

1 **Updating taxonomic and biometric knowledge of *Enchelyopus cimbrius* (Gadiformes,**
2 **Gaidropsaridae) through morphology and DNA barcoding**

3

4 Rafael Bañón^{1,*}, Alejandro de Carlos^{2,3}, Juan Carlos Arronte⁴, Ángel Sebastián Comesaña⁵,
5 José Daniel Barreiro Vázquez⁶, Cristina García-Fernández⁷, Francisco Baldó⁸

6 ¹Grupo de Estudio do Medio Mariño (GEMM), Edif. Club Náutico bajo, 15960 Ribeira, Spain;
7 anoplogaster@yahoo.es

8 ²Departamento de Bioquímica, Xenética e Inmunoloxía, Facultade de Bioloxía, Universidade
9 de Vigo, Rúa Fonte das Abelleiras s/n, 36310 Vigo, Spain; adcarlos@uvigo.es

10 ³Centro de Investigación Mariña, Universidade de Vigo, 36310 Vigo, Spain.

11 ⁴Centro Oceanográfico de Santander (COST-IEO), CSIC, Severiano Ballesteros 16, 39004
12 Santander, Spain; jcarlos.arronte@ieo.csic.es

13 ⁵Centro de Apoyo Científico y Tecnológico a la Investigación (CACTI), Universidade de
14 Vigo – Campus Lagoas Marcosende, Vigo, Spain. basti@uvigo.ga

15 ⁶Departamento de Anatomía, Producción Animal e Ciencias Clínicas Veterinarias Hospital
16 Veterinario Universitario Rof Codina, Facultade de Veterinaria, Lugo (Spain).

17 josedaniel.barreiro@usc.es

18 ⁷Centro Oceanográfico de Málaga (COMA-IEO), CSIC, Puerto Pesquero s/n, 29640
19 Fuengirola, Málaga, Spain; cristina.garcia.fernandez@ieo.csic.es

20 ⁸Centro Oceanográfico de Cádiz (COCAD-IEO), CSIC, Puerto Pesquero, Muelle de Levante
21 s/n, 11006 Cádiz, Spain; francisco.baldo@ieo.csic.es

22

23

24 *Corresponding author. Grupo de Estudos do Medio Mariño (GEMM), Spain. E-mail

25 addresses: anoplogaster@yahoo.es (R. Bañón).

26

27 **Abstract**

28 A taxonomic characterisation of *Enchelyopus cimbrius* (Gadiformes, Gaidropsaridae) is
29 presented on the basis of eleven specimens from the North Atlantic. Identification was carried
30 out by integrative taxonomy, combining the examination of morphological and molecular
31 characters. The former are consistent with previous descriptions, but new biometric and
32 meristic data for the species are provided, showing ontogenetic changes with respect to post-
33 larvae-pelagic juveniles. Length-weight relationships of 44 specimens showed isometric
34 growth, while the length-length relationships of eight body parts of the species showed
35 differential allometric growth. The molecular analysis resulted in the addition of 11 new
36 sequences of cytochrome c oxidase subunit 1 (*COI*) to the molecular repositories. DNA
37 barcoding supports the morphological identification of *Enchelyopus cimbrius* specimens and
38 confirms the amphi-Atlantic distribution of the species. Updating the taxonomic data can be
39 useful to confirm the current status or to identify divergences, and also to better characterise
40 and delimit each species, contributing to a better understanding of intraspecific variability,
41 both morphological and molecular.

42

43 **Keywords** *COI*, rocklings, barcoding, biogeography, mitochondrial DNA, allometric growth

44

45 **Introduction**

46

47 The family Gaidropsaridae Jordan & Evermann, 1898, as currently recognized, contains three
48 genera: *Gaidropsarus* Rafinesque, 1810, *Ciliata* Couch, 1832, and *Enchelyopus* Bloch &
49 Schneider 1801 and 17 species (Carnevale and Harzhauser 2013). Fishes of this family,
50 commonly known as rocklings, are characterized by an elongated and relatively slender body,

51 the presence of three barely separated dorsal fins (the first with a single thickened
52 unsegmented ray; the second with small, unsegmented rays in a fleshy ridge rising in a
53 groove; and the third with segmented rays in an elongated fin) and two to four prominent
54 individual barbels on the snout, in addition to the one at the tip of the lower jaw (Nelson et al.
55 2016). The genus *Enchelyopus* is a monotypic genus containing a single species, the
56 fourbeard rockling *Enchelyopus cimbrius* (Linnaeus, 1766). It is a demersal species found in
57 the North Atlantic and adjacent Arctic, on muddy and sandy bottoms at depths from 20 to 900
58 m (Moore et al. 2003). The distribution extends from the Gulf of Mexico and Florida to
59 Newfoundland and southwestern Greenland in the western Atlantic, around Iceland, and from
60 the Barents Sea to the Bay of Biscay in the eastern Atlantic, with only one record from
61 Mauritania (Cohen 1990; Mecklenburg et al. 2018). According to the Red List of the
62 International Union for Conservation of Nature (IUCN), *E. cimbrius* is considered globally to
63 be of least concern (Iwamoto et al., 2015).

64 The species has a carnivorous diet that varies depending on age and location. It has
65 been reported to consist primarily of bivalve molluscs, polychaetes, crustaceans (amphipods,
66 decapods, copepods, mysids and cumaceans) and fishes (Langton and Bowman 1980; Deree
67 1999)

68 According to Cohen (1990) the growth rate is relatively slow; the maximum age
69 recorded in the Baltic Sea is 13 years and 37.8 cm of total length (TL) (Lampart-Kałużnicka
70 and Heese 2015).

71 The spawning season is apparently protracted, lasting from January to August or even
72 to September/October, in waters less than 140 m deep (Cohen 1990). First maturity is reached
73 at three years of age (at about 15 cm total length) and females spawn between 5,000 and
74 45,000 planktonic eggs depending on their body size (Cohen 1990).

75 Molecular taxonomy has been successfully applied to the systematic study of fishes in
76 conjunction with traditional morphological analysis. The use of mitochondrial cytochrome c
77 oxidase subunit I (*COI*) in *E. cimbrius* for taxonomic or phylogenetic purposes has been
78 described previously (Von der Heyden and Matthee 2008; McCusker et al. 2012;
79 Knebelsberger et al. 2014).

