



The hidden companion of non-native fishes in Northeast Atlantic waters

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The hidden companion of non-native fishes in Northeast Atlantic waters

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Abstract

A tropicalisation phenomenon of the ichthyofauna has been described in the last decades in Galicia (north-eastern Atlantic), with increasing reports of tropical and subtropical fishes appearing northward of this distribution range. A search for parasites was carried out in the digestive tract of two specimens first captured in Galician waters: the Prickly puffer *Ephippion guttifer* (Tetraodontidae) and the African striped grunt *Parapristipoma octolineatum* (Haemulidae). The parasitological examination of *E. guttifer* showed a high intensity of nematodes, belonging to three different genera: *Cucullanus* (Cucullanidae), *Hysterothylacium* (Raphidascaridae) and *Anisakis* (Anisakidae), the last one with demonstrated pathogenicity to humans. Molecular identification allowed the identification of *Anisakis pegreffii* and the first report for European waters of *Cucullanus dodsworthi*, *Hysterothylacium reliquens* and a new *Hysterothylacium* sp. *P. octolineatum* showed far lower level of parasitation, with only two *Hysterothylacium* larvae, genetically identified as *Hysterothylacium deardorffoverstreetorum*, being thus also a first report of this species for the Eastern Atlantic. The possible ecological impact of the occurrence of non-native fish species in a new area reach a different point if we consider that only two individual fish can harbor more of one hundred nematoda belonging to five different species.

38 **Keywords:** tropicalization, non-native fish, *Anisakis pegreffii*, *Hysterothylacium* spp.,
39 *Cucullanus dodsworthi*
40

41 1. INTRODUCTION

42 There are multiple evidences that the climate of the planet is changing, and one of the most
43 patent consequences is the increasing of the average surface temperature in the seas.

44 Galicia is an autonomous region of Spain located in the north-western corner of the Iberian
45 Peninsula (41°–43°N), in the northern boundary of the Iberian upwelling system. In this
46 upwelling system, an increase in the SST of 0.68°C between 1982 and 2006 was observed,
47 but the prediction for the period 1960/1990–2070/2100 is between 1.4 and 2.4°C (Philippart
48 et al., 2011). Studies from Galicia region also show similar results: a rise of 0.24°C per
49 decade has been observed in the Galician sea waters since 1974 (Gómez-Gesteira et al.,
50 2011).

51 Oceanic changes in temperature due to global climate change are causing poleward shifts in
52 the latitudinal abundance and distribution ranges of fish species, which may cause dramatic
53 changes in assemblages and trophic webs and have been shown to affect ecosystems and
54 fisheries (Horta e Costa et al., 2014). As consequence, a tropicalization of coastal fish
55 communities has indeed been occurring in the NE Atlantic, including the Macaronesian
56 archipelagos, the Mediterranean Sea, and the European continental shelves, from the
57 Iberian Peninsula up to the North Sea (Afonso et al., 2013).

58 In Galician waters, this tropicalization phenomenon is also very apparent. In a revision of
59 the marine fish fauna, a total of 17 African fish species have been found in Galicia, most of
60 them recorded for the first time during the last decades (Bañón, Villegas-Ríos, Serrano,
61 Mucientes, & Arronte, 2010) and this migration persists to the present day. Among them,
62 there are several species whose finding represents the current northern distribution
63 boundary in the Eastern Atlantic, such as *Seriola fasciata* (Bloch, 1793) (Bañón &
64 Mucientes, 2009), *Fistularia petimba* (Lacepède, 1803) (Bañón & Sande, 2008) or
65 *Lagocephalus laevigatus* (Linnaeus, 1766) (Bañón & Santás, 2011).

66 The Prickly puffer *Ephippion guttifer* (Bennett, 1831) is a western African tetraodontid
67 species, ranging from Morocco to Angola, with sporadic intrusions in the western
68 Mediterranean (Bañón, Alonso-Fernández, Barros-García, Rios, & De Carlos, 2018). It is a

69 demersal fish species inhabiting shallow coastal and estuarine environments to depths of
70 approximately 50 m. The African striped grunt *Parapristipoma octolineatum*
71 (Valenciennes, 1833) is a haemulid demersal species that is found over sandy and rocky
72 areas from two to 180 m depth, ranging from Portugal to Angola and the western
73 Mediterranean (Carpenter & Johnson, 2016).

74 In spite of the continuous new arrivals of southern fishes, there is a lack of information on
75 those species that could be introduced hidden and simultaneously: their parasites. In
76 Galicia, and for extension in the Atlantic European, most studies of parasites are focused on
77 commercially exploited shellfish, mainly bivalves, due to their economic importance and
78 the mortalities they cause (Villalba et al., 2014). Studies of parasites in fish are less
79 numerous and focused in fishery species (Sanmartin-Duran, Quinteiro, & Ubeira, 1989),
80 including *Anisakis* infestation (Abollo, Gestal, & Pascual, 2001; Rodríguez, Abollo,
81 González, & Pascual, 2018), but also in farmed fishes (Iglesias et al., 2001). The public
82 concern about fish parasites increases when considering those which affect commercial
83 species, devaluating their market price, or those which are responsible for seafood-
84 associated infections.

85 This paper aims to describe the parasite fauna in non-native fishes detected in Galician
86 waters, emphasizing the increased impact of the occurrence of some southern fish out of
87 their habitual distribution range when we put the focus on their hidden companion.

