Using DNA barcoding to relate cystacanths and adults of Corynosoma australe (Acanthocephala: Polymorphidae) of the Southeastern Pacific Ocean (Off Peru Coast)

Aarón Mondragón-Martínez (aaron72.mondragon@gmail.com)
Universidad Ricardo Palma
Martín Dávila-Rios
Universidad Ricardo Palma
Rosa Martínez-Rojas
National University of San Marcos
Lidia Cruz-Neyra
Universidad Ricardo Palma
Juan C. Ramos Gorbeña
Universidad Ricardo Palma
Miguel Dávila-Robles
Universidad Ricardo Palma
Enrique Garcia-Candela
National University of San Marcos
Estrellita Rojas De-Los-Santos
National University of San Marcos
Abraham Delgado-Escalante
National University of San Marcos
J.R Sanchez-Venegas
National University of San Marcos
Eduardo A. Pulido-Murillo
Universidad Ricardo Palma

Research Article

Keywords: Acanthocephala, Corynosoma, DNA barcoding, pinnipeds, fishes, Peru

Posted Date: January 24th, 2023

DOI: https://doi.org/10.21203/rs.3.rs-2482271/v1

Additional Declarations: No competing interests reported.

Version of Record: A version of this preprint was published at Parasitology Research on June 9th, 2023.
See the published version at https://doi.org/10.1007/s00436-023-07889-1.

Abstract

The objective of this study is to use DNA barcoding to relate cystacanths and adults belonging to the acanthocephalans genus *Corynosoma* found in the southeastern Pacific Ocean off the coast of Peru. For this, we sampled three species of commercial fish (*Paralichthys adspersus*, *Paralabrax humeralis* and *Cheilodactylus variegatus*) and two South American sea lions *Otaria byronia* stranded on the beaches of the city of Huacho and Barranca, department of Lima. A total of 509 larvae were found in the body cavity of 95 fish (total prevalence 54.28%, total mean intensity 8.64), moreover, a total of 127 adults were found in the large intestine of two South American sea lion (P = 100%, MI = 63.5). We isolated 203 larvae of *P. humeralis* (P = 65.71%; MI = 8.83; MA = 5.8), 235 (P = 54.29%; MI = 12.37; MA = 6.71) of *C. variegatus* and 71 (P = 42.86%; MI = 4.73; MA = 2.03) of *P. adspersus*. All adult and larval specimens were morphologically identified as *Corynosoma* sp. We performed phylogenetic analysis and generated cytochrome c oxidase subunit 1 (cox1) gene sequences that were compared with sequences available from GenBank. Likewise, using maximum likelihood (ML) and Bayesian inference (BI) revealed that the 16 new sequences (four adults and twelve larvae) were grouped into a clade formed by *Corynosoma australe*. Therefore, our results contribute to broaden the range of paratenic hosts as well as to record the presence of *C. australe* in the definitive host. In addition, it is the first analysis that confirms the presence of *C. australe* using DNA barcoding, allowing its geographical distribution to be extended to the Southeast Pacific Ocean off the coast of Peru.

Introduction

About 40 species of the genus *Corynosoma* Lühe, have been recorded worldwide (García-Varela et al. 2021), with *C. australe* having the greatest range in the southern hemisphere from South Australia, Antarctica, South Africa, South America (Zdzitowiecki 1984; Aznar et al. 2012; Ionita et al. 2008; Hernandez-Orts et al. 2017; Lisitsyna et al. 2018) and most recently reported in North America. (United States of America and Mexico) (García-Varela et al. 2021). *Corynosoma* species generally use pinnipeds as their definitive host, but they have also been found parasitizing cetaceans and waterfowl. (Sardella et al. 2005; Aznar et al. 2012; Hernández-Orts et al. 2017; Lisitsyna et al. 2018). The complete life cycle comprises benthic amphipods as intermediate hosts (Hoberg 1986; Sinisalo and Valtonen 2003) and a wide range of fish as potential paratenic hosts (Valtonen 1983; Laskowski and Zdzitowiecki 2005; Sasaki et al. 2019). In addition, *Corynosoma* has been reported to naturally infect terrestrial mammals, considered accidental hosts (Noronha 1988; Cabrera et al. 1990; Tantaleán et al. 2007).