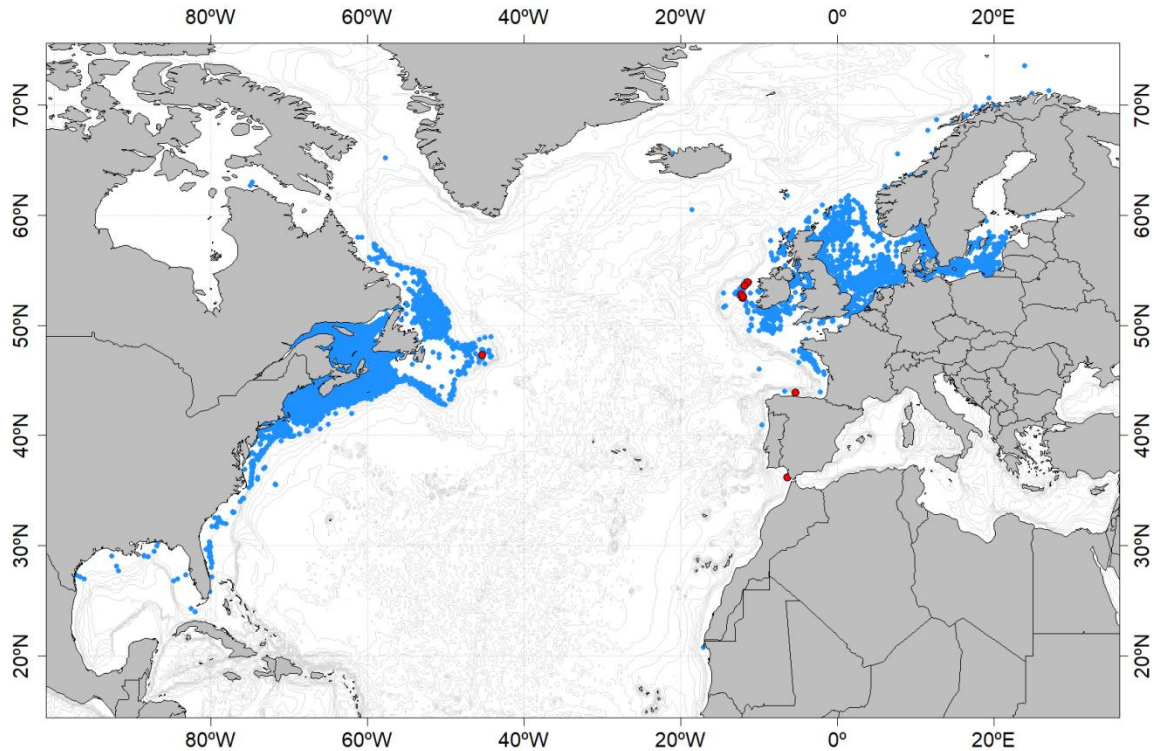
80 The aims of this research are: (i) to combine the use of morphological data and the
81 *COI* molecular marker to analyse specimens caught mainly in the eastern North Atlantic for
82 taxonomic purposes, and (ii) to establish length-weight and length-length relationships for the
83 species. The results are discussed in the context of the data available in the scientific
84 literature.

85

86 **Material and Methods**

87

88 **Sampling data and morphological analysis**



89
 90 **Fig. 1** Distribution of *Enchelyopus cimbrius* (light blue dots) and sampling locations of the
 91 analysed specimens in the current study (red dots). The distribution data were downloaded
 92 from Global Biodiversity Information Facility (GBIF, 2024) and Ocean Biogeographic
 93 Information System (OBIS, 2024).

94
 95 Eleven specimens of *E. cimbrius* were caught by trawling during several scientific research
 96 surveys carried out in different areas of the North Atlantic Ocean: i) Flemish Cap 2016,
 97 carried out in the Flemish Cap (Northwest Atlantic); ii) PORCUPINE 2023, conducted off the
 98 west coast of Ireland, and iii) Demersales2022, in the Cantabrian Sea and Galician waters
 99 (north and northwestern Spain), and iv) ARSA 2019 in the Gulf of Cadiz (southern Spain)
 100 (Fig. 1).

101 The specimens were preserved frozen on board. Once in the laboratory, they were
 102 defrosted at room temperature, thoroughly examined, photographed and deposited in the fish
 103 collection of the Universidade de Santiago de Compostela, Museo de Historia Natural Luis

104 Iglesias, in Galicia, Spain, under the reference numbers from MHN USC 25221-1 to MHN
105 USC 25221-11. Species identification was carried out following Cohen (1990), and
106 morphological measurements were recorded to the nearest mm using a digital caliper.
107 Vertebral counts were obtained from radiographs taken by a mammography computed
108 radiography equipment (Fujifilm Capsula XL II, Japan- using exposure factors of 44 kVp x
109 35 mAs) and do not include the terminal ural element. Standard length (SL) and head length
110 (HL) were used throughout.

111 The total length-weight relationship (TL-W, power relationship) (n=44) was explored
112 using data from specimens captured during scientific surveys on Porcupine Bank between
113 2001 and 2023, and the allometric growth of each body measurement (n=11) for the 2023
114 specimens. Eight body characters were used to analyse the allometric growth: Interorbital
115 length (IO), eye diameter (ED), pelvic fin length (VL), head length (HL), first dorsal height
116 (D1H), pectoral fin length (PL), body depth (BD) and caudal peduncle depth (CPD). Models
117 were fitted using linear regression after log-transformation all morphometric data according to
118 the equation: $Y = a \times X^b$, where 'Y' represents TL or the morphological parameter; 'X'
119 represents W o TL for the TL-W relationship and the allometric growth, respectively; 'a' was
120 the intercept and 'b' was the growth coefficient (Lleonart et al. 2000; Froese 2006; Karachle
121 and Stergiou 2012). Based on the b value, growth was classified as hypoallometric (negative
122 allometric growth; b significantly >3 for TL-W relationship and > 1 for allometric growth),
123 isometric (b not different from 3 for TL-W relationship and 1 for allometric growth) or
124 hyperallometric (positive allometric growth; b significantly < 3 for TL-W relationship and < 1
125 for allometric growth) (Lleonart et al. 2000; Froese 2006). All relationships were tested by
126 examining whether the slope estimates for 3 (TL-W relationship) or 1 (allogometric growth) fell
127 within the 95% confidence interval.