88

89 2. MATERIAL AND METHODS

90

91 2.1. Host 92 species

93 Two tropical fish species were caught alive for the first time in Galician waters, NW Spain.
94 A male specimen of *E. guttifer* of 570 mm TL was caught on 10 January 2017 with
95 trammel nets in the mouth of the Ría de Vigo, at 40° 42' 46.021" N, 8° 51' 24.998" W and at
96 a depth of approximately five metres (Bañón et al., 2018). The second specimen was a
97 female of *P. octolineatum* of 293 mm TL, caught by a spear fisherman in Punta Faxilda, in
98 the mouth of Ría de Pontevedra, on 21 July 2018, at 42°24.907N, 8°53.208W and 7 m

3

99 depth. Both specimens were deposited in the Museo de Historia Natural da Universidade de
100 Santiago de Compostela (MHNUSC, Santiago de Compostela, Spain) with the collection
101 number MHNUSC25103 for *E. guttifer* and MHNUSC 25124 for *P. octolineatum*.

102

103 **2.2. Parasite detection and morphological characterization**

104 Guts were dissected and examined under a dissecting microscope, and all the detected
105 parasites were recovered and morphologically classified. Then, viscera were processed by
106 peptic digestion for specific recovery of any remaining nematodes, following Llarena-
107 Reino et al. (2013). Again, different morphological types of nematodes were collected
108 separately. Data and samples were collected and coded in a BioBank platform, a certified
109 service (ISO9001) that hosts a collection of biological samples and organized as a technical
110 unit with defined quality criteria, order and destination, to ensure full traceability of
111 samples and data.

112 A scanning electron microscope (SEM) study of an adult female of *Hysterothylacium* was
113 also carried out. Adult female nematode identified as *Hysterothylacium* sp. isolated from
114 the digestive tract, were washed in PBS. Ova and the central part of the body were used for
115 molecular identification. The anterior and posterior ends of one of the worms were
116 processed at the CACTI Electron Microscopy Service (University of Vigo) for SEM. The
117 selected specimens were fixed in 1% glutaraldehyde in 0.01M PBS, pH 7.4, postfixed in
118 OsO₄ 1% in cacodylate buffer 0.01M pH 7.4, dehydrated using an acetone series and then
119 critical point dried. The specimens were coated with gold and examined using a FEI Quanta
120 200 scanning electron microscope in rough vacuum conditions at an accelerating voltage of
121 12.5 kV.

122

123 **2.3.**

124 **Molecular identification of nematode parasites**

125 Twenty four samples of those nematodes (23 from *E. guttifer* and one from *P.*
126 *octolineatum*), including all different morphological types were then selected and processed
127 for molecular identification. Genomic DNA purification of the nematode parasites was
128 performed employing NucleoSpin Tissue Kit (Macherey-Nagel, Easton, PA), according to
129 the manufacturers protocol for isolating genomic DNA from human or animal tissue and

130 cultured cells. DNA quality and quantity was checked in a spectrophotometer Nanodrop®
131 ND-2000 (Thermo Scientific). To identify the nematodes species, ITS rDNA region was
132 amplified using the primers NC5/NC2 described by Zhu et al. (2000), as well as a SSU
133 rDNA fragment using the primer 18SU467F/18SL1310R (Suzuki, Hoshino, Murakami,
134 Takeyama & Cho, 2008) in one case. Reactions were performed in a total volume of 25 ml
135 containing 1 µl of genomic DNA (10 ng), PCR buffer at 1x concentration, 0.3 µM primers,
136 0.2 mM nucleotides and 0.025 U. µl⁻¹ KAPA Taq DNA polymerase
137 (KAPABIOSYSTEMS). The PCR products were separated on a 2% agarose gel in Tris
138 acetate EDTA buffer, stained with Red Safe and scanned in a GelDoc XR documentation
139 system (Bio-Rad Laboratories). PCR products were cleaned for sequencing using
140 ExoProStar™ 1 Step (GE Healthcare, NJ, USA) for 15 min at 37 °C, followed by
141 inactivation for 15 min at 80 °C. Sequencing was performed in a specialised service
142 (StabVida, Portugal) and the chromatograms were analysed using ChromasPro v.1.41
143 Technelysium Pty Ltd. All generated sequences were searched for identity using BLAST
144 (Basic Local Alignment Search Tool) through web servers of the National Center for
145 Biotechnology Information (USA). Phylogenetic analysis was performed with ITS
146 sequences obtained in this study and with sequences of the genus *Hysterothylacium* and
147 *Anisakis* available in GenBank (Table 1). *Ascaridia columbae* (KF147909) was used as
148 outgroup. Alignments were performed using Clustal W (Thompson, Higgins, & Gibson,
149 1994) included in MEGA 7 (Kumar, Stecher, & Tamura, 2016). Maximum-likelihood
150 analysis (ML) implemented in MEGA 7 software was used to generate phylogenetic tree.
151 Kimura 2-parameter model was found the most appropriate evolutionary model for the
152 analysis. The ML tree was assessed by bootstrap analysis with 500 replicates.

153

154 3. RESULTS

155

156 3.1. Morphological features

157 Examination under a dissecting microscope and after artificial peptic digestion for
158 parasitological analysis showed the presence of 116 nematoda in the visceral tract of *E.*
159 *guttifer*. Two of them were female adults belonging to the genus *Hysterothylacium*, 111
160 were *Hysterothylacium* larvae, 1 was a *Cucullanus* sp. and 2 were L3 larvae of the genus

161 *Anisakis*. Different morphological features leading to this generic identification could be
162 seen in Figure 1. Figure 1a shows the anterior extremity of a *Hysterothylacium* adult female
163 with 3 lips, approximately equal in size, and with prominent lateral flanges. Figure 1b
164 shows the tail tip, with numbers of small nodular protuberances. Figure 1c provides an
165 image of the general aspect of a specimen of one of the *Hysterothylacium* larvae. Figure 1
166 also shows the characteristics boring tooth (bt, Figure 1d) and tail mucron (m, Figure 1e)
167 of a L3 larvae of the genus *Anisakis* and Figures 1f and 1g showed the characteristic
168 muscular esophagus, expanded in width at both ends (Figure 1f) and the cephalic end
169 (Figure 1g) of a *Cucullanus* nematode.

