-7	+	ATG	TAG
ND4	CDS	12602	13973	1372	0	+	ATG	T—
tRNA-His	tRNA	13974	14039	66	1	+		
ND5	CDS	14041	15756	1716	4	+	ATG	TAA
COX3	CDS	1	732	732	11	+	???	TAA
tRNA-Lys	tRNA	744	812	69	16	+		
tRNA-Ala	tRNA	829	894	66	0	+		
tRNA-Arg	tRNA	895	963	69	23	+		
tRNA-Asn	tRNA	987	1055	69	13	+		
tRNA-Ile	tRNA	1069	1137	69	3	+		
ND3	CDS	1141	1494	354	0	+	ATG	TAG
tRNA-Ser (agc)	tRNA	1495	1556	62	6	+		
ND2	CDS	1563	2614	1052	0	+	ATG	TA—

***Clavatulatripartita* (Clavatulidae)**

Product (gene)	Type	Start	Stop	Length	Intergenic	Strand	Start Codon	Stop Codon
COX1	CDS	2651	4189	1539	41	+	ATG	TAA
COX2	CDS	4231	4915	685	0	+	ATG	T—
tRNA-Asp	tRNA	4916	4983	68	0	+		
ATP8	CDS	4984	5139	156	5	+		
ATP6	CDS	5145	5843	699	38	+		
tRNA-Met	tRNA	5882	5949	68	10	-		
tRNA-Tyr	tRNA	5960	6026	67	1	-		
tRNA-Cys	tRNA	6028	6093	66	11	-		
tRNA-Trp	tRNA	6105	6170	66	1	-		
tRNA-Gln	tRNA	6172	6233	62	5	-		
tRNA-Gly	tRNA	6239	6305	67	1	-		
tRNA-Glu	tRNA	6307	6375	69	0	-		
r-rRNA	rRNA	6376	7340	965	0	+		
tRNA-Val	tRNA	7341	7408	68	0	+		
l-rRNA	rRNA	7409	8770	1362	0	+		
tRNA-Leu (cta)	tRNA	8771	8839	69	2	+		
tRNA-Leu (tta)	tRNA	8842	8911	70	0	+		
ND1	CDS	8912	9853	942	4	+	ATG	TAA
tRNA-Pro	tRNA	9858	9925	68	1	+		
ND6	CDS	9927	10427	501	157	+	ATG	TAA
tRNA-Ser (tca)	tRNA	10585	10650	66	225	+		
CYTB	CDS	10876	12015	114	209	+	ATG	TAA
tRNA-Thr	tRNA	12225	12292	68	3	-		
ND4L	CDS	12296	12592	297	-7	+	ATG	TAG
ND4	CDS	12586	13957	1372	0	+	ATG	T—
tRNA-His	tRNA	13958	14022	65	1	+		
ND5	CDS	14024	15739	1716	4	+	ATG	TAA
COX3	CDS	1	774	774	9	+	???	TAA
tRNA-Lys	tRNA	784	850	67	17	+		
tRNA-Ala	tRNA	868	933	66	0	+		
tRNA-Arg	tRNA	934	1002	69	21	+		
tRNA-Asn	tRNA	1024	1092	69	11	+		
tRNA-Ile	tRNA	1104	1172	69	3	+		
ND3	CDS	1176	1529	354	1	+	ATG	TAG
tRNA-Ser (agc)	tRNA	1531	1598	68	0	+		
ND2	CDS	1599	2650	1052	0	+	ATG	TA—

***Gemmuloborsonia moosai* (Clavatulidae?)**

Product (gene)	Type	Start	Stop	Length	Intergenic	Strand	Start Codon	Stop Codon
COX1	CDS	1	1533	1533	26	+	ATG	TAA
COX2	CDS	1560	2244	685	0	+	ATG	T—
tRNA-Asp	tRNA	2245	2312	68	0	+		
ATP8	CDS	2313	2471	159	2	+	ATG	TAA
ATP6	CDS	2474	3169	696	34	+	ATG	TAA
tRNA-Met	tRNA	3204	3270	67	10	-		
tRNA-Tyr	tRNA	3281	3348	68	1	-		
tRNA-Cys	tRNA	3350	3415	66	1	-		
tRNA-Trp	tRNA	3417	3482	66	1	-		
tRNA-Gln	tRNA	3484	3546	63	5	-		
tRNA-Gly	tRNA	3552	3618	67	1	-		
tRNA-Glu	tRNA	3620	3689	70	0	-		
r-rRNA	rRNA	3690	4653	964	0	+		
tRNA-Val	tRNA	4654	4720	67	0	+		
l-rRNA	rRNA	4721	6074	1354	0	+		
tRNA-Leu (cta)	tRNA	6075	6143	69	24	+		
tRNA-Leu (tta)	tRNA	6168	6237	70	0	+		
ND1	CDS	6238	7179	942	10	+	ATG	TAG
tRNA-Pro	tRNA	7190	7257	68	1	+		
ND6	CDS	7259	7756	498	11	+	ATG	TAA
CYTB	CDS	7768	8907	1140	5	+	ATG	TAA
tRNA-Ser (tca)	tRNA	8913	8978	66	31	+		
tRNA-Phe	tRNA	9010	9076	67	190	+		
tRNA-Thr	tRNA	9267	9333	67	12	-		
ND4L	CDS	9346	9642	297	-7	+	ATG	TAG
ND4	CDS	9636	11007	1372	0	+	ATG	T—
tRNA-His	tRNA	11008	11073	66	1	+		
ND5	CDS	11075	12790	1716	123	+	ATG	TAA
COX3	CDS	12914	13693	780	12	+	GTG	TAA
tRNA-Lys	tRNA	13706	13777	72	8	+		
tRNA-Ala	tRNA	13786	13851	66	0	+		
tRNA-Arg	tRNA	13852	13921	70	5	+		
tRNA-Asn	tRNA	13927	13994	68	1	+		
tRNA-Ile	tRNA	13996	14065	70	3	+		
ND3	CDS	14069	14420	352	0	+	ATG	T—
tRNA-Ser (agc)	tRNA	14421	14488	68	0	+		
ND2	CDS	14489	15541	1053	0	+	ATG	TAA

***Lucerapex sp. (Turridae?)***

<b>Product (gene)</b>	<b>Type</b>	<b>Start</b>	<b>Stop</b>	<b>Lenght</b>	<b>Intergenic</b>	<b>Strand</b>	<b>Start Codon</b>	<b>Stop Codon</b>
COX1	CDS	2595	4139	1545	12	+	ATG	TAG
COX2	CDS	4152	4838	687	5	+	ATG	TAA
tRNA-Asp	tRNA	4844	4911	68	0	+		
ATP8	CDS	4912	5070	159	2	+	ATG	TAA
ATP6	CDS	5073	5768	696	36	+	ATG	TAA
tRNA-Met	tRNA	5805	5870	66	10	-		
tRNA-Tyr	tRNA	5881	5946	66	1	-		
tRNA-Cys	tRNA	5948	6012	65	0	-		
tRNA-Trp	tRNA	6013	6078	66	1	-		
tRNA-Gln	tRNA	6080	6142	63	2	-		
tRNA-Gly	tRNA	6145	6211	67	1	-		
tRNA-Glu	tRNA	6213	6281	69	0	-		
r-rRNA	rRNA	6282	7235	954	0	+		
tRNA-Val	tRNA	7236	7303	68	0	+		
l-rRNA	rRNA	7304	8654	1351	0	+		
tRNA-Leu (cta)	tRNA	8655	8723	69	1	+		
tRNA-Leu (tta)	tRNA	8725	8795	71	0	+		
ND1	CDS	8796	9737	942	5	+	ATG	TAA
tRNA-Pro	tRNA	9743	9810	68	1	+		
ND6	CDS	9812	10312	501	7	+	ATG	TAA
CYTB	CDS	10320	11459	1140	7	+	ATG	TAG
tRNA-Ser (tca)	tRNA	11467	11532	66	283	+		
tRNA-Thr	tRNA	11816	11880	65	12	-		
ND4L	CDS	11893	12189	297	-7	+	ATG	TAG
ND4	CDS	12183	13554	1372	0	+	ATG	T—
tRNA-His	tRNA	13555	13618	64	1	+		
ND5	CDS	13620	15338	1719	0	+	ATG	TAA
COX3	CDS	1	744	7440	10	+	???	TAA
tRNA-Lys	tRNA	755	825	71	6	+		
tRNA-Ala	tRNA	832	898	67	-1	+		
tRNA-Arg	tRNA	898	967	70	8	+		
tRNA-Asn	tRNA	976	1043	68	4	+		
tRNA-Ile	tRNA	1048	1117	70	3	+		
ND3	CDS	1121	1474	354	0	+	ATG	TAA
tRNA-Ser (agc)	tRNA	1475	1542	68	0	+		
ND2	CDS	1543	2594	1052	0	+	ATG	TA—