128

129 **Molecular analysis**

130

131 DNA was extracted from muscle, using the E.Z.N.A. Tissue DNA Kit (Omega BIO-TEK,
132 Norcross, GA, USA) following to the manufacturer's instructions, with a single 200 µL
133 elution step. The 5' end of *COI* gene was amplified using 2 µL of template DNA, the universal
134 primer cocktail for fish DNA barcoding C_FishF1t1-C_FishR1t1 (Ivanova et al. 2007), and
135 the Phire Green Hot Start II PCR Master Mix (Thermo Scientific, Waltham, MA, USA), in a
136 final volume of 20 µL. The PCR cycling profile consisted of 30 s at 98 °C, followed by 35
137 cycles at 98 °C for 5 s, 52 °C for 10 s and 72 °C for 15 s, 72 °C for 1 min and cooling to 12 °C.
138 The PCR products were purified by treatment with ExoSAP-IT, subjected to sequencing
139 reactions using the BigDye v3.1 cycle sequencing kit. The sequencing was performed in both
140 directions using the M13F (-21) and M13R (-27) primers (Messing 1983), using a SeqStudio
141 Genetic Analyser (Applied Biosystems, Foster City, CA, USA) at the Centro de Apoyo
142 Científico y Tecnológico a la Investigación of the Universidade de Vigo (CACTI) facilities.
143 Sequence quality was verified using MEGA v11 (Tamura et al. 2021) and, for each
144 individual, the direct and reverse sequences were assembled into a consensus sequence.

145 The DNA sequence data, specimen photographs and other metadata have been
146 deposited in the Barcode of Life Database (BOLD Systems; www.boldsystems.org) as part of
147 the projects entitled "Fishes of the Porcupine Bank" (code PORCU), with process IDs
148 PORCU029-24 to PORCU36-24, "Fishes of the Western Atlantic Ocean" (code FIWA), with
149 process ID FIWA020-24 and "Unusual Atlantic Fishes" (code UNAFI) with process IDs
150 UNAFI 011-24 and UNAFI 012-24. The barcode sequences have also been deposited in
151 GenBank (<https://www.ncbi.nlm.nih.gov/genbank/>) under accession numbers PP131287-
152 PP131297.

153 The *COI* data were utilised for two purposes: (a) double-check the morphological
154 identification of voucher specimens through DNA barcoding and (b) to evaluate potential
155 genetic structure among individuals from different sampling sites. To achieve this, a Median
156 Joining Network (Bandelt et al. 1999) was constructed using PopART 1.7 (Leigh and Bryant
157 2015), with $\varepsilon = 0$.

158 The sequences used to elaboration of the haplotype network, including those
159 contributed by the present research, were obtained from the BOLD database, selecting those
160 with a length of more than 600 nucleotides. The set of 51 sequences was collapsed into 12
161 haplotypes using FaBox 1.61 (Vilesen, 2007).

162

163 **Results**

164

165 **Taxonomic account**

166

167 *Enchelyopus cimbrius* (Linnaeus, 1766) Fig. 2 and 3

168 *Gadus cimbrius* Linnaeus [C.] (ex Strussenfelt) 1766: 440. Bigelow and Schroeder (1953):

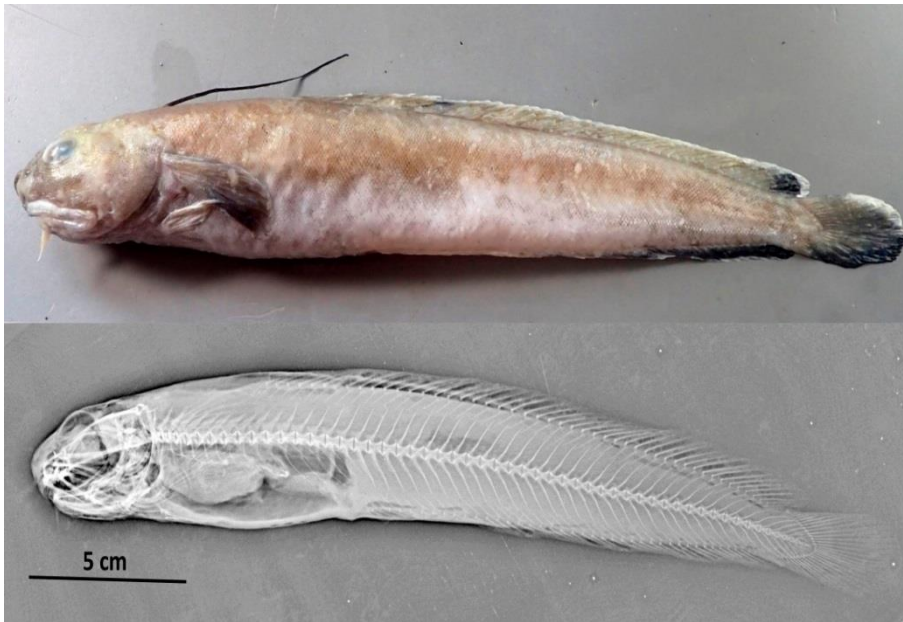
169 234-238 (description); Cohen and Russo (1979): description; Demir et al. (1985); Cohen

170 (1990): description; Deree (1999): feeding, age and growth; Lampart-Kałużnicka and Heese

171 (2015): biology; Iwamoto and Cohen (2016): keys.

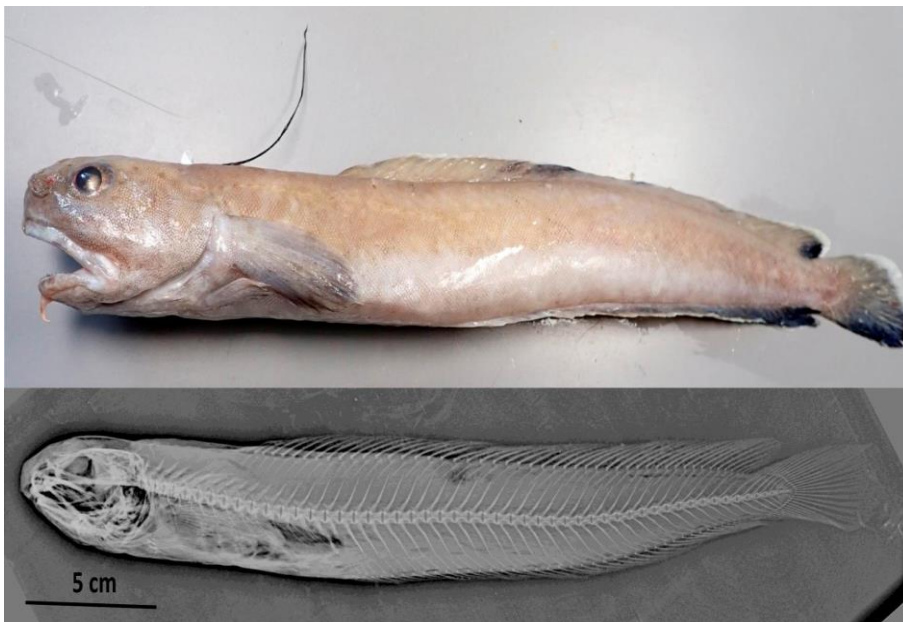
172

173 **Material examined**



174
175 **Fig. 2** *Enchelyopus cimbrius* MHN USC 25221-5, 281.5 mm TL (top) and the corresponding
176 radiograph of the specimen (below).