170 In *P. octolineatum*, only two nematode larvae were detected, and morphologically
171 identified as belonging to the genus *Hysterothylacium* (Figures 1h, 1i and 1j), with some
172 very distinctive features, such as tail mucron presence (m, Figures 1h and 1i).

173

174 **3.2. Molecular identification**

175 Blast search of ITS1-5.8S-ITS2 sequences obtained of the nematode parasites from *E.*
176 *guttifer* showed the following results: 3 sequences (from ova and adults of
177 *Hysterothylacium* sp.) were 99-100% similar to *Hysterothylacium reliquens* sequences
178 deposited in GenBank; 18 sequences from the larval stages of the genus *Hysterothylacium*
179 were 91-92% similar to those of *Hysterothylacium rigidum* and one of the samples
180 morphologically identified as *Anisakis* sp. shared 100% nucleotide identity with *Anisakis*
181 *pegreffii* sequences deposited in GenBank. The *Cucullanus* sp. nematode could not be
182 identified with NC5/NC2 primers and then 18S sequence was obtained. Its sequence was
183 100% similar to that of *Cucullanus dodsworthi* from a checkered puffer *Sphoeroides*
184 *testudineus* from Mexico (HQ241923).

185 *Hysterothylacium* larvae sequence from *P. octolineatum* was 100% similar to a
186 *Hysterothylacium* sp. sequence from *Zenopsis conchifer* from Brazil (KU594488) and to
187 *Hysterothylacium deardorffoverstreetorum* sequences from *Paralichthys isosceles*, also
188 from Brazilian coast (JF730200).

189 The sequences reported in this study have been deposited in GenBank under accession
190 numbers: KY781734-KY781736 (*H. reliquens*), KY781737 (*A. pegreffii*), MK039143-

191 MK039160 (*Hysterothylacium* sp. from *E. guttifer*), MK039161 (*H.*
192 *deardorffoverstreetorum*) and MK045808 (*C. dodsworthi*).

193 An ITS tree constructed with a total of 423 sites and 43 sequences showed two clearly
194 differentiate clades (Figure 2): one of them belonging to *Anisakis* sequences with bootstrap
195 value of 99%, which included the *A. pegreffii* sequence obtained in this study grouped with
196 other *A. pegreffii* sequences deposited in GenBank; and the other clade including
197 *Hysterothylacium* sequences with bootstrap value of 92%. Within this clade, *H. reliquens*
198 sequences from *E. guttifer* were placed in a subclade with other *H. reliquens* sequences
199 with bootstrap value of 99% whereas the 18 *Hysterothylacium* sequences similar to *H.*
200 *rigidum* (91% similarity in BLAST) formed an only subclade with strong bootstrap value of
201 99%. The *Hysterothylacium* sequence obtained from *P. octolineatum* was grouped in the
202 clade of *H. deardorffoverstreetorum* sequences with bootstrap value of 100%.

203

204 4. DISCUSSION

205 This study provides information about the parasitological condition of two non-native
206 fishes reported recently for the first time in Galician waters (NW Spain) in order to give an
207 insight of the potential risk of these occurrences as a vehicle for alien parasites in a new
208 area.

209 Both the two host species are tropical species caught northward of its habitual distribution
210 range in the eastern Atlantic, which supposes a new northern limit for *E. guttifer* (Bañón et
211 al., 2018) and the second northernmost record for *P. octolineatum*, only further south than a
212 specimen recently observed, but not examined, in the South of Bay of Biscay (Casamajor,
213 2016).

214 *Ephippion guttifer* showed a high parasitization by different nematodes in the digestive
215 tract. Molecular identification allowed first reports of *A. pegreffii*, *C. dodsworthi* *H.*
216 *reliquens* and a new *Hysterothylacium* sp. in this species. Previously, only copepod
217 ectoparasites (Walter, 2015a, b), trematodes (Fischthal & Thomas, 1970) and mixosporidia
218 (Kpatcha, 1994) were reported. Regarding other tetraodontid species, the presence of
219 Anisakidae (*Anisakis* sp.) and Raphidascaridae, *Hysterothylacium aduncum* (Rudolphi,
220 1802) have been described in *Lagocephalus sceleratus* (Bakopoulos, Karoubali, & Diakou,
221 2017).

222 *Parapristipoma octolineatum* showed a very lower level of parasitation, with only two
223 *Hysterothylacium* larvae, genetically identified as *H. deardorffoverstreetorum*. There are
224 also scarce parasitological studies available about the parasitic fauna of *P. octolineatus*. To
225 our knowledge, only protozoa belonging to microsporidia (Kpatcha, Diebakate, Faye, &
226 Toguebaye, 1995) and coccidia (Diouf, 1993) have been found, together with metazoan
227 trematodes (Aleshkina & Gaevskaya, 1985; Diagne et al., 2015, 2016). There are no
228 records of nematode parasites in this species, although a high diversity of parasitic
229 nematode have been described in other haemulids, including larvae of *Contracaecum* sp.,
230 *Pseudoterranova* sp., *Rhapidascaris* sp. and *Hysterothylacium* sp. (Chero et al., 2014;
231 Moravec & Justine, 2017; Paschoal, Cezar, & Luque, 2015).