In the Peruvian sea, cystacanths of the genus *Corynosoma* have been reported morphologically characterized in various fish of commercial importance (Tantaleán et al. 2005; Chero et al. 2014; Iannacone et al. 2015; Minaya et al. 2016), also in the South American sea lion *Otaria byronia* (Tantaleán 1993; Cabrera et al. 1994; Naupay et al. 2019). Evidence from a study of controlled infections in experimental hosts in Peru showed the process of development from juveniles to adults that reached full sexual maturity with oviposition, registering *Corynosoma obtuscens* (now syn. *C. australe*) as a parasite of great infective capacity and non-specific for the definitive host (Castro and Martínez 2002), likewise, it

has been recorded in terrestrial mammals (Cabrera et al. 1999; Castro et al. 2004; Tantaleán et al. 2007; Acosta et al. 2015) and reproductive adults of *C. australe* have been reported in the Magellanic penguin *Spheniscus magellanicus* in Brazil, as a new avian host. (Hernández-Orts et al. 2017). In the present study, we used morphological data and the first analysis using DNA barcoding to confirm the identification of cystacanths and adults of *Corynosoma australe* present in the southeastern Pacific Ocean off the coast of Peru where we expanded its geographic distribution for the southern hemisphere of America and recorded new commercially important paratenic hosts.

Material And Methods

Sample collection

Between January and March 2018, 95 specimens of three commercial fish species were examined, *Paralichthys adspersus* (length 34.83 ± 2.32 cm; weight: 325.78 ± 54.7 g), *Paralabrax humeralis* (length 39.17 ± 2.6 cm; weight 459.2 ± 45.2 g) and *Cheilodactylus variegatus* (length: 33 ± 2.7 cm; 315.5 ± 34.15 g) off the coast of the Peruvian Sea (Chorrillos, Lima, 12° 9'57.59”S 77° 1'46.3”O). Specimens were examined in fresh conditions in the laboratory of Parasitology in Wildlife and Zoonosis of “Universidad Nacional Mayor de San Marcos”, fishes were identified according to Chirichigno and Cornejo (2001).

In 2015, another research project had already collected acanthocephalans from two stranded specimens of *O. byronia* stranded on the beaches of Huacho (11° 06' S and 77° 36' W) and Barranca (10° 45' S and 77° 46' W), department of Lima.

Parasitological examination

A total of 509 cystacanths, mostly alive, were found encysted on the serosal surface of the intestine, stomach, and body cavity of *P. adpersus*, *P. humeralis* and *C. variegatus*, removed from their capsule and repeatedly washed in 0.9% saline solution and morphologically identified at genus level by optical microscope (Leica EZ4, Germany) following Sardella et al. (2005). Some cystacanths larvae were fixed and stored in 2 ml tubes with 70% alcohol for molecular analysis, furthermore, larvae and adults were fixed in 2.5% glutaraldehyde to be analyzed under the scanning electron microscope (SEM). The ethanol-preserved adult samples contained 127 acanthocephalan specimens that were used in this study to perform previous morphological descriptions (Zdzitowiecki, 1984; Serdella et al. 2005; Lisitsyna et al. 2019; García-Varela et al. 2021).

Molecular identification

DNA was extracted with the DNeasy tissue Kit (Qiagen, Chatsworth, California, USA), DNA quality and quantity was verified in a spectrophotometer Nanodrop®ND-2000 (Thermo Scientific). The primers used were CORY-COIF 5´ AGTTCTAATCATAARGATATYGG-3´ (Nadler et al., 2006) and CORY-COIR 5 ´TAAACTTCAGGGTGACCAAAAAATCA-3´ (Folmer et al. 1994). The locus was amplified by PCR in a Veriti™ 96-well thermocycler (Applied Biosystems, California, USA) with a final volume of 50 µL, including 5 µL of genomic DNA. The reaction mixture contained 2.5 U/µl Taq polymerase (Hot Star Taq DNA Polymerase

Qiagen Kit, Hilden, Germany), and 0.5 µM of each primer (Macrogen, South Korea). The amplification condition was optimized as follows: one cycle at 94°C for 3 min; 35 cycles of 94°C for 1 min, 40°C for 60 sec, 72°C for 1 min, and a final cycle of 72°C for 5 min; storage at 4˚C. Amplied fragments were visualized on agarose gel (1.5%) detected by the gel documentation system (ENDURO™ GDS Touch, USA) and fragment sizes were determined by comparison with a GeneRuler Express DNA Ladder marker (#SM 1551, Thermo Scientific). The PCR products were sent to Macrogen Inc. (Seoul, South Korea) for purification and sequencing. The PCR primers were used for sequencing. Nucleotide sequences obtained by PCR were subjected to known sequences by BLAST search. (http://blast.ncbi.nlm.nih.gov/Blast.cgi). All sequences have been deposited in Genbank data set (Table 1).