***Cochlespira sp. (Cochlespiridae)***

<b>Product (gene)</b>	<b>Type</b>	<b>Start</b>	<b>Stop</b>	<b>Lenght</b>	<b>Intergenic</b>	<b>Strand</b>	<b>Start Codon</b>	<b>Stop Codon</b>
COX1	CDS	3109	4641	1533	26	+	ATG	TAA
COX2	CDS	4668	5352	685	0	+	ATG	T—
tRNA-Asp	tRNA	5353	5419	67	0	+		
ATP8	CDS	5420	5578	159	2	+	ATG	TAA
ATP6	CDS	5581	6276	696	39	+	ATG	TAA
tRNA-Met	tRNA	6316	6384	69	8	-		
tRNA-Tyr	tRNA	6393	6458	66	1	-		
tRNA-Cys	tRNA	6460	6524	65	0	-		
tRNA-Trp	tRNA	6525	6591	67	0	-		
tRNA-Gln	tRNA	6592	6655	64	13	-		
tRNA-Gly	tRNA	6669	6736	68	0	-		
tRNA-Glu	tRNA	6737	6802	66	0	-		
s-rRNA	rRNA	6803	7757	955	0	+		
tRNA-Val	tRNA	7758	7825	68	0	+		
l-rRNA	rRNA	7826	9173	1348	0	+		
tRNA-Leu (cta)	tRNA	9174	9243	70	10	+		
tRNA-Leu (tta)	tRNA	9254	9322	69	0	+		
ND1	CDS	9323	10264	942	6	+	ATG	TAA
tRNA-Pro	tRNA	10271	10339	69	0	+		
ND6	CDS	10340	10840	501	5	+	ATG	TAA
CYTB	CDS	10846	11985	1140	6	+	ATG	TAA
tRNA-Ser (tca)	tRNA	11992	12056	65	1	+		
tRNA-Thr	tRNA	12058	12124	67	9	-		
ND4L	CDS	12134	12430	297	-7	+	ATG	TAG
ND4	CDS	12424	13795	1372	0	+	ATG	T—
tRNA-His	tRNA	13796	13861	66	1	+		
ND5	CDS	13863	15581	1719	0	+	ATG	TAA
COX3	CDS	1	747	747	112	+	???	TAA
tRNA-Ile	tRNA	860	928	69	3	+		
ND3	CDS	932	1285	354	98	+	ATG	TAA
tRNA-Asn	tRNA	1384	1451	68	122	+		
tRNA-Lys	tRNA	1574	1641	68	1	+		
tRNA-Ala	tRNA	1643	1709	67	0	+		
tRNA-Arg	tRNA	1710	1779	70	208	+		
tRNA-Ser (agc)	tRNA	1988	2055	68	0	+		
ND2	CDS	2056	3108	1053	0	+	ATG	TAA

***Splendrillia* sp. 1 (Drilliidae)**

<b>Product (gene)</b>	<b>Type</b>	<b>Start</b>	<b>Stop</b>	<b>Lenght</b>	<b>Intergenic</b>	<b>Strand</b>	<b>Start Codon</b>	<b>Stop Codon</b>
COX1	CDS	1	1533	1533	26	+	ATG	TAG
COX2	CDS	1560	2244	685	0	+	ATG	T—
tRNA-Asp	tRNA	2245	2312	68	0	+		
ATP8	CDS	2313	2471	159	2	+	ATG	TAA
ATP6	CDS	2474	3169	696	33	+	ATG	TAA
tRNA-Met	tRNA	3203	3271	69	5	-		
tRNA-Tyr	tRNA	3277	3343	67	1	-		
tRNA-Cys	tRNA	3345	3410	66	19	-		
tRNA-Trp	tRNA	3430	3497	68	1	-		
tRNA-Gln	tRNA	3499	3560	62	8	-		
tRNA-Gly	tRNA	3569	3634	66	0	-		
tRNA-Glu	tRNA	3635	3702	68	0	-		
s-rRNA	rRNA	3703	4672	970	0	+		
tRNA-Val	tRNA	4673	4739	67	0	+		
l-rRNA	rRNA	4740	6111	1372	0	+		
tRNA-Leu (cta)	tRNA	6112	6181	70	2	+		
tRNA-Leu (taa)	tRNA	6184	6252	69	0	+		
ND1	CDS	6253	7194	942	1	+	ATG	TAA
tRNA-Pro	tRNA	7196	7261	66	3	+		
ND6	CDS	7265	7765	501	12	+	ATG	TAA
CYTB	CDS	7778	8917	1140	3	+	ATG	TAA
tRNA-Ser (tca)	tRNA	8921	8985	65	28	+		
tRNA-Thr	tRNA	9014	9079	66	19	-		
ND4L	CDS	9099	9395	297	-7	+	ATG	TAG
ND4	CDS	9389	10760	1372	0	+	ATG	T—
tRNA-His	tRNA	10761	10825	65	0	+		
ND5	CDS	10826	12544	1719	1	+	ATG	TAA
tRNA-Phe	tRNA	12546	12609	64	54	+		
COX3	CDS	12664	13443	780	20	+	ATG	TAA
tRNA-Lys	tRNA	13464	13538	75	19	+		
tRNA-Ala	tRNA	13558	13624	67	4	+		
tRNA-Arg	tRNA	13629	13697	69	1	+		
tRNA-Asn	tRNA	13699	13764	66	17	+		
tRNA-Ile	tRNA	13782	13849	68	4	+		
ND3	CDS	13854	14207	354	1	+	ATG	TAG
tRNA-Ser (agc)	tRNA	14209	14275	67	0	+		
ND2	CDS	14276	15331	1056	27	+	ATG	TAA



***Splendrillia* sp. 2 (Drilliidae)**

<b>Product (gene)</b>	<b>Type</b>	<b>Start</b>	<b>Stop</b>	<b>Lenght</b>	<b>Intergenic</b>	<b>Strand</b>	<b>Start Codon</b>	<b>Stop Codon</b>
COX1	CDS	2648	4180	1533	26	+	ATG	TAA
COX2	CDS	4207	4891	685	0	+	ATG	T—
tRNA-Asp	tRNA	4892	4959	68	0	+		
ATP8	CDS	4960	5118	159	3	+	ATG	TAA
ATP6	CDS	5122	5817	696	33	+	ATG	TAA
tRNA-Met	tRNA	5851	5919	69	13	-		
tRNA-Tyr	tRNA	5933	6000	68	1	-		
tRNA-Cys	tRNA	6002	6064	63	21	-		
tRNA-Trp	tRNA	6086	6152	67	1	-		
tRNA-Gln	tRNA	6154	6215	62	10	-		
tRNA-Gly	tRNA	6226	6292	67	0	-		
tRNA-Glu	tRNA	6293	6361	69	0	-		
s-rRNA	rRNA	6362	7332	971	0	+		
tRNA-Val	tRNA	7333	7399	67	0	+		
l-rRNA	rRNA	7400	8772	1373	0	+		
tRNA-Leu (cta)	tRNA	8773	8842	70	4	+		
tRNA-Leu (taa)	tRNA	8847	8915	69	0	+		
ND1	CDS	8916	9857	942	1	+	ATG	TAA
tRNA-Pro	tRNA	9859	9925	67	3	+		
ND6	CDS	9929	10429	501	18	+	ATG	TAA
CYTB	CDS	10448	11587	1140	4	+	ATG	TAA
tRNA-Ser (tca)	tRNA	11592	11656	65	40	+		
tRNA-Thr	tRNA	11697	11762	66	17	-		
ND4L	CDS	11780	12076	297	-7	+	ATG	TAG
ND4	CDS	12070	13441	1372	0	+	ATG	T—
tRNA-His	tRNA	13442	13507	66	0	+		
ND5	CDS	13508	15231	1724	0	+	ATG	???
COX3	CDS	1	756	756	19	+	???	TAA
tRNA-Lys	tRNA	776	849	74	9	+		
tRNA-Ala	tRNA	859	926	68	6	+		
tRNA-Arg	tRNA	933	998	66	4	+		
tRNA-Asn	tRNA	1003	1069	67	7	+		
tRNA-Ile	tRNA	1077	1145	69	4	+		
ND3	CDS	1150	1503	354	1	+	ATG	TAA
tRNA-Ser (agc)	tRNA	1505	1571	67	0	+		
ND2	CDS	1572	2627	1056	20	+	ATG	TAA