232 Nematodes belonging to the families Anisakidae and Raphidascaridae are widespread in
233 fish population worldwide (Mattiucci & Nascetii, 2008; Mattiucci et al., 2018; Nadler et al.,
234 2005). Only *E. guttifer* presented *Anisakis* larvae, but in a low number, molecularly
235 identified as *A. pegreffii*. In European waters, that is the most prevalent species of the genus
236 in the Mediterranean Sea, whereas *Anisakis simplex* is the most common one in North
237 Atlantic waters with a sympatric area between both species from the Alborán Sea
238 (Mediterranean Gibraltar area) to the Spanish Galician coast (Mattiucci et al., 2018).

239 With regards to *H. reliquens*, this species has been described in 25 fish species belonging to
240 eight different orders, from Indian, western Atlantic and eastern Atlantic, off Morocco
241 (Zhao et al., 2017). Therefore, this represents the first record of this parasite species from
242 European waters and a northward extension of its geographic distribution range in the
243 eastern Atlantic, through a translocation of its host species. The two individuals were live
244 mature females and they were ovopositing when detected, and this constitutes an increased
245 risk for parasite dissemination in the ecosystem. Moreover, a high number of
246 *Hysterothylacium* larvae were detected in the digestive tract of *E. guttifer* and the molecular
247 identification did not allow to find correspondence to sequences of any described species of
248 the genus. Specific diagnosis was not possible as all the individuals were third stage larvae
249 (as the lips were poorly or not developed).

250 Another species from the genus *Hysterothylacium*, *H. deardorffoverstreetorum*, was the
251 only parasite detected in *P. octolineatum*. This species was first described parasitizing the
252 flounder *Paralichthys isosceles* (Jordan, 1891) from Brazilian coast (Knoff et al., 2012)

253 and it has also been found afterwards in many other Brazilian fishes (Di Azevedo &
254 Iñiguez, 2018; Kuraiem et al., 2017; Silva et al., 2017). Therefore, this also represents a
255 first record for this nematode species in the eastern Atlantic, from European waters.
256 Although our L3 larvae fits morphologically and molecularly with *H.*
257 *deardorffoverstreetorum*, described by Knoff et al. (2012) as a new species, this species has
258 recently been considered species inquirenda due to its problematic description and
259 diagnosis which are based only on larvae (Pantoja, Pereira, Santos, & Luque, 2016).

260 Among anisakids, *A. simplex*, *A. pegreffii* and *Pseudoterranova decipiens* are the main
261 species responsible for anisakidosis and gastroallergic reactions in humans (Arizono,
262 Yamada, Tegoshi, & Yoshikawa, 2012; Mattiucci et al., 2013). The Raphidascaridae genus
263 *Hysterothylacium* has been commonly considered not pathogenic to humans, although
264 recent data pointed to a case of invasive gastroallergic infection caused by the third stage
265 larvae of *H. aduncum* (González-Amores, Clavijo-Frutos, Salas-Casanova, & Alcain-
266 Martínez, 2015). Thus, in the case of *E. guttifer*, apart from its own toxicity derived from
267 the presence of tetrodotoxin, the presence of zoonotic parasites could be an additional risk
268 for human health. Although it has not been possible the examination of the edible part of
269 the fish to detect nematode parasites, the presence of zoonotic nematodes in viscera and the
270 demonstrated migration capacity from viscera to flesh of *A. pegreffii* (Cipriani et al., 2016)
271 might pose a threat of human infection.

272 In the case of Cucullanidae, nematodes of genus *Cucullanus* comprise a large number of
273 species that parasitize a variety of fresh, brackish, and marine fishes (Lanfranchi, Timi, &
274 Sardella, 2004; Moravec & Justine, 2017; Moravec, Levron, & de Buron, 2011; Moravec &
275 Scholz, 2017). Up to now, *C. dodsworthi* is the only species of this genus infecting
276 tetraodontiforms, specifically the checkered puffer *Sphoeroides testudineus* (type host)
277 from Bahia de Guanabara, Brazil (Barreto, 1922) and from Mexican waters off the Yucatán
278 Peninsula (Mejía-Madrid & Aguirre-Macedo, 2011) as well as parasitizing *Lagocephalus*
279 *laevigatus* from the eastern Atlantic coast of Africa (Campana-Rouget, 1957). It has also
280 been reported from *Mugil cephalus* from Biscayne Bay (Florida) (Boucher, 1974; Skinner,
281 1975), although it was considered an accidental host (Mejía-Madrid & Aguirre-Macedo,
282 2011). So, the detection of *C. dodsworthi* in *E. guttifer* widens the host range of this
283 parasite and represents the first record in European waters.

284 Climate change affects parasite species directly, enhancing transmission rates and the
285 virulence, but also through changes in the distribution and abundance of their hosts (Palm,
286 2011). These changes could be even enhanced if we consider that introduction of only one
287 fish individual in a new ecosystem can imply the introduction of a far higher number and
288 species diversity (more than one hundred individuals and four different species in *E.*
289 *guttifer*) when we consider the parasite fauna. Even, in the case of the prickly puffer, two of
290 the parasites were completely mature females of *H. reliquens*, which started laying a huge
291 amount of ova during parasitological examination. All the parasitic species and genus
292 described in this paper has been found as parasites of different fish species, so we cannot
293 discard that these species could find a suitable host between the local fish species.