Table 1
List of species used in the phylogenetic analyses, with data on the life-cycle stage, host locality and GenBank accession number for sequences mitochondrial cytochrome c oxidase subunit 1 (*cox*1) gene. Abbreviations: A, adult; C, cystacanth.

Species	Stage	Locality	Hosts species	Genbank access.	Reference
OUTGROUP					
Andracantha phalacrocoracis	C	Japón: Hokkaido, Nemuro	*Osmerus dentex*	LC465354	Sasaki et al. 2019
Andracantha sigma	A	New Zealand	*Phalacrocorax punctatus*	MF527035	Presswell et al. 2017
INGROUP					
Corynosoma villosum	A	USA: Alaska, isla St. Paul	*Callorhinus ursinus*	MK119251	Lisitsyna et al. 2018
Corynosoma villosum	C	Japan: Hokkaido, Hamatonbetsu	*Platichthys stellatus*	LC465388	Sasaki et al. 2019
Corynosoma validum	A	USA: Alaska, isla St. Paul	*Callorhinus ursinus*	JX442193	García-Varela et al. 2013
Corynosoma validum	A	USA: Alaska, isla St. Paul	*Callorhinus ursinus*	MK119252	Lisitsyna et al. 2018
Corynosoma enhydri	A	USA: Monterey Bay, California	*Enhydra lutris*	DQ089719	García-Varela and Nadler, 2006
Corynosoma magdaleni	A	Baltic Sea	*Phoca vitulina*	MF078642	Waindok et al. 2018
Corynosoma magdaleni	A	Lake Saimaa, Finland	*Phoca hispida saimensis*	EF467872	García-Varela et al. 2006
Corynosoma strumosum	A	USA: California, Sausalito	*Zalophus californianus*	MK119250	Lisitsyna et al. 2018
Corynosoma strumosum	A	Japan: Hokkaido, Erimo	*Phoca vitulina*	LC465394	Sasaki et al. 2019
Corynosoma semerme	C	Japan: Hokkaido, Nemuro	*Osmerus dentex*	LC465392	Sasaki et al. 2029
Corynosoma semerme	A	USA: Alaska, isla St. Paul	*Callorhinus ursinus*	MK119253	Lisitsyna et al. 2018
Corynosoma obtuscens	A	USA: Alaska, isla St. Paul	*Callorhinus ursinus*	JX442192	García-Varela et al. 2013

Species	Stage	Locality	Hosts species	Genbank access.	Reference
OUTGROUP					
Corynosoma hannae	C	New Zealand: Kaka Point, Otago	*Peltorhamphus novaezeelandiae*	KX957726	Hernandez-Orts et al. 2016
Corynosoma hannae	C	New Zealand: Kaka Point, Otago	*Colistium guntheri*	KY909263	Anglade and Randhawa, 2017
Corynosoma australe	A	Mexico: Isla Guadalupe, Baja California Norte	*Zalophus californianus*	MT676814	Garcia-Varela et al. 2020
Corynosoma australe	A	Mexico: Isla Guadalupe, Baja California Norte	*Zalophus californianus*	MT676815	Garcia-Varela et al. 2020
Corynosoma australe	A	Mexico: Isla San Pedro Nolasco, Sonora	*Zalophus californianus*	MT676809	Garcia-Varela et al. 2020
Corynosoma australe	A	Mexico: Isla San Pedro Nolasco, Sonora	*Zalophus californianus*	MT676811	Garcia-Varela et al. 2020
Corynosoma australe	A	USA: California, Sausalito	*Zalophus californianus*	MK119249	Lisitsyna et al. 2018
Corynosoma australe	A	Mexico: Isla Guadalupe, Baja California Norte	*Zalophus californianus*	MT676813	Garcia-Varela et al. 2020
Corynosoma australe	A	Brazil: Rio de Janeiro	*Spheniscus magellanicus*	MF497335	Hernandez-Orts et al.2017
Corynosoma australe	A	Brazil: Rio de Janeiro	*Spheniscus magellanicus*	MF497334	Hernandez-Orts et al.2017
Corynosoma australe	C	Argentina	*Raneya brasiliensis*	MT676823	Garcia-Varela et al. 2020
Corynosoma australe	C	Argentina: Golfo de San Matias	*Merluccius hubbsi*	MT676821	Garcia-Varela et al. 2020
Corynosoma australe	C	Argentina	*Raneya brasiliensis*	MT676824	Garcia-Varela et al. 2020