***Anguloclavus* sp. 1 (Horaiclavidae)**

Product (gene)	Type	Start	Stop	Length	Intergenic	Strand	Start Codon	Stop Codon
COX1	CDS	2600	4138	1539	15	+	ATG	TAA
COX2	CDS	4154	4838	685	0	+	ATG	T—
tRNA-Asp	tRNA	4839	4907	69	1	+		
ATP8	CDS	4909	5064	156	42	+	ATG	TAA
ATP6	CDS	5107	5805	699	28	+	ATG	TAA
tRNA-Met	tRNA	5834	5898	65	8	-		
tRNA-Tyr	tRNA	5907	5972	66	1	-		
tRNA-Cys	tRNA	5974	6038	65	0	-		
tRNA-Trp	tRNA	6039	6106	68	1	-		
tRNA-Gln	tRNA	6108	6170	63	3	-		
tRNA-Gly	tRNA	6174	6239	66	0	-		
tRNA-Glu	tRNA	6240	6307	68	0	-		
s-rRNA	rRNA	6308	7262	955	0	+		
tRNA-Val	tRNA	7263	7330	68	0	+		
l-rRNA	rRNA	7331	8674	1344	6	+		
tRNA-Leu (cta)	tRNA	8681	8749	69	1	+		
tRNA-Leu (tta)	tRNA	8751	8819	69	0	+		
ND1	CDS	8820	9761	942	2	+	ATG	TAA
tRNA-Pro	tRNA	9764	9831	68	1	+		
ND6	CDS	9833	10333	501	14	+	ATG	TAA
tRNA-Ser (tca)	tRNA	10348	10413	66	7	+		
CYTB	CDS	10421	11560	1140	4	+	ATG	TAA
tRNA-Thr	tRNA	11565	11630	66	5	-		
ND4L	CDS	11636	11932	297	-7	+	ATG	TAG
ND4	CDS	11926	13294	1369	0	+	ATG	T—
tRNA-His	tRNA	13295	13361	67	1	+		
ND5	CDS	13363	15078	1716	0	+	ATG	TAA
COX3	CDS	1	759	759	11	+	???	TAA
tRNA-Lys	tRNA	771	835	65	2	+		
tRNA-Ala	tRNA	838	903	66	0	+		
tRNA-Arg	tRNA	904	973	70	2	+		
tRNA-Asn	tRNA	976	1042	67	13	+		
tRNA-Ile	tRNA	1056	1119	64	1	+		
ND3	CDS	1121	1474	354	0	+	ATG	TAA
tRNA-Ser (agc)	tRNA	1475	1542	68	0	+		
ND2	CDS	1543	2599	1057	0	+	ATG	T—

***Marshallena* sp. (Horiaclavidae)**

<b>Product (gene)</b>	<b>Type</b>	<b>Start</b>	<b>Stop</b>	<b>Length</b>	<b>Intergenic</b>	<b>Strand</b>	<b>Start Codon</b>	<b>Stop Codon</b>
COX1	CDS	2650	4185	1536	28	+	ATG	TAG
COX2	CDS	4214	4900	687	55	+	ATG	TAA
tRNA-Asp	tRNA	4956	5023	68	0	+		
ATP8	CDS	5024	5182	159	18	+	ATG	TAA
ATP6	CDS	5201	5896	696	38	+	ATG	TAA
tRNA-Met	tRNA	5935	6000	66	8	-		
tRNA-Tyr	tRNA	6009	6075	67	5	-		
tRNA-Cys	tRNA	6081	6146	66	1	-		
tRNA-Trp	tRNA	6148	6215	68	0	-		
tRNA-Gln	tRNA	6216	6279	64	3	-		
tRNA-Gly	tRNA	6283	6349	67	0	-		
tRNA-Glu	tRNA	6350	6419	70	0	-		
s-rRNA	rRNA	6420	7378	959	0	+		
tRNA-Val	tRNA	7379	7445	67	0	+		
l-rRNA	rRNA	7446	8803	1358	0	+		
tRNA-Leu (cta)	tRNA	8804	8872	69	0	+		
tRNA-Leu (tta)	tRNA	8873	8941	69	0	+		
ND1	CDS	8942	9883	942	5	+	ATG	TAG
tRNA-Pro	tRNA	9889	9955	67	1	+		
MD6	CDS	9957	10457	501	6	+	ATG	TAG
CYBT	CDS	10464	11603	1140	8	+	ATG	TAA
tRNA-Ser (tca)	tRNA	11612	11676	65	4	+		
tRNA-Thr	tRNA	11681	11748	68	15	-		
ND4L	CDS	11764	12060	297	-7	+	ATG	TAG
ND4	CDS	12054	13425	1372	0	+	ATG	T—
tRNA-His	tRNA	13426	13491	66	0	+		
ND5	CDS	13492	15210	1719	0	+	ATG	TAA
COX3	CDS	1	771	771	33	+		
tRNA-Lys	tRNA	805	869	65	10	+		
tRNA-Ala	tRNA	880	948	69	1	+		
tRNA-Arg	tRNA	950	1017	68	7	+		
tRNA-Asn	tRNA	1025	1093	69	3	+		
tRNA-Ile	tRNA	1097	1164	68	1	+		
ND3	CDS	1166	1519	354	0	+		
tRNA-Ser (agc)	tRNA	1520	1587	68	0	+		
ND2	CDS	1588	2643	1056	6	+		

***Anguloclavus* sp. 2 (Horaiclavidae)**

Product (gene)	Type	Start	Stop	Lenght	Intergenic	Strand	Start Codon	Stop Codon
COX1	CDS	2584	4122	1539	15	+	ATG	TAA
COX2	CDS	4138	4822	685	0	+	ATG	T—
tRNA-Asp	tRNA	4823	4891	69	1	+		
ATP8	CDS	4893	5048	156	42	+	ATG	TAA
ATP6	CDS	5091	5789	699	28	+	ATG	TAA
tRNA-Met	tRNA	5818	5882	65	8	-		
tRNA-Tyr	tRNA	5891	5956	66	1	-		
tRNA-Cys	tRNA	5958	6022	65	0	-		
tRNA-Trp	tRNA	6023	6090	68	1	-		
tRNA-Gln	tRNA	6092	6154	63	4	-		
tRNA-Gly	tRNA	6159	6224	66	1	-		
tRNA-Glu	tRNA	6226	6293	68	0	-		
s-rRNA	rRNA	6294	7248	955	0	+		
tRNA-Val	tRNA	7249	7316	68	0	+		
l-rRNA	rRNA	7317	8671	1355	0	+		
tRNA-Leu (cta)	tRNA	8672	8740	69	1	+		
tRNA-Leu (tta)	tRNA	8742	8810	69	0	+		
ND1	CDS	8811	9752	942	2	+	ATG	TAA
tRNA-Pro	tRNA	9755	9822	68	1	+		
ND6	CDS	9824	10324	501	16	+	ATG	TAA
tRNA-Ser (tca)	tRNA	10341	10406	66	7	+		
CYTB	CDS	10414	11553	1140	4	+	ATG	TAA
tRNA-Thr	tRNA	11558	11623	66	5	-		
ND4L	CDS	11629	11925	297	-7	+	ATG	TAG
ND4	CDS	11919	13287	1369	0	+	ATG	T—
tRNA-His	tRNA	13288	13351	64	1	+		
ND5	CDS	13353	15068	1716	35	+	ATG	TAA
COX3	CDS	1	744	744	11	+	???	TAA
tRNA-Lys	tRNA	756	820	65	2	+		
tRNA-Ala	tRNA	823	888	66	0	+		
tRNA-Arg	tRNA	889	958	70	2	+		
tRNA-Asn	tRNA	961	1026	66	13	+		
tRNA-Ile	tRNA	1040	1103	64	1	+		
ND3	CDS	1105	1458	354	0	+	ATG	TAA
tRNA-Ser (agc)	tRNA	1459	1526	68	0	+		
ND2	CDS	1527	2583	1057	0	+	ATG	T—