294 The effect of these changes in parasite distribution through host species translocation has a
295 good example looking at migrations through the Suez Canal, so-called Lessepsian
296 migrations. Thus, the cornetfish *Fistularia commersonii* has spread right across the
297 Mediterranean Sea along with its parasite *Allolepidapedon fistulariae* (and other worms)
298 (Pais, Merella, Follesa, & Garipa, 2007). It is not yet known if these Lessepsian migrant
299 parasites have spread into the open Atlantic Ocean (Bray, Diaz, & Cribb, 2016). With the
300 opening in August 2015 of a new channel parallel to the old one, the exchange of fauna
301 between the Red and Mediterranean Seas is bound to increase (Galil et al., 2015). Also, this
302 migration has affected species of nematoda such as *Anisakis typica*, which have reached the
303 Mediterranean Sea as a result of the migration of its intermediate/paratenic hosts from the
304 Indian Ocean (Mattiucci et al., 2018). Lessepsian migrant may affect native fish hosts by
305 potentially altering the dynamics of native and invasive parasite-host interactions via
306 parasite release, parasite co-introduction and parasite acquisition (Boussellaa, Neifar,
307 Goedknecht, & Thielges, 2018).

308 According a recent terminology, the parasites which have entered in a new area outside of
309 their native range with an alien host species are defined as co-introduced parasites
310 (LyMBERY et al., 2014). This is in agreement with the new findings of *C. dodsworthi*, *H.*
311 *reliquens*, *H. deardorffoverstreetorum* and a *Hysterothylacium* sp., although it is not always
312 straightforward to determine whether a newly discovered parasite is alien or native to a
313 region.

314 The combination of the oceanographic and topographic features makes Galician waters be
315 very productive, able to support extensive costal fisheries and shellfish harvesting (Surís-
316 Regueiro & Santiago, 2014). On the other hand, the introduction of parasite species in a
317 new marine environment could affect negatively to native fauna but also can seriously
318 endanger marine production in the area, causing important mortalities and economic losses,
319 as have been probed in shellfishes (Cigarría & Elston, 1997; Ramilo et al., 2014; Villalba et
320 al., 2014). Although this is the first attempt to investigate parasitic fauna introduced into
321 European Atlantic waters by exotic fish species, more attention needs to be paid to how this
322 parasitic fauna affects both the host species and the new ecosystem into which it is
323 introduced.