177



178
179 **Fig. 3** *Enchelyopus cimbrius* MHN USC 25221-10, 325.1 mm TL (top) and the corresponding
180 radiograph of the specimen (below).

181

182 Eleven specimens were caught in the North Atlantic, one specimen from the western and ten
183 from the eastern North Atlantic (Fig. 1): MHN USC 25221-1, Cantabrian Sea, 245.3 mm TL,
184 10 October 2022, 43.873 °N, 5.379 °W, 300 m depth, 11.6 °C, salinity (S)=35.5; MHN USC

185 25221-2, 211.5 mm TL, 5 July 2016; 47.261°N, 45.294°W, 261 m depth; MHN USC 25221-3,
186 81 mm TL, 24 February 2019; 36.198 °N, 6.396 °W, 294 m depth, 14.7 °C, S=36.5; MHN
187 USC 25221-4, Porcupine Bank, 234.7 mm TL, 26 September 2023; 52.781 °N, 12.293 °W,
188 344 m depth, 11.3 °C, S=35.5; MHN USC 25221-5, Porcupine Bank, 281.5 mm TL (Fig. 2),
189 27 September 2023, 53.571 °N, 11.841 °W, 270 m depth, 11.7 °C, S=35.5; MHN USC 25221-
190 6, Porcupine Bank, 314.2 mm TL, 26 September 2023, 52.781 °N, 12.293 °W, 344 m depth,
191 11.3 °C, S=35.5; MHN USC 25221-7, Porcupine Bank, 281.7 mm TL, 26 September 2023,
192 52.467 °N, 12.080 °W; 327 m depth, 11.3 °C, 35.5; MHN USC 25221-8, Porcupine Bank,
193 317.3 mm TL, 18 September 2023, 53.858 °N, 11.395 °W; 258 m depth, 11.5 °C, S=35.5;
194 MHN USC 25221-9, Porcupine Bank, 277.4 mm TL, 26 September 2023, 52.619 °N, 12.056
195 °W; 267 m depth, 11.1 °C, 35.4; MHN USC 25221-10, Porcupine Bank, 325.1 mm TL (Fig.
196 3), 18 September 2023, 53.858 °N, 11.395 °W; 258 m depth, 11.5 °C, S=35.5; MHN USC
197 25221-11, Porcupine Bank, 358.2 mm TL, 27 September 2023, 53.571 °N, 11.841 °W, 270 m
198 depth, 11.7 °C, 35.5.

199

200 **Description**

201

202 Elongated body, cylindrical anteriorly and compressed posteriorly (Figs. 2 and 3), body depth
203 5.8-9 times in SL; the head above is flattened posteriorly and rounded anterior to the eyes,
204 head length 4.5-5.8 in SL; snout short and blunted, 3.5-5.1 times in HL; eyes horizontally
205 oblong, horizontal eye diameter 4.4-5.4 in HL; four barbels, one on the chin, one on at the tip
206 of the snout, and one on each nostril; small chin barbel 5.8-10.8 times in HL; mouth large,
207 inferior; upper jaw prominent, extending beyond the posterior margin of the eye, upper jaw
208 length 1.7-2.3 in HL; first dorsal fin with a single elongated ray, 4-4.7 times in SL; second
209 dorsal fin with a series of short filaments in a groove, its base 1.6-3.2 times in HL; third

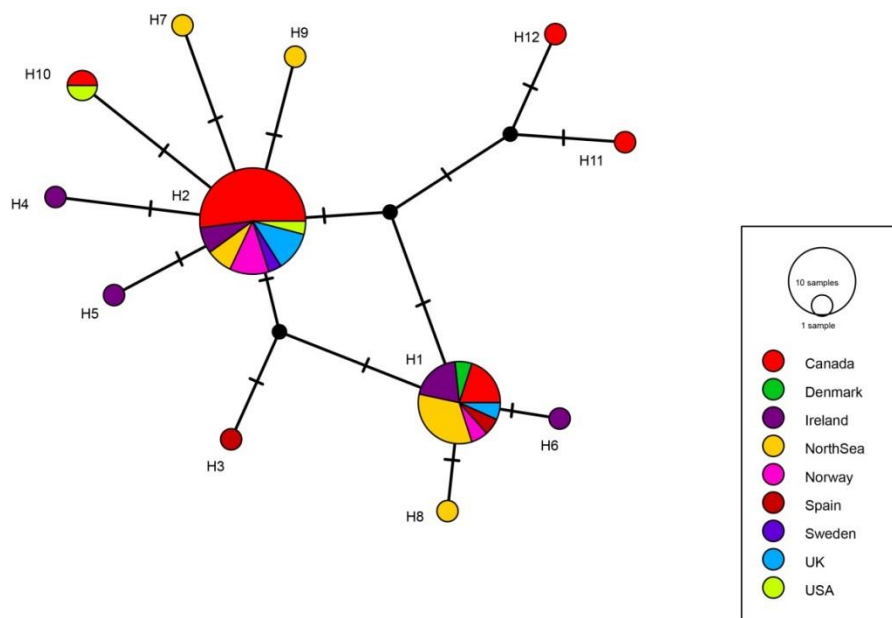
210 dorsal fin longer with normal soft rays, its base 1.5-2 times in SL; pelvic fin jugular, anterior
 211 to the base of the pectoral fin; the lateral line is interrupted along its entire length; the colour
 212 is brownish on the back, lighter on the sides, dirty white on the belly, dark oval spot on the
 213 posterior end of the third dorsal and anal fins and on the lower part of the caudal fin. The
 214 inside of the mouth, the gill cavities and the first dorsal fin ray are blackish. Table 1 shows the
 215 morphological results while Tables 2 and 3 provide a comparison of the morphometric and
 216 meristic data, respectively.