***Benthomangelia* sp. 2 (Mangeliidae)**

Product (gene)	Type	Start	Stop	Length	Intergenic	Strand	Start Codon	Stop Codon
COX1	CDS	2592	4142	1551	62	+	ATG	TAA
COX2	CDS	4205	4889	685	0	+	ATG	T—
tRNA-Asp	tRNA	4890	4956	67	0	+		
ATP8	CDS	4957	5115	159	2	+	ATG	TAA
ATP6	CDS	5118	5813	696	35	+	ATG	TAA
tRNA-Met	tRNA	5849	5916	68	0	-		
tRNA-Tyr	tRNA	5917	5981	65	1	-		
tRNA-Cys	tRNA	5983	6044	62	0	-		
tRNA-Trp	tRNA	6045	6110	66	0	-		
tRNA-Gln	tRNA	6111	6175	65	3	-		
tRNA-Gly	tRNA	6179	6243	65	0	-		
tRNA-Glu	tRNA	6244	6308	65	0	-		
s-rRNA	rRNA	6309	7261	953	0	+		
tRNA-Val	tRNA	7262	7324	63	0	+		
l-rRNA	rRNA	7325	8656	1332	0	+		
tRNA-Leu (cta)	tRNA	8657	8724	68	0	+		
tRNA-Leu (tta)	tRNA	8725	8793	69	0	+		
ND1	CDS	8794	9735	942	3	+	ATG	TAA
tRNA-Pro	tRNA	9739	9806	68	0	+		
ND6	CDS	9807	10309	504	0	+	ATG	TA—
CYTB	CDS	10310	11449	1140	10	+	ATG	TAA
tRNA-Ser (tca)	tRNA	11460	11524	65	0	+		
tRNA-Thr	tRNA	11525	11588	64	5	-		
ND4L	CDS	11594	11890	297	-7	+	ATG	TAG
ND4	CDS	11884	13255	1372	0	+	ATG	T—
tRNA-His	tRNA	13256	13320	65	1	+		
ND5	CDS	13322	15037	1716	0	+	ATG	TAA
COX3	CDS	1	771	771	6	+	???	TAA
tRNA-Lys	tRNA	778	842	65	0	+		
tRNA-Ala	tRNA	843	909	67	0	+		
tRNA-Arg	tRNA	910	975	66	6	+		
tRNA-Asn	tRNA	982	1047	66	5	+		
tRNA-Ile	tRNA	1053	1119	67	1	+		
ND3	CDS	1121	1472	352	0	+	ATG	T—
tRNA-Ser (agc)	tRNA	1473	1540	68	0	+		
ND2	CDS	1541	2591	1051	0	+	ATG	T—

***Toxicochlespira* sp. (Mangeliidae)**

<b>Product (gene)</b>	<b>Type</b>	<b>Start</b>	<b>Stop</b>	<b>Length</b>	<b>Intergenic</b>	<b>Strand</b>	<b>Start Codon</b>	<b>Stop Codon</b>
COX1	CDS	2604	4151	1548	73	+	ATG	TAA
COX2	CDS	4225	4909	685	0	+	ATG	T—
tRNA-Asp	tRNA	4910	4975	66	0	+		
ATP8	CDS	4976	5134	159	2	+	ATG	TAA
ATP6	CDS	5137	5832	696	30	+	ATG	TAA
tRNA-Met	tRNA	5863	5929	67	0	-		
tRNA-Tyr	tRNA	5930	5994	65	1	-		
tRNA-Cys	tRNA	5996	6059	64	0	-		
tRNA-Trp	tRNA	6060	6125	66	0	-		
tRNA-Gln	tRNA	6126	6188	63	4	-		
tRNA-Gly	tRNA	6193	6258	66	3	-		
tRNA-Glu	tRNA	6262	6327	66	0	-		
s-rRNA	rRNA	6328	7275	948	0	+		
tRNA-Val	tRNA	7276	7338	63	0	+		
l-rRNA	rRNA	7339	8677	1339	0	+		
tRNA-Leu (cta)	tRNA	8678	8746	69	0	+		
tRNA-Leu (tta)	tRNA	8747	8814	68	0	+		
ND1	CDS	8815	9756	942	3	+	ATG	TAA
tRNA-Pro	tRNA	9760	9827	68	0	+		
ND6	CDS	9828	10331	504	4	+	ATG	TAA
CYTB	CDS	10336	11475	1140	12	+	ATG	TAA
tRNA-Ser (tca)	tRNA	11488	11552	65	8	+		
tRNA-Thr	tRNA	11561	11625	65	8	-		
ND4L	CDS	11634	11930	297	-7	+	ATG	TAG
ND4	CDS	11924	13295	1372	0	+	ATG	T—
tRNA-His	tRNA	13296	13360	65	0	+		
ND5	CDS	13361	15076	1716	0	+	ATG	TAA
COX3	CDS	1	771	771	4	+	???	TAA
tRNA-Lys	tRNA	776	841	66	0	+		
tRNA-Ala	tRNA	842	908	67	2	+		
tRNA-Arg	tRNA	911	978	68	8	+		
tRNA-Asn	tRNA	987	1052	66	12	+		
tRNA-Ile	tRNA	1065	1131	67	1	+		
ND3	CDS	1133	1484	352	0	+	ATG	T—
tRNA-Ser (agc)	tRNA	1485	1552	68	0	+		
ND2	CDS	1553	2602	1050	1	+	ATG	TAA

***Mitromorpha fischeri* (Mitromorphidae)**

<b>Product (gene)</b>	<b>Type</b>	<b>Start</b>	<b>Stop</b>	<b>Length</b>	<b>Intergenic</b>	<b>Strand</b>	<b>Start Codon</b>	<b>Stop Codon</b>
COX1	CDS	2642	4207	1566	83	+	ATG	TAG
COX2	CDS	4291	4977	687	1	+	ATG	TAA
tRNA-Asp	tRNA	4979	5047	69	0	+		
ATP8	CDS	5048	5206	159	25	+	ATG	TAA
ATP6	CDS	5232	5927	696	34	+	ATG	TAA
tRNA-Met	tRNA	5962	6027	66	4	-		
tRNA-Tyr	tRNA	6032	6097	66	20	-		
tRNA-Cys	tRNA	6118	6180	63	0	-		
tRNA-Trp	tRNA	6181	6246	66	0	-		
tRNA-Gln	tRNA	6247	6310	64	4	-		
tRNA-Gly	tRNA	6315	6380	66	0	-		
tRNA-Glu	tRNA	6381	6446	66	0	-		
s-rRNA	rRNA	6447	7390	944	0	+		
tRNA-Val	tRNA	7391	7458	68	0	+		
l-rRNA	rRNA	7459	8829	1371	0	+		
tRNA-Leu (cta)	tRNA	8830	8897	68	4	+		
tRNA-Leu (tta)	tRNA	8902	8970	69	3	+		
ND1	CDS	8974	9915	942	6	+	ATG	TAG
tRNA-Pro	tRNA	9922	9988	67	0	+		
ND6	CDS	9989	10489	501	5	+	ATG	TAG
CYTB	CDS	10495	11634	1140	12	+	ATG	TAA
tRNA-Ser (tca)	tRNA	11647	11711	65	0	+		
tRNA-Thr	tRNA	11712	11777	66	20	-		
ND4L	CDS	11798	12094	297	-7	+	ATG	TAG
ND4	CDS	12088	13459	1372	0	+	ATG	T—
tRNA-His	tRNA	13460	13523	64	1	+		
ND5	CDS	13525	15243	1719	0	+	ATG	TAG
COX3	CDS	1	756	756	32	+	???	TAG
tRNA-Lys	tRNA	789	858	70	4	+		
tRNA-Ala	tRNA	863	930	68	0	+		
tRNA-Arg	tRNA	931	1000	70	15	+		
tRNA-Asn	tRNA	1016	1081	66	19	+		
tRNA-Ile	tRNA	1101	1167	67	0	+		
ND3	CDS	1168	1521	354	0	+	ATG	TAA
tRNA-Ser (agc)	tRNA	1522	1589	68	0	+		
ND2	CDS	1590	2641	1052	0	+	ATG	TA—