324

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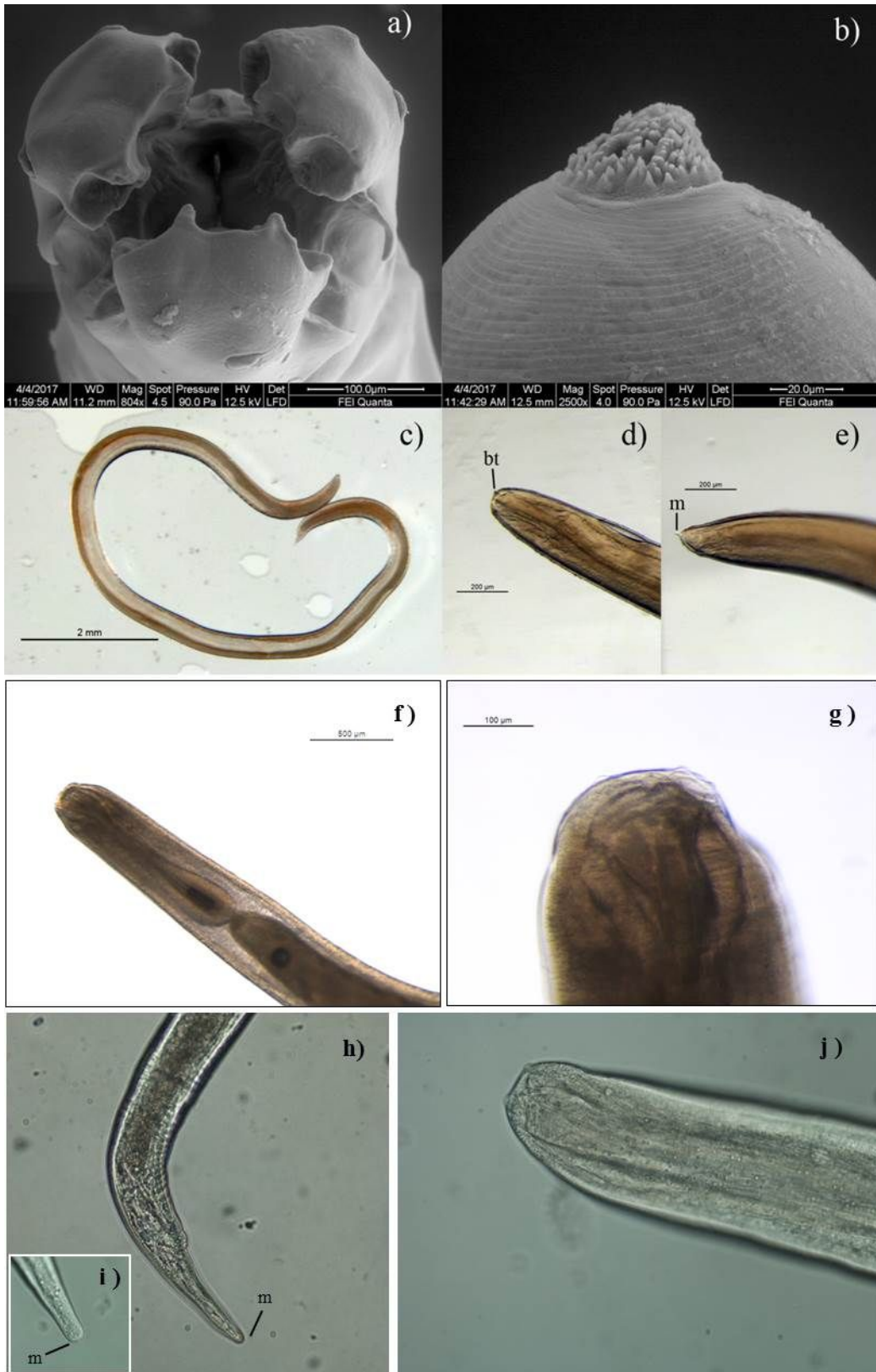
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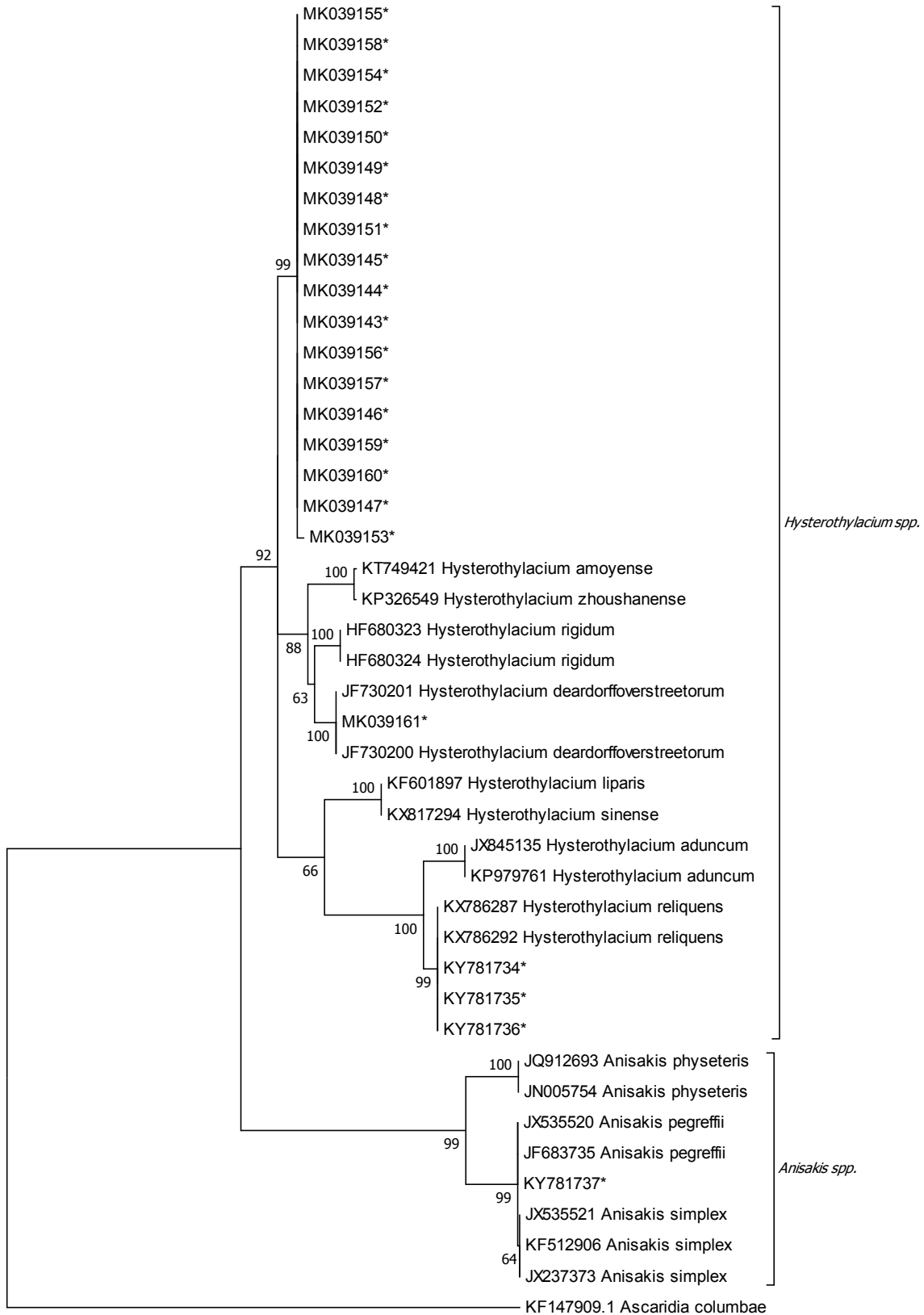
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572

573 **FIGURE 1.** Nematode parasites from the digestive tract of *E. guttifer* and *P. octolineatus*:
574 scanning electron micrographs of an adult female of *H. reliquens* from *E. guttifer*, showing
575 the cephalic extremity (a) and the tail tip (b); general aspect of the *Hysterothylacium* sp.
576 larvae isolated from prickly puffer stomach (c); L3 larvae of the genus *Anisakis* isolated
577 from *E. guttifer* stomach wall and identified by molecular analysis as *A. pegreffii*, showing
578 the genus characteristics anterior boring tooth (d), and tail mucrom (e); *Cucullanus*
579 nematode also from prickly puffer (genetically identified as *C. dodsworthi*), with their
580 characteristic muscular esophagus, expanded in width at both ends (f) and an image of the
581 cephalic end (g); *Hysterothylacium* larvae from *P. octolineatum* digestive tract (*H.*
582 *deardorffoverstreetorum*) showing the tail mucron (h, i) and the cephalic end (j)
583 bt= boring tooth, m= tail mucrom.
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588 **FIGURE 2.** Maximum-likelihood analysis showing the taxonomic position of the
589 *Hysterothylacium* and *Anisakis* sequences obtained in this study. Numbers at branch nodes
590 indicate bootstrap confidence values in percent. (*) Sequences obtained in this study.
591