Species	Stage	Locality	Hosts species	Genbank access.	Reference
OUTGROUP					
Corynosoma australe	C	Peru: Lima	*Paralichthys adspersus*	MZ920052	This study
Corynosoma australe	C	Peru: Lima	*Paralichthys adspersus*	MZ920053	This study
Corynosoma australe	C	Peru: Lima	*Paralichthys adspersus*	MZ920054	This study
Corynosoma australe	C	Peru: Lima	*Paralichthys adspersus*	MZ920055	This study
Corynosoma australe	C	Peru: Lima	*Paralabrax humeralis*	MZ920056	This study
Corynosoma australe	C	Peru: Lima	*Paralabrax humeralis*	MZ920057	This study
Corynosoma australe	C	Peru: Lima	*Paralabrax humeralis*	MZ920058	This study
Corynosoma australe	C	Peru: Lima	*Paralabrax humeralis*	MZ920059	This study
Corynosoma australe	C	Peru: Lima	*Cheilodactylus variegatus*	MZ920060	This study
Corynosoma australe	C	Peru: Lima	*Cheilodactylus variegatus*	MZ920061	This study
Corynosoma australe	C	Peru: Lima	*Cheilodactylus variegatus*	MZ920062	This study
Corynosoma australe	C	Peru: Lima	*Cheilodactylus variegatus*	MZ920063	This study
Corynosoma australe	A	Peru: Lima	*Otaria byronia*	MZ920064	This study
Corynosoma australe	A	Peru: Lima	*Otaria byronia*	MZ920065	This study
Corynosoma australe	A	Peru: Lima	*Otaria byronia*	MZ920066	This study
Corynosoma australe	A	Peru: Lima	*Otaria byronia*	MZ920067	This study

Phylogenetic analyses

The sequences obtained were assembled and edited in the ChromasPro version 2.0.1 (Technelysium Pty Ltd., South Brisbane, Queensland, Australia). Generated contigs were compared with sequences available for species of the genus *Corynosoma*. Two members of the genus *Andracantha* Schmidt, 1975, A. sigma Presswell, García-Varela & Smales, 2017 and *A. phalacrocoracis* (Yamaguti, 1939), were chosen as outgroups according to Lisitsyna et al. 2018. The alignment was obtained using the ClustalW method implemented in the MEGA version X program (Kumar et al. 2018). The resulting alignment was also corrected (removing misaligned positions and divergent regions) and trimmed using Gblock web server (http://phylogeny.lirmm.fr/; Dereeper et al. 2008), with adjustments for less stringent parameters.

Phylogenetic reconstructions were performed using Bayesian inference (BI) and maximum likelihood (ML) algorithms. The best nucleotide substitution model, HKY + G + I, was selected according to Bayesian information criterion. ML analysis was performed using MEGA X and nodal supports were inferred based on 1000 bootstrap replicates. The BI analysis was conducted using Mr. Bayes v.3.2.6 (Ronquist et al. 2012), running two independent Markov Chain Monte Carlo runs of four chains setting for 1,000,000 generations and sampling every 100 generations. The first 25% of the trees sampled were discarded as “burn-in”, and consensus topology and posterior probability values were calculated from the remaining trees and visualized in FigTree v. 1.4.3 (http://tree.bio.ed.ac.uk/software/fgtree/). Uncorrected p distances were calculated using MEGA X.

Parameters of parasitological analyses

Descriptors quantitative of parasite infection such as prevalence (P%), mean intensity (MI) and mean abundance (MA) were calculated using the software Quantitative Parasitology 3.0 (Reiczigel and Rózsa 2005). Sterne's exact test was used at 95% confidence limits for prevalence. To compare MI and MA, the bootstrap procedure was applied with 1000 replications at the 95% confidence interval. Differences were considered significant when $p < 0.05$.