***Inquisitor* sp. (Pseudomelatomidae)**

<b>Product (gene)</b>	<b>Type</b>	<b>Start</b>	<b>Stop</b>	<b>Length</b>	<b>Intergenic</b>	<b>Strand</b>	<b>Start Codon</b>	<b>Stop Codon</b>
COX1	CDS	1	1533	1533	20	+	ATG	TAA
COX2	CDS	1554	2238	685	0	+	ATG	T—
tRNA-Asp	tRNA	2239	2306	68	0	+		
ATP8	CDS	2307	2465	159	2	+	ATG	TAA
ATP6	CDS	2468	3163	696	36	+	ATG	TAA
tRNA-Met	tRNA	3200	3265	66	3	-		
tRNA-Tyr	tRNA	3269	3336	68	3	-		
tRNA-Cys	tRNA	3340	3404	65	2	-		
tRNA-Trp	tRNA	3407	3473	67	1	-		
tRNA-Gln	tRNA	3475	3536	62	4	-		
tRNA-Gly	tRNA	3541	3606	66	0	-		
tRNA-Glu	tRNA	3607	3671	65	0	-		
s-rRNA	rRNA	3672	4633	962	0	+		
tRNA-Val	tRNA	4634	4701	68	0	+		
l-rRNA	rRNA	4702	6049	1348	0	+		
tRNA-Leu (cta)	tRNA	6050	6118	69	2	+		
tRNA-Leu (tta)	tRNA	6121	6189	69	0	+		
ND1	CDS	6190	7131	942	3	+	ATG	TAA
tRNA-Pro	tRNA	7135	7202	68	1	+		
ND6	CDS	7204	7704	501	1	+	ATG	TAA
CYTB	CDS	7706	8845	1140	3	+	ATG	TAA
tRNA-Ser (tca)	tRNA	8849	8913	65	55	+		
tRNA-Thr	tRNA	8969	9034	66	13	-		
ND4L	CDS	9048	9344	297	-7	+	ATG	TAA
ND4	CDS	9338	10709	1372	0	+	ATG	T—
tRNA-His	tRNA	10710	10774	65	0	+		
ND5	CDS	10775	12487	1713	7	+	ATG	TAG
tRNA-Phe	tRNA	12495	12561	67	57	+		
COX3	CDS	12619	13398	780	6	+	ATG	TAA
tRNA-Lys	tRNA	13405	13477	73	4	+		
tRNA-Ala	tRNA	13482	13547	66	0	+		
tRNA-Arg	tRNA	13548	13617	70	11	+		
tRNA-Asn	tRNA	13629	13699	71	5	+		
tRNA-Ile	tRNA	13705	13772	68	3	+		
ND3	CDS	13776	14129	354	0	+	ATG	TA—
tRNA-Ser (agc)	tRNA	14129	14196	68	0	+		
ND2	CDS	14197	15248	1052	0	+	ATG	TA—



***Leucosyrinx* sp. (Pseudomelatomidae?)**

Product (gene)	Type	Start	Stop	Length	Intergenic	Strand	Start Codon	Stop Codon
COX1	CDS	1	1533	1533	26 +		ATG	TAA
COX2	CDS	1560	2244	685	0 +		ATG	T—
tRNA-Asp	tRNA	2245	2313	69	0 +			
ATP8	CDS	2314	2472	159	2 +		ATG	TAA
ATP6	CDS	2475	3170	696	32 +		ATG	TAA
tRNA-Met	tRNA	3203	3267	65	11 -			
tRNA-Tyr	tRNA	3279	3345	67	1 -			
tRNA-Cys	tRNA	3347	3408	62	2 -			
tRNA-Trp	tRNA	3411	3476	66	1 -			
tRNA-Gln	tRNA	3478	3539	62	1 -			
tRNA-Gly	tRNA	3541	3607	67	0 -			
tRNA-Glu	tRNA	3608	3674	67	0 -			
s-rRNA	rRNA	3675	4655	981	0 +			
tRNA-Val	tRNA	4656	4722	67	0 +			
l-rRNA	rRNA	4723	6081	1359	0 +			
tRNA-Leu (cta)	tRNA	6082	6150	69	2 +			
tRNA-Leu (tta)	tRNA	6153	6221	69	0 +			
ND1	CDS	6222	7163	942	7 +		ATG	TAA
tRNA-Pro	tRNA	7171	7239	69	1 +			
ND6	CDS	7241	7741	501	2 +		ATG	TAA
CYTB	CDS	7744	8883	1140	6 +		ATG	TAA
tRNA-Ser (tca)	tRNA	8890	8954	65	122 +			
tRNA-Thr	tRNA	9077	9143	67	11 -			
ND4L	CDS	9155	9451	297	-7 +		ATG	TAG
ND4	CDS	9445	10816	1372	0 +		ATG	T—
tRNA-His	tRNA	10817	10881	65	0 +			
ND5	CDS	10882	12597	1716	5 +		ATG	TAA
tRNA-Phe	tRNA	12603	12669	67	55 +			
COX3	CDS	12725	13504	780	9 +		ATG	TAG
tRNA-Lys	tRNA	13514	13586	73	7 +			
tRNA-Ala	tRNA	13594	13659	66	0 +			
tRNA-Arg	tRNA	13660	13728	69	7 +			
tRNA-Asn	tRNA	13736	13804	69	8 +			
tRNA-Ile	tRNA	13813	13882	70	3 +			
ND3	CDS	13886	14239	354	0 +		ATG	TAG
tRNA-Ser (agc)	tRNA	14240	14306	67	0 +			
ND2	CDS	14307	15358	1052	0 +		ATG	TA—

***Otitoma* sp. (Pseudomelatomidae)**

Product (gene)	Type	Start	Stop	Length	Intergenic	Strand	Start Codon	Stop Codon
COX1	CDS	1	1533	1533	20	+	ATG	TAA
COX2	CDS	1554	2238	685	0	+	ATG	T—
tRNA-Asp	tRNA	2239	2306	68	1	+		
ATP8	CDS	2308	2466	159	2	+	ATG	TAA
ATP6	CDS	2469	3164	696	38	+	ATG	TAA
tRNA-Met	tRNA	3203	3269	67	8	-		
tRNA-Tyr	tRNA	3278	3345	68	0	-		
tRNA-Cys	tRNA	3346	3410	65	3	-		
tRNA-Trp	tRNA	3414	3480	67	0	-		
tRNA-Gln	tRNA	3481	3544	64	8	-		
tRNA-Gly	tRNA	3553	3619	67	0	-		
tRNA-Glu	tRNA	3620	3688	69	0	-		
s-rRNA	rRNA	3689	4655	967	0	+		
tRNA-Val	tRNA	4656	4723	68	0	+		
l-rRNA	rRNA	4724	6083	1360	0	+		
tRNA-Leu (cta)	tRNA	6084	6154	71	12	+		
tRNA-Leu (tta)	tRNA	6167	6235	69	0	+		
ND1	CDS	6236	7177	942	3	+	ATG	TAA
tRNA-Pro	tRNA	7181	7247	67	1	+		
ND6	CDS	7249	7749	501	15	+	ATG	TAA
CYTB	CDS	7765	8903	1139	0	+	ATG	TA—
tRNA-Ser (tca)	tRNA	8904	8969	66	51	+		
tRNA-Thr	tRNA	9021	9087	67	15	-		
ND4L	CDS	9103	9399	297	-7	+	ATG	TAG
ND4	CDS	9393	10764	1372	0	+	ATG	T—
tRNA-His	tRNA	10765	10832	68	0	+		
ND5	CDS	10833	12548	1716	7	+	ATG	TAA
tRNA-Phe	tRNA	12556	12623	68	319	+		
COX3	CDS	12943	13722	780	6	+	ATG	TAA
tRNA-Lys	tRNA	13729	13799	71	3	+		
tRNA-Ala	tRNA	13803	13869	67	0	+		
tRNA-Arg	tRNA	13870	13938	69	14	+		
tRNA-Asn	tRNA	13953	14021	69	5	+		
tRNA-Ile	tRNA	14027	14096	70	3	+		
ND3	CDS	14100	14453	354	11	+	ATG	TAA
tRNA-Ser (agc)	tRNA	14465	14532	68	0	+		
ND2	CDS	14533	15584	1052	0	+	ATG	TA—