217

218 Genetic features

219

220 Considering all mitochondrial *COI* sequences, 12 haplotypes were recognized, of which four
 221 (H3 to H6) were obtained for the first time for this species (Fig. 4). As can be seen, the two
 222 main haplotypes, H1 and H2, which account for 78% of the sequences, are present in 7 of the
 223 9 locations, on both sides of the Atlantic Ocean.



224

225

226 **Fig. 4** Haplotype network of *COI* sequences (623 nucleotides) from *Enchelyopus cimbrius* (n

227 = 51). Median Joining Network ($\epsilon = 0$) created in PopART v1.7. Each circle represents a

228 haplotype; the size of the circles corresponds to the number of individuals with that
229 haplotype. Colours indicate sampling locations. Bars indicate the number of mutations
230 between two haplotypes. Small black circles indicate hypothetical haplotypes, predicted by
231 the model.

232

233 **Weight-length relationships**

234

235 The TL-W results of the manuscript along with results from other areas are shown in Table 4.
236 The individuals showed equal growth in weight and length ($b = 3.049$; CI $b = 2.797- 3.303$; p
237 < 0.001). Only in one other published case is this relationship provided, also isometric, while
238 in all other cases this information is missing.

239

240 **Allometric morphological growth**

241

242 The linear regression relationship between total body length (TL) and different morphometric
243 characters for *E. cimbrius* are presented in Table 5. The findings showed strong and
244 significant correlations ($r > 0.974$; $p < 0.001$) between TL and morphometric characters,
245 indicating a direct relationship between total body length and growth of various body parts of
246 this species. However, there are differences in allometric growth between characters. IO and
247 D1H showed positive allometry with TL, while ED, VL, HL, and PL exhibited negative
248 allometry with respect to TL. BD and CPD, on the other hand, showed isometry.

249

250 **Discussion**

251

252 The under-description of many fish species is mainly due to a current lack of interest in fish
253 taxonomic studies at institutional, individual and editorial levels. This limited knowledge of
254 intraspecific variation makes it difficult to recognise species boundaries and thus to assess the
255 actual diversity and distribution of species (Frutos et al. 2022). Integrative taxonomic studies
256 combining morphology and molecular tools should be increasingly applied in fishes. These
257 studies can support the current taxonomic status or reveal the presence of cryptic and
258 synonymous species, indicating hidden biodiversity (Bañón et al. 2023).

259 In the eastern Atlantic, although *E. cimbrius* occupies a considerable area, only a small
260 sample has been taxonomically studied, mainly from Denmark and Norway (Cohen and
261 Russo 1979). Additionally, there is a significant knowledge gap between the southernmost
262 documented record in the eastern Atlantic, at Cape Blanc, Mauritania and the more common
263 distribution northwards from the northern part of the Bay of Biscay (Mecklenburg et al.
264 2018). The present study partially fills this gap, although the southern occurrence of this
265 species in the eastern Atlantic is too sparse to provide valuable information. This species has
266 previously been reported in the northern part of the Bay of Biscay, in the Grande Vasière and
267 Quiberon Bay (Quéro et al. 1989) with only one specimen found in the southern part,
268 specifically, in the Cantabrian Sea (Sánchez et al. 1995).

269 The morphological description of *E. cimbrius* is mainly based on meristic characters
270 (Bigelow and Schroeder 1953; Cohen and Ruso 1979), as biometrics characters are poorly
271 described. Exceptions are found in Demir et al. (1985) for post-larvae and juveniles, and
272 Svetovidov (1948) for adults. In the latter case, however, relative measurements were
273 obtained with respect to TL rather than the more commonly used SL, making taxonomic
274 comparisons difficult.

275 The TL-W relationship estimated in the study showed an isometric growth, suggesting
276 that the specimens maintain the same shape during the growth process, without changing their

277 density (Lleonart et al. 2000). Even with the limited data, the growth allometry of the species
278 showed similar patterns to other studies. Considerable ontogenetic changes have been
279 described in *E. cimbrius*, including a progressive increase in the length of the elongated first
280 dorsal fin ray during development (Demir et al. 1985). These authors reported a range of 1.2-
281 32.4% HL in specimens between 8 and 29.9 mm TL, prior to the 118.3-138.8% HL obtained
282 in this study. Other morphological characters, such as pelvic fin length, showed differences
283 between post-larval pelagic juveniles and adults. Although Demir et al. (1985) reported a
284 range of 15.8-32.1% SL, the present study obtains lower values for this character (6.9-15.8%
285 SL). A comparison of the relative biometric ranges between post-larval pelagic juveniles and
286 adults showed an increase in the first dorsal fin length, the interorbital width and the peduncle
287 height with growth. Conversely, there is a decrease in body depth, head length, eye diameter
288 and pelvic fin length. Body depth and caudal peduncle length followed an isometric growth
289 pattern. This suggests a growth strategy that prioritises the development of certain body parts
290 over others. In *E. cimbrius* there is a greater development of some body features in the
291 anterior part of the body as individuals become longer.

292 Ontogenetic growth in fishes is a complex and multifaceted process, influenced by
293 multiple factors (Sibly et al. 2015). Most fishes undergo dramatic changes in body size as
294 they grow, because they occupy multiple niches throughout their ontogenetic development,
295 and may experience different selective pressures within each sequential niche (Searle et al.
296 2021). In general, juveniles have larger eyes and heads relative to body size, while adults have
297 smaller eyes and heads relative to body size (Searle et al. 2021), as it was observed in the
298 current study. Younger gadiforms often have relatively more expanded and elongated pelvic
299 fins than adults, which seems to assist with buoyancy (Fahay and Marckle 1984).