593 **TABLE 1.** GenBank accession numbers of the sequences of rRNA ITS genes of the genus
 594 *Hysterothylacium* and *Anisakis* used in phylogenetic analysis
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Species	GenBank accession	Host	Location
<i>H. rigidum</i>	HF680323 HF680324	<i>Lophius piscatorius</i>	Ireland
<i>H. deardorffoverstreetorum</i>	JF730200, JF730201	<i>Paralichthys isosceles</i>	Brazil
<i>H. aduncum</i>	JX845135	<i>Zoarcetes viviparus</i>	Denmark
	KP979761	<i>Engraulis encrasicolus</i>	Adriatic Sea
<i>H. reliquens</i>	KX786287, KX786292	<i>Brachirus orientalis</i>	Iraq
<i>H. amoyense</i>	KT749421	<i>Platycephalus indicus</i>	Iran
<i>H. zhoushanense</i>	KP326549	<i>Lepidotrigla japonica</i>	China
<i>H. liparis</i>	KF601897	<i>Liparis tanakae</i>	China
<i>H. sinense</i>	KX817294	<i>Conger myriaster</i>	China
<i>A. physeteris</i>	JQ912693	<i>Physeter macrocephalus</i>	Mediterranean Sea
	JN005754	<i>Pagellus bogaraveo</i>	Azores
<i>A. pegreffii</i>	JX535520	<i>Stenella coeruleoalba</i>	Mediterranean Sea
	JF683735	<i>Gadus macrocephalus</i>	South Korea
<i>A. simplex</i>	JX535521	<i>Balaenoptera acutorostrata</i>	Norwegian coast
	KF512906	<i>Merluccius merluccius</i>	Ireland
	JX237373	<i>Clupea harengus</i>	Denmark

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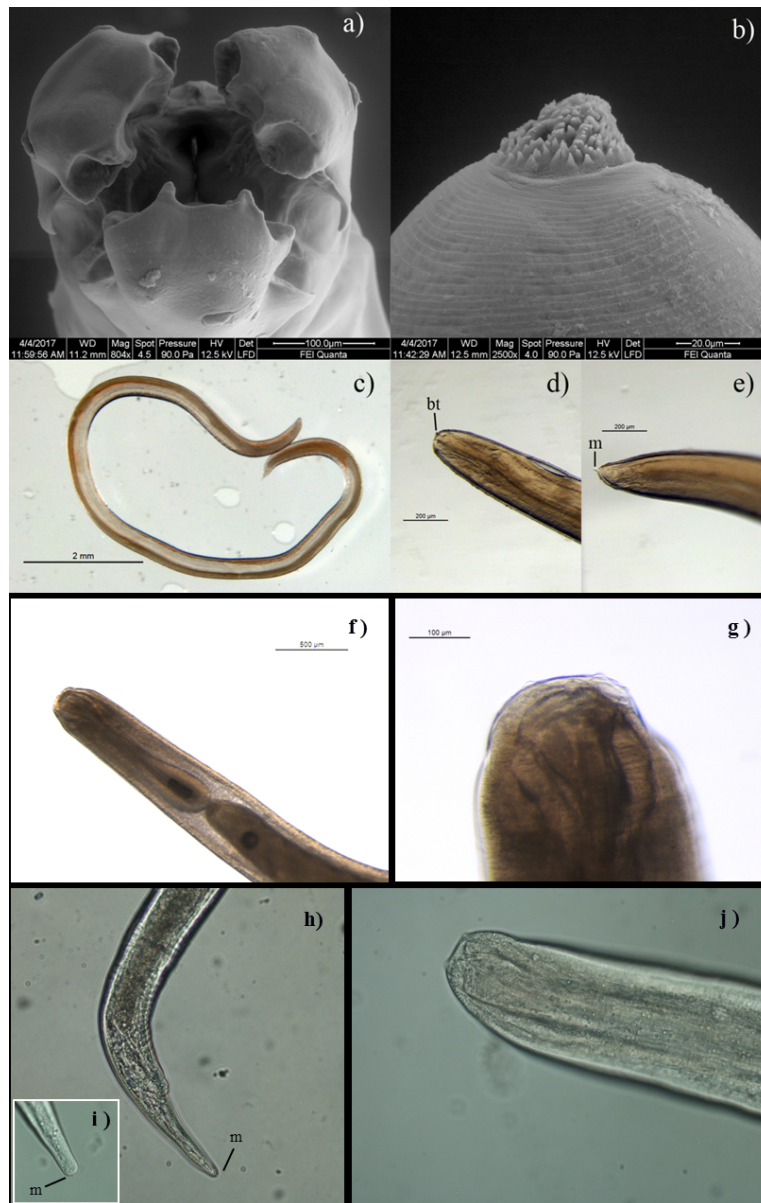


FIGURE 1. Nematode parasites from the digestive tract of *E. guttifer* and *P. octolineatus*: scanning electron micrographs of an adult female of *H. reliquens* from *E. guttifer*, showing the cephalic extremity (a) and the tail tip (b); general aspect of the *Hysterothylacium* sp. larvae isolated from prickly puffer stomach (c); L3 larvae of the genus *Anisakis* isolated from *E. guttifer* stomach wall and identified by molecular analysis as *A. pegreffii*, showing the genus characteristics anterior boring tooth (d), and tail mucrom (e); *Cucullanus* nematode also from prickly puffer (genetically identified as *C. dodsworthi*), with their characteristic muscular esophagus, expanded in width at both ends (f) and an image of the cephalic end (g); *Hysterothylacium* larvae from *P. octolineatum* digestive tract (*H. deardorffoverstreetorum*) showing the tail mucrom (h, i) and the cephalic end (j)
bt= boring tooth, m= tail mucrom.