***Eubela* sp. (Raphitomidae)**

<b>Product (gene)</b>	<b>Type</b>	<b>Start</b>	<b>Stop</b>	<b>Lenght</b>	<b>Intergenic</b>	<b>Strand</b>	<b>Start Codon</b>	<b>Stop Codon</b>
COX1	CDS	2613	4151	1539	73	+	ATG	TAA
COX2	CDS	4225	4911	687	18	+	ATG	TAG
tRNA-Asp	trna	4930	4994	65	67	+		
ATP8	CDS	5062	5223	162	18	+	ATG	TAA
ATP6	CDS	5242	5934	693	36	+	ATG	TAA
tRNA-Met	tRNA	5971	6036	66	3	-		
tRNA-Tyr	tRNA	6040	6105	66	8	-		
tRNA-Cys	tRNA	6114	6176	63	0	-		
tRNA-Trp	tRNA	6177	6241	65	1	-		
tRNA-Gln	tRNA	6243	6305	63	2	-		
tRNA-Gly	tRNA	6308	6372	65	0	-		
tRNA-Glu	tRNA	6373	6438	66	0	-		
s-rRNA	rRNA	6439	7369	931	0	+		
tRNA-Val	tRNA	7370	7433	64	0	+		
l-rRNA	rRNA	7434	8757	1324	0	+		
tRNA-Leu (cta)	tRNA	8758	8826	69	8	+		
tRNA-Leu (tta)	tRNA	8835	8902	68	1	+		
ND1	CDS	8904	9845	942	0	+	ATG	TAA
tRNA-Pro	tRNA	9846	9909	64	1	+		
ND6	CDS	9911	10415	505	0	+	ATG	T—
CYTB	CDS	10416	11555	1140	10	+	ATG	TAA
tRNA-Ser (tca)	tRNA	11566	11629	64	4	+		
tRNA-Thr	trna	11634	11698	65	7	-		
ND4L	CDS	11706	12002	297	-7	+	ATG	TAG
ND4	CDS	11996	13370	1375	0	+	ATG	T—
tRNA-His	tRNA	13371	13431	61	0	+		
ND5	CDS	13432	15153	1722	0	+	ATG	TAA
COX3	CDS	1	759	759	11	+	???	TAA
tRNA-Lys	tRNA	771	839	69	4	+		
tRNA-Ala	tRNA	844	910	67	2	+		
tRNA-Arg	tRNA	913	980	68	1	+		
tRNA-Asn	tRNA	982	1048	67	5	+		
tRNA-Ile	tRNA	1054	1122	69	2	+		
ND3	CDS	1125	1478	354	2	+	ATG	TAA
tRNA-Ser (agc)	tRNA	1481	1548	68	0	+		
ND2	CDS	1549	2607	1059	5	+	ATG	TAA

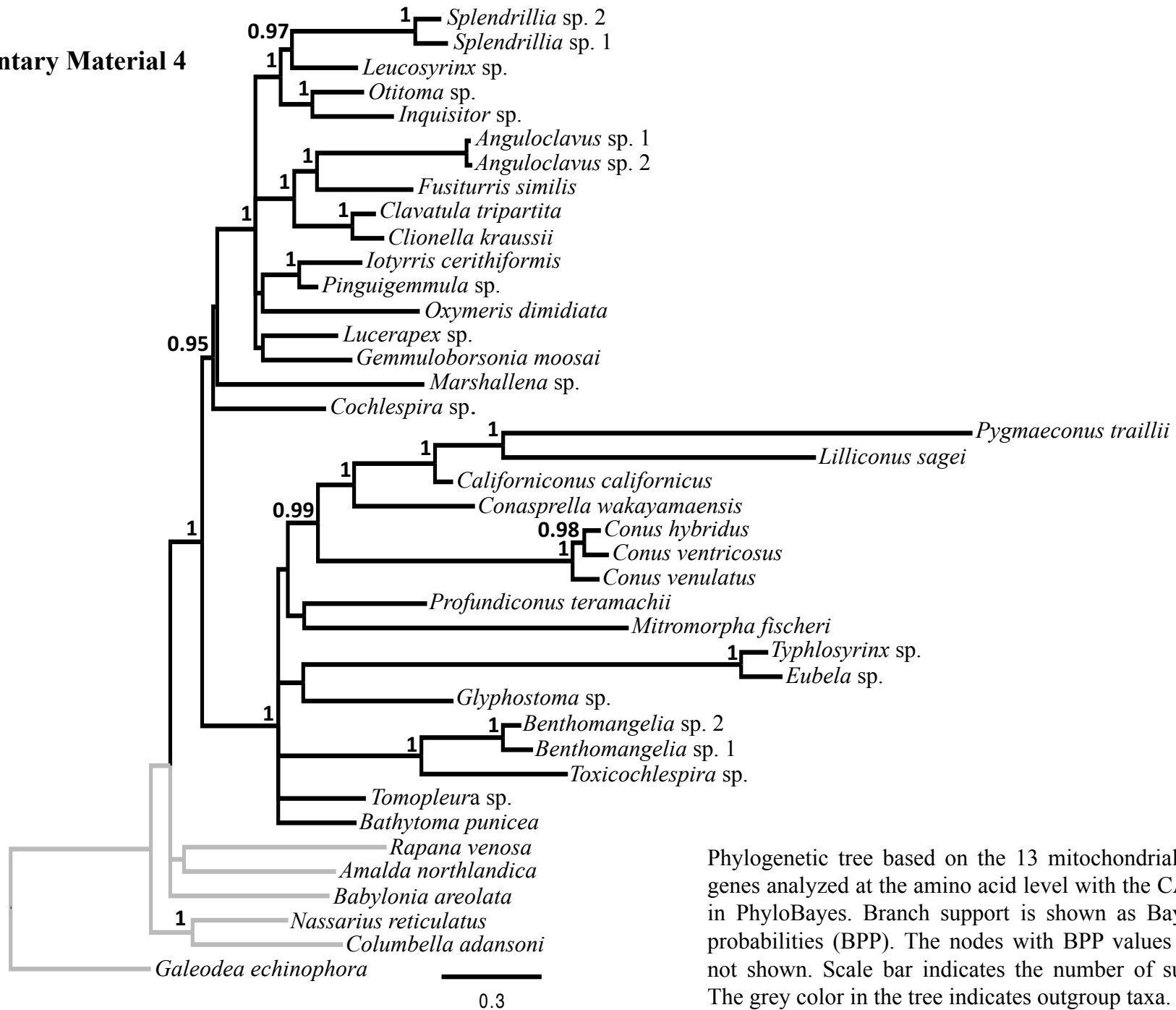
***Typhlosyrinx* sp. (Raphitomidae)**

Product (gene)	Type	Start	Stop	Length	Intergenic	Strand	Start Codon	Stop Codon
COX1	CDS	1	1.539	1539	66	+	ATG	TAA
COX2	CDS	1.606	2.292	687	22	+	ATG	TAA
tRNA-Asp	tRNA	2.315	2.379	65	68	+		
ATP8	CDS	2.448	2.609	162	19	+	ATG	TAA
ATP6	CDS	2.629	3.321	693	36	+	ATG	TAA
tRNA-Met	tRNA	3.358	3.423	66	5	-		
tRNA-Tyr	tRNA	3.429	3.493	65	4	-		
tRNA-Cys	tRNA	3.498	3.559	62	0	-		
tRNA-Trp	tRNA	3.560	3.623	64	1	-		
tRNA-Gln	tRNA	3.625	3.686	62	2	-		
tRNA-Gly	tRNA	3.689	3.753	65	0	-		
tRNA-Glu	tRNA	3.754	3.818	65	0	-		
s-rRNA	rRNA	3.819	4.750	932	0	+		
tRNA-Val	tRNA	4.751	4.814	64	0	+		
l-rRNA	rRNA	4.815	6.129	1315	0	+		
tRNA-Leu (cta)	tRNA	6.130	6.198	69	8	+		
tRNA-Leu (tta)	tRNA	6.207	6.274	68	1	+		
ND1	CDS	6.276	7.217	942	0	+	ATG	TAA
tRNA-Pro	tRNA	7.218	7.281	64	1	+		
ND6	CDS	7.283	7.787	505	0	+	ATG	T—
CYTB	CDS	7.788	8.927	1140	11	+	ATG	TAA
tRNA-Ser (tca)	tRNA	8.939	9.002	64	0	+		
tRNA-Thr	tRNA	9.003	9.067	65	5	-		
ND4L	CDS	9.073	9.369	297	-7	+	ATG	TAG
ND4	CDS	9.363	10.737	1375	0	+	ATG	T—
tRNA-His	tRNA	10.738	10.799	62	0	+		
ND5	CDS	10.800	12.521	1722	8	+	ATG	TAA
tRNA-Phe	tRNA	12.530	12.594	65	582	+		
COX3	CDS	13.177	13.956	780	11	+	ATG	TAA
tRNA-Lys	tRNA	13.968	14.035	68	2	+		
tRNA-Ala	tRNA	14.038	14.104	67	2	+		
tRNA-Arg	tRNA	14.107	14.174	68	1	+		
tRNA-Asn	tRNA	14.176	14.242	67	5	+		
tRNA-Ile	tRNA	14.248	14.314	67	2	+		
ND3	CDS	14.317	14.670	354	2	+	ATG	TAA
tRNA-Ser (agc)	tRNA	14.673	14.740	68	0	+		
ND2	CDS	14.741	15.799	1059	5	+	ATG	TAA