300 Several differences from Svetovidov (1948) were identified. For instance, the length
301 of the first dorsal fin ray was 13.2-14.2% TL, which is lower than the 19-22% TL found in this

302 study. The interorbital space was narrower in our samples (1.9-4.7% TL) compared to 7.9-
303 8.9% TL in Svetovidov (1948). In addition, the lateral line is interrupted along its entire
304 length (Cohen 1990), with about 29 pores in Svetovidov (1948) and 29-36 pores in this study.
305 Svetovidov did not provide information on the number, size, or origin of the specimens
306 examined. Therefore, it is possible that the differences found are related to any of these
307 variables. Additionally, transcription errors cannot be ruled out. Svetovidov (1948) reported
308 lower values for the length of the upper jaw (43.9-48 %HL) compared to the lower jaw (48.7-
309 55.8%HL). However, since the mouth of *E. cimbrius* is inferior, it is likely that these values
310 were erroneously interchanged. The interorbital space also seems to be an error, as this author
311 state that "the interorbital space is very narrow", but the reported range (7.9-8.9% TL)
312 suggests otherwise and it is far from our values and from the theoretical values based on the
313 calculated linear regression.

314 The sample size (n=11) used for allometric growth analysis is a limitation of this
315 study, reflecting the scarcity of *E. cimbrius* in the sampling areas. Despite this, the consistent
316 patterns observed provide valuable preliminary insights into the morphological development
317 of the species, although future studies with larger samples would help to confirm these
318 findings.

319 Integrative studies are particularly recommended for species with high intraspecific
320 variability in order to find taxonomic divergences. Geographical and morphological
321 differences have been noted previously (Cohen and Russo 1979), which, together with
322 allometric growth, accounts for the high intraspecific variability of this species. Despite this,
323 the species can be easily distinguished from other gadiformes by several taxonomic
324 characters, such as the presence of four barbels and the blackish colouration of the posterior
325 end of the third dorsal and the anal fins as well as the lower part of the caudal fin. Molecular
326 analysis also confirms the amphiatlantic distribution of the species.

327

328 **Acknowledgments** The authors would like to thank the staff involved in the research surveys
329 Flemish Cap 2016, ARSA 0319, Demersales 2022 and Porcupine 2023 carried out by the
330 Spanish Institute of Oceanography (IEO, CSIC) on board the R/V Vizconde de Eza and R/V
331 Miguel Oliver (Ministry of Agriculture, Fisheries and Food, Spain). These surveys were
332 partly funded by the EU through the European Maritime and Fisheries Fund (EMFF) and
333 European Maritime, Fisheries and Aquaculture Fund (EMFAF), as part of the Spanish
334 National Programme for the Collection, Management and Use of Data in the Fisheries Sector
335 and Support for Scientific Advice in relation to the Common Fisheries Policy.

336

337 **Funding**

338 This study was funded by the European Maritime and Fisheries Fund (EMFF) and the
339 European Maritime, Fisheries and Aquaculture Fund (EMFAF): PORCUDEM-
340 20233FMP001.

341

342 **Declarations**

343 **Conflict of interest** The authors declare that they have no known competing financial
344 interests or personal relationships that could have appeared to influence the work reported in
345 this paper.

346

347 **Ethics approval** No animal testing was performed during this study.

348

349 **Sampling and field studies** All necessary permits for sampling and observational field
350 studies have been obtained by the authors from the competent authorities and are mentioned
351 in the acknowledgements. The study is compliant with CBD and Nagoya protocols.

352

353 **Data availability** The sequences employed in the current study are available in the BOLD
354 systems (<https://www.boldsystems.org/>, accessed on 21 December 2023) and GenBank
355 (<https://www.ncbi.nlm.nih.gov/genbank/>, accessed on 21 December 2023) repositories. All
356 specimens used in this study for taxonomical purposes are deposited in the fish collection of
357 the Universidade de Santiago de Compostela, Museo de Historia Natural Luis Iglesias, in
358 Santiago de Compostela, Spain (see methods). All other data are included in this article.

359

360 **Author contribution** RB conceived the study. ADC and ASC conducted molecular analyses.
361 FB and JCA compiled the specimens. JDBV make the X-ray photographs. RB and CGF
362 conducted morphological analysis. RB, FB, CGF and ADC wrote the manuscript and all
363 authors critically reviewed and approved the manuscript.