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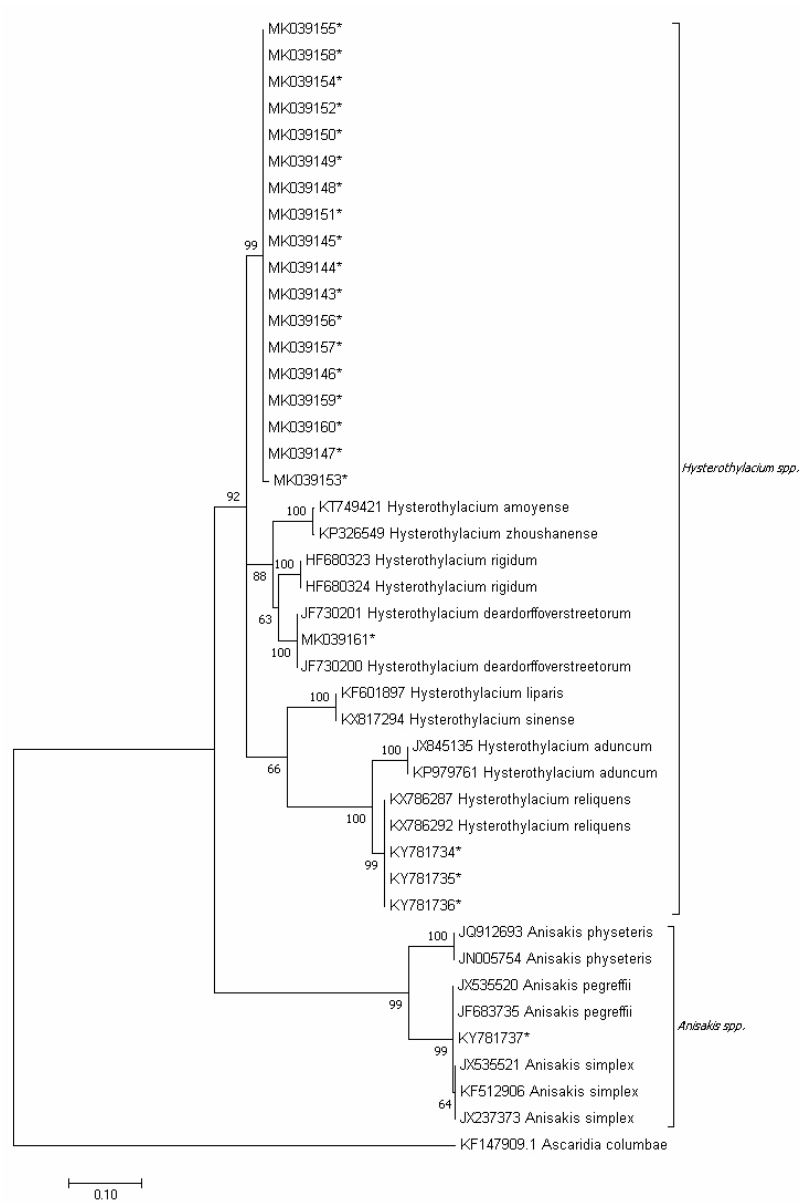


FIGURE 2. Maximum-likelihood analysis showing the taxonomic position of the *Hysterothylacium* and *Anisakis* sequences obtained in this study. Numbers at branch nodes indicate bootstrap confidence values in percent. (*) Sequences obtained in this study.

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<i>H. deardorffoverstreetorum</i>	JF730200, JF730201	<i>Paralichthys isosceles</i>	Brazil
<i>H. aduncum</i>	JX845135	<i>Zoarcetes viviparus</i>	Denmark
	KP979761	<i>Engraulis encrasicolus</i>	Adriatic Sea
<i>H. reliquens</i>	KX786287, KX786292	<i>Brachirus orientalis</i>	Iraq
<i>H. amoyense</i>	KT749421	<i>Platycephalus indicus</i>	Iran
<i>H. zhoushanense</i>	KP326549	<i>Lepidotrigla japonica</i>	China
<i>H. liparis</i>	KF601897	<i>Liparis tanakae</i>	China
<i>H. sinense</i>	KX817294	<i>Conger myriaster</i>	China
<i>A. physeteris</i>	JQ912693	<i>Physeter macrocephalus</i>	Mediterranean Sea
	JN005754	<i>Pagellus bogaraveo</i>	Azores
<i>A. pegreffii</i>	JX535520	<i>Stenella coeruleoalba</i>	Mediterranean Sea
	JF683735	<i>Gadus macrocephalus</i>	South Korea
<i>A. simplex</i>	JX535521	<i>Balaenoptera acutorostrata</i>	Norwegian coast
	KF512906	<i>Merluccius merluccius</i>	Ireland
	JX237373	<i>Clupea harengus</i>	Denmark

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