***Pinguiggemula* sp. (Turridae)**

Product (gene)	Type	Start	Stop	Lenght	Intergenic	Strand	Start Codon	Stop Codon
COX1	CDS	2.590	4.134	1545	17	+	ATG	TAA
COX2	CDS	4.152	4.836	685	0	+	ATG	T—
tRNA-Asp	tRNA	4.837	4.906	70	0	+		
ATP8	CDS	4.907	5.065	159	2	+	ATG	TAA
ATP6	CDS	5.068	5.763	696	35	+	ATG	TAA
tRNA-Met	tRNA	5.799	5.866	68	11	-		
tRNA-Tyr	tRNA	5.878	5.945	68	1	-		
tRNA-Cys	tRNA	5.947	6.010	64	0	-		
tRNA-Trp	tRNA	6.011	6.077	67	1	-		
tRNA-Gln	tRNA	6.079	6.140	62	9	-		
tRNA-Gly	tRNA	6.150	6.217	68	0	-		
tRNA-Glu	tRNA	6.218	6.286	69	0	-		
s-rRNA	rRNA	6.287	7.244	958	0	+		
tRNA-Val	tRNA	7.245	7.311	67	0	+		
l-rRNA	rRNA	7.312	8.672	1361	0	+		
tRNA-Leu (cta)	tRNA	8.673	8.742	70	15	+		
tRNA-Leu (tta)	tRNA	8.758	8.827	70	0	+		
ND1	CDS	8.828	9.769	942	12	+	ATG	TAG
tRNA-Pro	tRNA	9.782	9.850	69	1	+		
ND6	CDS	9.852	10.352	501	5	+	ATG	TAA
CYTB	CDS	10.358	11.497	1140	13	+	ATG	TAA
tRNA-Ser (tca)	tRNA	11.511	11.576	66	1	+		
tRNA-Thr	tRNA	11.578	11.643	66	11	-		
ND4L	CDS	11.655	11.951	297	-7	+	ATG	TAG
ND4	CDS	11.945	13.316	1372	0	+	ATG	T—
tRNA-His	tRNA	13.317	13.381	65	0	+		
ND5	CDS	13.382	15.097	1716	0	+	ATG	TAA
COX3	CDS	1	732	732	11	+	???	TAA
tRNA-Lys	tRNA	744	811	68	18	+		
tRNA-Ala	tRNA	830	896	67	0	+		
tRNA-Arg	tRNA	897	965	69	3	+		
tRNA-Asn	tRNA	969	1.037	69	6	+		
tRNA-Ile	tRNA	1.044	1.111	68	4	+		
ND3	CDS	1.116	1.469	354	1	+	ATG	TAA
tRNA-Ser (agc)	tRNA	1.471	1.538	68	0	+		
ND2	CDS	1.539	2.589	1051	0	+	ATG	T—

Supplementary Material 4



Phylogenetic tree based on the 13 mitochondrial protein-coding genes analyzed at the amino acid level with the CAT+GTR model in PhyloBayes. Branch support is shown as Bayesian posterior probabilities (BPP). The nodes with BPP values below 0.95 are not shown. Scale bar indicates the number of substitutions/site. The grey color in the tree indicates outgroup taxa.