364

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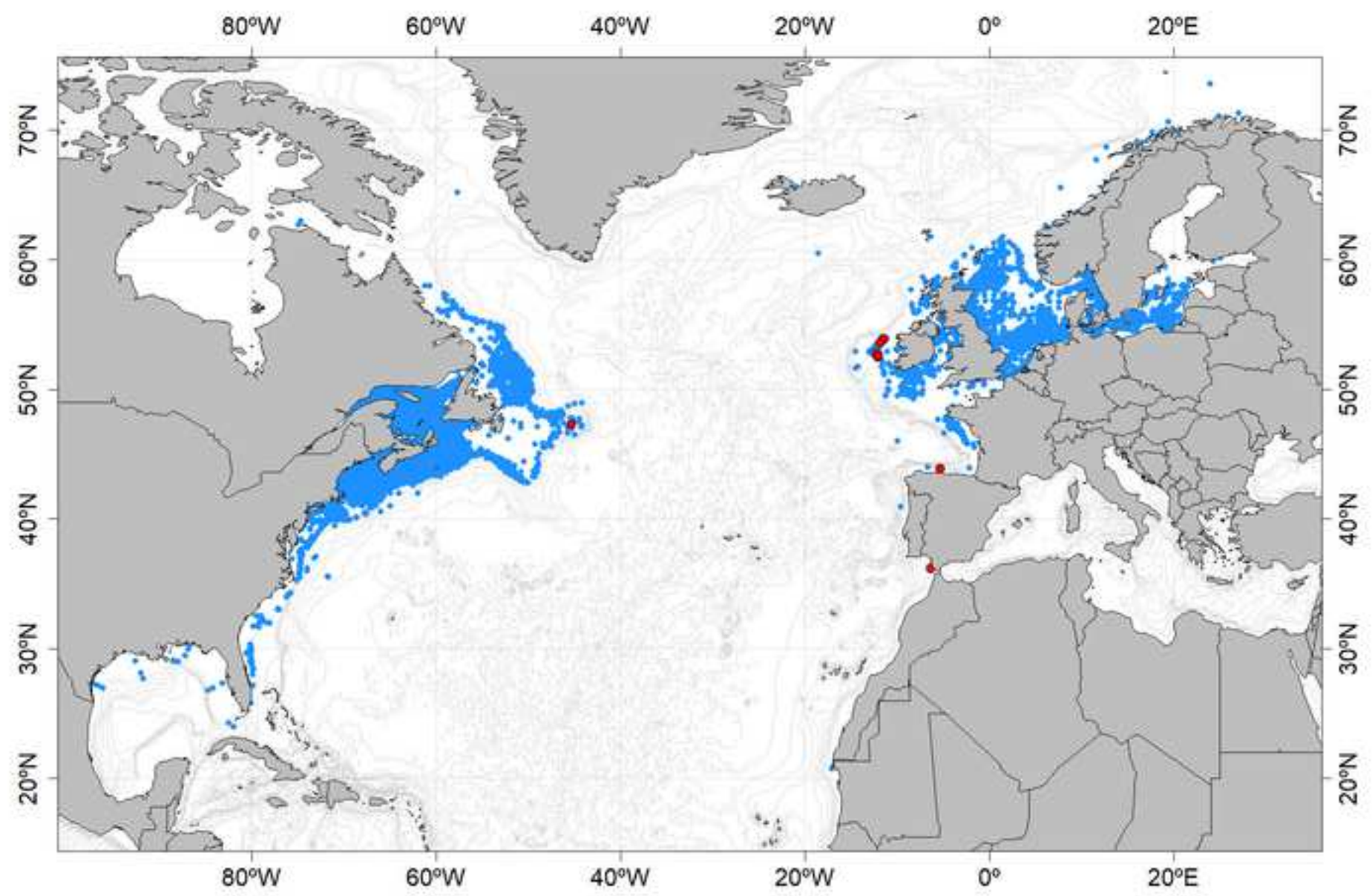
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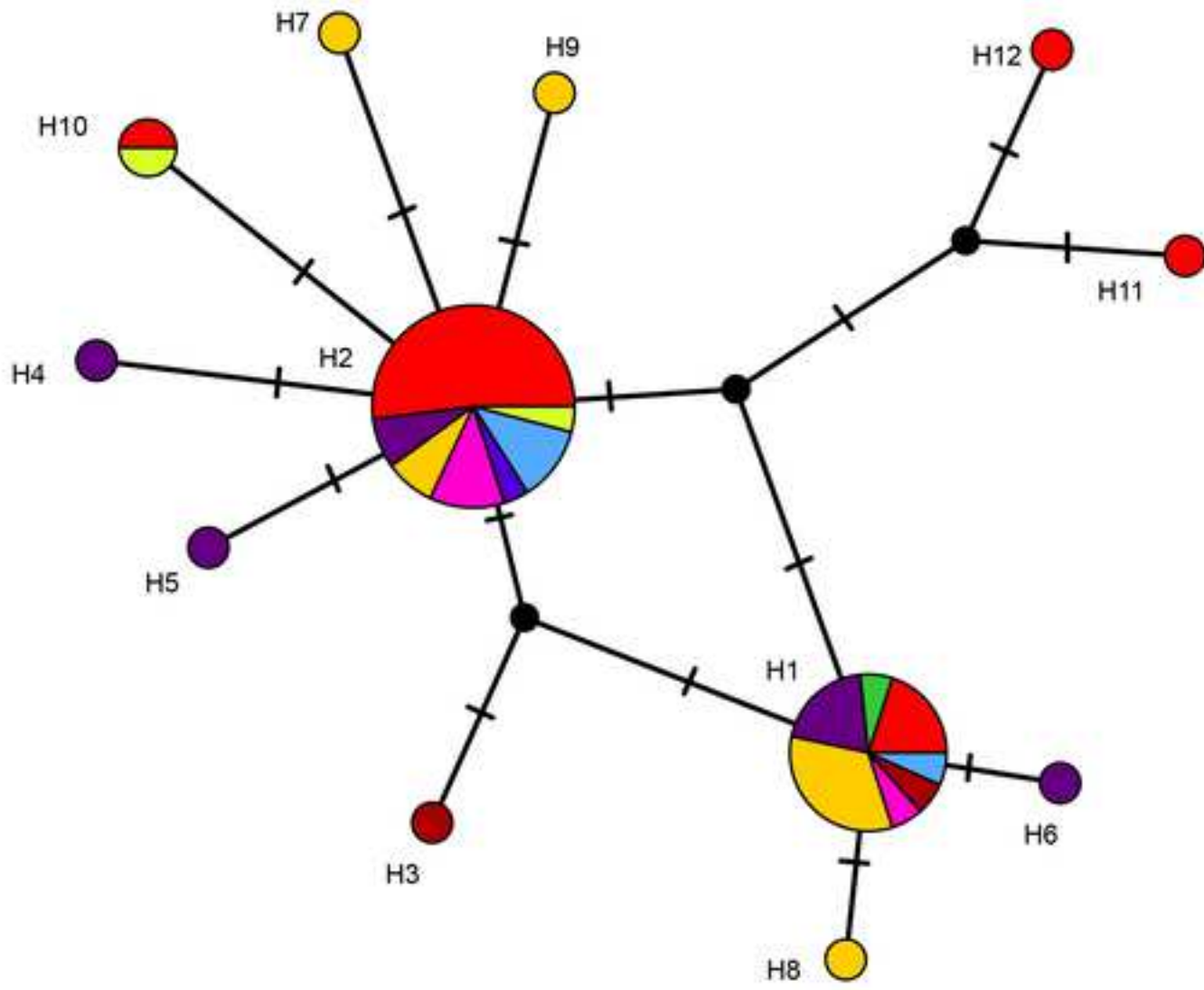


Table 1 Morphometric and meristic data of *Enchelyopus cimbricus* based on the examination of 11 specimens from the North Atlantic. The number of specimens is indicated in brackets.