# Supplementary Material 5

*atp6*

	1	10	20	30	40	50	60	70	80	90	100	110	120	130	140	150
1Bathytoma_punicea	ATGCTTGTAGATATTTTTCTCTTTGACGATAAATAACCAAGT	TTTTATATCACTTTACATATTAATAATGAATTTTTTCATTA	ATAATACAAATTATCTCTTTAGGTCTTCTTACTGAGTAAATG	CAAC	CCCGCATGAAATAGGGCTATTAGGTT											
2Clionella_kraussii	ATGCTAAATGATATCTTTCTCTTCGACGATAAACAATCAGG	TTTTATGTCATTGTATATCTAATATGATTATTTCCACTT	GTAACAGTGTAGTTTATTAGATTATCTTATTGAACTATGC	CCCCCTCAATGAGCCTCAATACAAGAA												
3Clavatulatripartita	ATGCTTATAGATATTTTTCTCTCTTTGATGATAAACAATC	AGGTTTTATGTCATTATATATTTAATGTGGTTATCCCGT	TAGCAACAGTGTAGCTATTTAGGGTGTCTATTGAACTAT	GCTCCACCTCAATGAACCTCAGTTGTAAGAA												
4Gemuloborsoniamoosai	ATGCTTATAGATATTTTTCTCTTTGATGATAAATAACCA	AGGTTTTATATCTTTATATATTTAATGTGAATTTTTCC	CCGTGAGAACGATTTTTCTCTTTAGTTATCTTATTGAG	TAATGTTA	CCAAAAATGAACTAGTATTATTAGAA											
5Lucerapex_sp	ATGCTTATGATATTTTTCTCTTTGATGATAAATAACCA	AGTTTTTATATCCCTATATATATTAATATGAACTTTT	CTTTAGCCACAATTTACTTTATTAGATCCTCTACTGAG	TTCATCT	CCCCGTTGAATTAGAATTATTAGAA											
6Cochlespirasp	ATGCTTATAGATATTTTTCTCTTCGATGATAAATAAC	CAGTTTTTATGTCATTATATGTTCTTATATGAATGTT	TCGTTATATTAATCTTCTTTTATAGTTCTAATTACT	GAGTTATGGCT	CCCCGATGAACAAGATAATAAGAA											
7Splendrilliasp1	ATGTTTATAGATATTTTTCTCTTCGATGATAAATAAC	CAGTTTTTATGTCATTATATGTTCTTATATGAATGTT	TCGTTATATTAATCTTCTTTTATAGTTCTAATTACT	GAGTTATGGCT	CCCCGATGAACAAGATAATAAGAA											
8Splendrilliasp2	ATGTTTATAGATATTTTTCTCTTTGATGATAAACAAT	CAGGTTTTATGTCATTATATGTTCTTATATGAATAT	TTTCACTCAGATTAATTTCTTTTAGCTCTAATTATT	GAGTTATGGCT	CCTCGTTGAATAAAAAACAAGAA											
9Anguloclavus_sp1	ATGCTTATGATATTTTTCTCTTTGACGATAAACAAT	CAAGTTTTATATCTTTTATGTAATGTTATTTCCAAT	TTTCTACCTCATGCTTTTTAGGTTATCTTATTGAG	TAACTGTCC	CCCAATGAACTCAATTTATTAGAA											
10Marshallenasp	ATGCTTGTAGATATTTCTCTTCGACGATAAATAAC	AGTTTTTATATCTTTATACATTTAATATGAGGCTT	TCGCTTAAACAATAGCCTTTTAGCCTATCTACTGG	TAGATTCC	CCTCGATGGTTGAGCATCATTAGAG											
11Anguloclavus_sp2	ATGCTGATAGACATTTCTCTTTCGACGATAAACAAT	CAAGTTTTATATCTTTTATATCTAATGTAATTTT	CCAATTTCTACCTCATGCTTTTTAGGTTATCTT	ATTGAGTAACTGTCC	CCCAATGAACTCAATTTATTAGAA											
12Benthomangaliasp2	ATGCTAGTTGACATTTTTCTCGTTGATGATAAATA	CAAGTTTTATATCAATATATTTTTAATGTGAATTT	TTTCTTTTACAACAATTTATTATTAGTTCTTCTT	ATTGAATGAAGC	CCCAGTTGAATCAATTTAATTT											
13Toxicochlespirasp	ATGCTCGTAGATATTTTTCTCATTGTGACAAATA	CAAGTCTTTATATCATTATATATTTAATATGAAT	TTTTCTTTTATAAGAAATGTTTACTCAGATCATCT	ATTGAATAGAGAAT	CCTCAGTGAATGAAATAATTAAT											
14Mitromorphafischeri	ATGCTTGTAGATATTTTTCTCTTTGATGATAAATA	CAGGTTTTATATCACTGTATATCTTGATATGAT	GTTTTCTTTAGTAAACAATCTTAACTTTAGACCT	CGTTTTGATTAATTTAC	CCCGCATGAATATCTTTATATATT											
15Inquisitorsp	ATGTTTATAGATATTTTTCTCTTCGACGATAAATA	CAAGTTTTATATCAATATATTTAATATGGGTTT	TTTCTTTAGCTACTATCTGTTTTTAGGTCATCT	CTCAGTAACTGCT	CCTCGTGGCAAAGTTAGTTAGAA											
16Leucosyrinxsp	ATGTTTATAGATATTTTTCTCTTTGATGATAAACA	ATCAGTTTTTATATCATTATATATTTAATATGACT	TTTTCTCATTAGTACTATTTATTTCTTTAGTTCT	TCTTATTGAAATAGATTT	CCTCGTGGACAAGAATTTAGTA											
17Otitomasp	ATGTTTATAGATATTTTTCTCTTTGATGATAAATA	CAGGTTTTATATCACTATATGCTTTGATGTGAAT	ATTTTCATTAGTCACTATTTGTTTTTTTAGTT	CATCTTATTGGGTTGCATCT	CCACGGTGAATAAGCATAATTAGAA											
18Eubelasp	ATGCTTGTAGATATTTTTCTCTTCGATGATAAATA	CAACAACTTTTATGTCATTTTATATTAACTTGA	ATTTTTCTGTTACTGATAAATTTTTTTTAGTTCT	TCTTACTGAGTTATAAAT	CCTAAGTGAATTTCTATTATTAAT											
19Typhlosyrinxsp	ATGCTTGTAGATATTTTTCTCTTCGATGATAAATA	CAAACTTTATGTCATTTTATATTAACTTGAAT	TTTTCTTAAATTAATAATTTACTTTTAGTTGTT	ATTATTAAGC	CCTAAATGAAATTTCTATCATTAAAT											
20Pinguigemmulasp	ATGTTTATAGATATTTTTCTCTTTGATGATAAATA	CAAGTTTTATATCGTTATATATTAATATGGAAT	TTTTCTGCTTAAACAATATTTTTTTAGCTCATCT	ATTGAGTAATATTA	CCACGATGATCTAGAGTTATTAGAA											
21Conasprellawakayamaensis	ATGCTTGTAGATATTTTTCTCTTTGACGATAAACA	CAAGTTTTATATCATTTTATGTAATATGTAAT	TTTTCTCCCTAGTAACTATTTAGTTTCTTATTG	ATTTGATTTGATTT	CCTCGTTGAAACAAGAAATTTAATCT											
22Conus_ventricosus	ATGCTTGTGATATTTTTCTCGTTGATGATAAATA	CAAGTTTTATGTCGTTGATATTTAATATGGGTT	TTTTCTTGTATTAGTTGTTCTTTTAGTTCTCT	TTTTGATTAGTGAC	CCTCGTGAACAACCTTTTTATTAAT											
23Conus_venulatus	ATGCTTGTGATATTTTTCTCATTGTGATGATAAATA	CAAGTTTTATGTCGTTGATGTTAATGTGAATTT	TTTCTTATTATAGTTGTTCTTTTAGTTCTCT	TTTTGGCTAGTATAC	CCTCGTTGAAATTTCTTTGTCAAT											
24Conus_hybridus	ATGCTTGTGATATTTTTCTCGTTGATGATAAATA	CAAGTTTTATGTCGTTGATATTTAATGTGAATTT	TTTCTTGTATTAGTTGTCCTTTTAGTTCTCT	TTTTGATTGGTACAT	CCTCGATGGAATTTCTTTATTAACA											
25Californiconus_californicus	ATGCTTGTAGATATTTTTCTCGTTGATGATAAATA	CAAGTTTTATATCACTGTATGTAATATGGCTTT	TTTCTTATTACAACCTGTCCTTTTAGCTCATCT	TTTTGACTGAGATTT	CCACGATGAACAAGTATCATTAACT											
26Lilliconus_sagei	ATGCTTGTAGATATTTTTCTCTTTGATGATAAATA	CAGATTTTTATATCTCATACATTTTTGACGTG	AAATTTCTCTTAAITTCACITATTTTTTAGTCT	TGTTTTGATTTGATTT	CCACGATGAGGAATAATTTAATCT											
27Pygmaeconustrailii	ATGTTAACAGATATTTTTCTCTTTGACGATAAATA	CAAGTATTTATGTCCTTTATATATTTAATGTGG	TTTTCTTCTTAGTATTATTTATTTTAGTT	CATCTTTTGATATGATCT	CCCGCTGAAGATCATTATCAACT											
28Profundiconusteramachii	ATGCTTGTAGATATTTTTCTCGTTGATGACAACA	ATCAGGTTTTATGTCCTTTATATTTAATATGA	ATTTTTCTTAAATAACAATGTTTTATTAGTT	CATCGTATTGAATAGCATT	CCACGATGAAATACTGTTATTAAT											
29Tomopleurasp	ATGCTTGTGATATTTTTCTCTTTGATGATAAATA	CAAGTTTTATATCGTTTTATGTTTTAATATG	AGTTTTTCTTAAATAACAATTTATTATTAG	TTTCTTATTGAATAAAGC	CCAAATGAAATGAAATTAATTAAT											
30Benthomangaliasp1	ATGCTAGTTGACATTTTTCTCATTGTGATGATAA	ATCAGGTTTTATATCAATATATTTTAAATATGA	ATTTTTCTTTTGAACAATTTATTATTAGTT	CATCTTATTGAATAAAGC	CCAAATGAAATGAAATTAATTAAT											
31Glyphostomasp	ATGCTTGTAGATATTTTTCTCATTGACGATAAATA	CAAGTTTTATATCTTTCTATTTTGTGATGACT	TTTTCTTATTACAGTTTTCTTTTAGGTTAT	GTGCTT	CCTCGATGAAATCAGTTTATTAGAA											
32Fusiturris_similis	ATGCTTATGGATATTTTTCTCTTTGATGATAAATA	CAAGTTTTATATCTTTGATGATAATGAAATTT	TTTCTTAAATGACTATTTCTTTATTAGATTAT	CTACTGGCAATGCTCT	CTCAATGAGCATCGTTATTAGAA											
33Oxymymerisdimidiata	ATGTTTATGGATATTTTTCTCTTTGATGATAAACA	ATCAGGTTTTATATCTTTATGTTTGTATGA	AGGTTTTACATTTAAACAGTTGTTTTTTAG	TCTCTTATTGAGTAATTA	CCTCGCTGAAGAAGTATTACTAGTA											
34Iotyrris_cerithiformis	ATGTTTATAGATATTTTTCTCTTCGATGATAAATA	CAAGTTTTATATCATTATATATTAATGTGAAT	TTTTCTCATTATAAATATTTGCTTTTAGCT	CATCATACTGAGTAATATTA	CCCGCTGATCAAGAATTTATTAGAA											
35Amalda_northlandica	ATGCTAGTAGATATTTTTCTCATTGTGATGATAA	CAACAATTTTTATATCTTTGACATTTAATGT	AGTTTTTCTTAAATAACAATGTTTTATTAG	ATCATCATACTGAGTTATGTT	CCACGATGAGTTTCTCTAGTGAGAA											
36Babylonia_aeolata	ATGCTTGTAGATATTTTTCTCATTGACGATAAACA	CAAGTTTTATATCGTTTATATGTTTGTGAGT	TTTTCTTAAATAACAATTTACTTTTTAGG	TCTTATTGAGTTCTCT	CCCGTGAATTTCTATTTAGTA											
37Rapanavenosa	ATGCTTGTGATATTTTTCTCGTTGATGACAATA	CAAGTTTTATATCTCTATATATTTAATATGG	TGTTTTCTTATTGAACAATGTTCTTTAG	TCTTATTTGAATATATCT	CCCGCATGAACTAGTGTAGTTGAA											
38Columbellaadasoni	ATGCTAGTAGATATTTTTCTCATTGACGATAAATA	CAAGTTTTATATCTTTATGTTTAAATGTGG	TTTTCTTTAGTAACTATGTTCTTATTTAG	TCTTATTTGAGTTATGACT	CCTCGTTGAGTAAGTGAATTAGAG											
39Nassarius_reticulatus	ATGCTTGTAGATATTTTTCTCTTTGATGATAAATA	CAAGTTTTATATCGCTATATGTTAATATGA	ATTTTTCTGTTAACTAATTTGTTTTATTG	AGTTCTCTACTGAGTTATATCT	CCTCGTTGATTAAAGAATGTGAGTG											
40Galeodea_echinophora	ATGCTTGTAGACATTTCTCTTTGATGATAAATA	CAAGTTTTATATCTTTATATTTAATATGAG	TTTTCTTAAAGCACAATTTATTTTTAGAT	CTACCTATTGAACTATATCT	CCTCGTTGAGTAAGCCTAATTTAA											

127

Alignment showing the beginning of the *atp6* gene in different species of Conoidea. An insertion of three nucleotides (one amino acid in the open reading frame) is found at position 127 in several species from the same clade in the reconstructed phylogeny. The inserted codon translates into Proline in *Clionella kraussii*, *Clavatulatripartitato*, and *Fusiturris similis*, and into Alanine in the two species of *Anguloclavus*.