	Range (n)	Mean±SD
Total length (mm)	81-358.2(11)	
Standard length (mm)	73-319(11)	
<i>As % SL</i>		
Head length	17.2-22.2(11)	18.7±1.5
Pre-dorsal 1-fin length	12.2-21.1(11)	16.5±2.1
Pre-dorsal 3-fin length	27-32.9 (11)	29.3±1.4
Pre-anal-fin length	39.6-48.2 (11)	43.9±2.4
Pre-pectoral-fin length	18-23.6 (11)	19.6±1.5
Pre-pelvic-fin length	16.3-19.3 (11)	17.7±0.9
Pectoral-fin length	12.1-14.7 (11)	13±0.7
Pelvic-fin length	6.9-15.8 (11)	9.2±2.3
Dorsal 3-fin base	49.3-66.9 (11)	63.8±4.9
Anal-fin base	43.6-53.6 (11)	50.8±2.8
Body depth (maximum)	11.1-17.2 (11)	24.3±0.4
Dorsal 1-fin height	19.3-24.8 (5)	22.8±2.5
Caudal-peduncle depth	4.6-5.3 (11)	5±0.3
<i>As % HL</i>		
Pre-orbital length	19.8-28.9 (11)	24.5±2.5
Post-orbital length	52.5-63.4 (11)	55.6±3
Eye diameter	18.4-22.6 (11)	20.7±1.4
Interorbital width	9.3-30.8 (11)	23.7±6.1
Upper jaw length	43.2-60.5 (11)	53.4±5.1
Lower jaw length	35.4-47.6 (11)	42.7±3.8
Barbel length	9.3-16.7 (11)	14.2±2.6
<i>Meristic</i>		
Dorsal fin rays	48 (1), 49 (4), 50 (4), 51 (2)	49.6±0.9
Anal fin rays	42 (3), 43 (4), 44 (4)	43.1±0.8
Pectoral fin rays	15 (3), 16 (4), 17 (3), 18 (1)	16.2±1
Pelvic fin rays	5 (1), 6 (10)	5.9± 0.3
Branchiostegal rays	7 (11)	
Gill rakers	1+8 (2), 1+9 (7), 1+10 (2)	10± 0.6
Pores in lateral line	29-36 (10)	32.1±2.6
Vertebrae	52 (1), 53 (1)	

Table 2 Comparative in relative percentages of *Enchelyopus cimbrius* morphometric data.

	As %SL		As % TL		As %HL		
	This study	Demir et al. 1985	This study	Svetovidov (1948)	This study	Svetovidov (1948)	Demir et al. 1985
Head length	17.2-22.2	22.9-32.6	15.3-20	16-17.2	—	—	—
Pre-dorsal 1-fin length	—	—	10.8-19	14.4-15.1	—	—	—
Pre-anal-fin length	—	—	35.2-42.3	37.4-43	—	—	—
Pre-orbital length	—	—	—	—	19.8-28.9	24.4-27.1	—
Eye diameter	—	—	—	—	18.4-22.6	22.2-24.4	27.7-50
Interorbital width	—	—	1.9-4.7	7.9-8.9	—	—	—
Upper jaw length	—	—	—	—	43.2-60.5	43.9-48	—
Lower jaw length	—	—	—	—	35.4-47.6	48.7-55.8	—
Barbel length	—	—	—	—	9.3-16.7	—	6-23.1
Dorsal 2-fin base	—	—	6.3-10.3	10.5-11.8	—	—	—
Dorsal 3-fin base	—	—	44.4-59.4	58.3-59.2	—	—	—
Anal-fin base	—	—	39.3-47.6	41.7-45.3	—	—	—
First dorsal fin length	—	—	19-22	13.2-14.2	118.3-138.8	—	1.2-32.4
Pectoral-fin length	12.1-14.7	5.6-16.7	10.7-13.2	13.4-14.9	—	—	—
Pelvic-fin length	6.9-15.8	15.8-32.1	6.1-14.2	7.4-8.9	—	—	—
Body depth	11.1-17.2	18.9-30.2	—	—	—	—	—
Caudal-peduncle depth	—	—	4.1-4.9	3.3-3.7	—	—	—

Table 3 Comparative of meristic data of *Enchelyopus cimbrius*. The number of vertebrae obtained in this study corresponds to only two radiographed specimens.

	This study	Svetovidov (1948)	Cohen and Russo (1979)	Demir et al. (1985)
Third dorsal fin rays	48-51	45-50	45-55	38-40
Anal fin rays	42-44	37-41	36-49	38-40
Pectoral fin rays	15-18	15-16	15-19	14-17
Pelvic fin rays	5-6	5	–	5-6
Branchiostegal rays	7	–	–	–
Gill rakers	9-11	9-10	5-13	–
Pores in lateral line	29-36	29	–	–
Vertebrae	52-53	54	–	51-55

Table 4 Parameters of allometric relationships between total length (TL, mm) and total weight (TW, g) of *Enchelyopus cimbrius* in this study and in the literature fitted to a potential equation $Y = a \times X^b$ (where b is the growth coefficient and a is the intercept). n: number of measurements for each study; r^2 : adjusted R-squared; Allo: allometry (I, isometric)

N	Min. length (cm)	Max. length (cm)	a	b	r^2	Allo	Source
44	11	31	0.0043	3.0496	0.93	I	This manuscript
43	3.4	22	0.0044	3.003	0.99	I	Froese and Pauly (2023)
63	11	29	0.0035	3.106	0.70	–	Froese and Pauly (2023)
448	4.7	28.5	0.0032	3.144	0.95	–	Froese and Pauly 2023)
334	6	31	0.0080	2.8377	0.966	–	Silva et al. 2013
174	–	29	0.00335	3.095	0.95	–	Noble and Clark (2019)
529	–	38	0.00254	3.188	0.97	–	Noble and Clark (2019)
27	–	–	0.0016	3.37	–	–	Alpoim et al. (2002)

Table 5 Parameters of allometric relationships between total body length (TL) and different morphometric characters for *Enchelyopus cimbrius* fitted to a potential equation $Y = a \times X^b$ (where b is the growth coefficient and a is the intercept). CI b: coefficient interval of the growth coefficient; n: number of measurements of each morphometric character; Allo: allometry (+ indicates positive allometry, – indicates negative allometry and I indicates isometry); Abbreviations as follow: Interorbital length (IO), eye diameter (ED), pelvic fin length (VL), head length (HL), first dorsal height (D1H), pectoral fin length (PL), body depth (BD), caudal peduncle depth (CPD).

Total length	Morphometric character	Regression coefficients						
		a	b	CI b	r ²	n	P-value	Allo
X	Y							
TL	IO	0.001	1.621	1.417-1.826	0.969	11	<0.001	+
TL	ED	0.095	0.814	0.703-0.925	0.965	11	<0.001	-
TL	VL	1.213	0.507	0.375-0.640	0.881	11	<0.001	-
TL	HL	0.421	0.831	0.759-0.904	0.985	11	<0.001	-
TL	D1H	0.0002	2.190	1.829-2.552	0.983	6	<0.001	+
TL	PL	0.198	0.903	0.825-0.981	0.986	11	<0.001	-
TL	BD	0.057	1.138	0.906-1.369	0.924	11	<0.001	I
TL	CPD	0.033	1.056	0.945-1.167	0.979	11	<0.001	I