Results

Morphological analysis

All the larval stage collected from *P. adspersus, P. humeralis* and *C. variegatus* were morphologically characterized as *Corynosoma* sp. We observed 30 larvae has a thick and short trunk with length 1950 ± 200 µm and SEM showed the presence of cylindrical proboscis is 560 ± 40 µm long and 195 ± 15 µm wide, armed with 18–20 longitudinal rows consisting of 12–14 hooks per each row, like also, tegumental spines in the body (Fig. 1). The adult stage collected from South American sea lions *O. byronia*, were examined in this study and exhibited similarity morphological characteristics like cystacanths, but with larger morphometrics. We observed that 30 adults have a thick trunk with length 2300 ± 200 µm and SEM showed the presence of cylindrical proboscis is almost of same size as cystacanths with 2–4 spiniform hooks, 17–19 hook rows, 11–14 hooks per row and 8–11 rooted hooks (Fig. 2).

Molecular Identification and phylogenetic analyses

The amplification of 16 partial sequences of cox1 (524 bp) were obtained for *C. australe* from paratenics hosts (*C. variegatus, P. humeralis and P. adspersus*) and definitive host (*O. byronia*) from the coast of Peru. The newly generated sequences were 100% identical, with the exception of two isolates (MZ920054, MZ920063), which detected 0.4% genetic divergence. The phylogenetic trees based on cox1 sequences performed by ML and BI were almost identical, with a better resolution in the ML reconstruction. The isolates of the present study are nested in a strongly supported clade with other isolates of *C. australe* and this species appears as a sister taxon of *Corynosoma hannae* (Fig. 3). The differences between groups of isolates of *C. australe* were evidenced with the uncorrected p-distance. The genetic divergence between Peruvian sequences of *C. australe* and other registered in the American continent ranged from 1.3 to 3.8% (Table 2). In ML tree was recovered a clade formed by Peruvian isolates, separated from isolates registered in other countries (Argentina, Brazil, Mexico, United States). The reference sequences and newly generated sequences deposited in GenBank are summarized in Table 1.

Table 2. Uncorrected p-distance (%) between *cox*1 sequences of *Corynosoma australe* from Peru and other American countries.

Corynosoma australe isolates	*Corynosoma australe* Peru	
	MZ920052-53, MZ920055-62, MZ920064-67	MZ920054, MZ920063
Peru		
- MZ920052-53, MZ920055-62, MZ920064-67	0	0.4
- MZ920054, MZ920063	0.4	0
Argentina	1.3-1.9	1.7-2.3
Brazil	2.1	2.1
Mexico	3.4	3.8
USA	2.3	2.7

Ecological analysis

A total of 509 cystacanths larvae were found in 95 fish (total prevalence 54.28%, total mean intensity 8.64). After morphological analysis and molecular identification, all cystacanths larvae isolated were identified as *C. australe.* The hosts examined during 2018, presented the following ecological indices: *P. humeralis* (P = 65.71%; MI = 8.83; MA = 5.8), *C. variegatus* (P = 54.29%; MI = 12.37; MA = 6.71) and *P. adspersus* (P = 42.86%; MI = 4.73; MA = 2.03), in addition, the intensity and mean abundance was significantly higher in *C. variegatus* than in the other hosts.

Discussion

In this study, we report for the first-time using DNA barcoding the presence of cystacanths larvae and adults of *Corynosoma australe* obtained from three different commercial fish species (*P. humeralis, P. adspersus and C. variegatus)* and from South American sea lions (*O. byronia*) from the Southeast Pacific Ocean off Peru. This parasite turned out to be the only dominant acanthocephalan isolated from the intestine, stomach, and body cavity of paratenic hosts. The elucidation of *C. australe* in *P. adspersus, P. humeralis* and *C. variegatus represent* new host records for this species of parasite and expands its distribution range in Peruvian sea waters. Studies carried on more than 20 species of marine teleost fishes located in the waters of the southwestern Atlantic Ocean (off the coasts of Argentina and Brazil) recorded cystacanths of *C. australe* (Santos et al. 2008; Hernández-Orts et al. 2019a; Hernández-Orts et al. 2019b). Similarly, for the southeastern Pacific Ocean (off the coasts of Peru and Chile) they have recorded *Corynosoma* spp. morphologically characterized in more than 40 species of marine teleost fishes (Tantaleán et al. 2005; Muñoz and Olmos 2008; Chero et al. 2014; Chero et al. 2016). Our molecular data confirmed the phylogenetic relationship of cystacanths larvae and adults strongly supported in a clade together with *C. australe* sequences from the northern and southern hemisphere of the Americas (García-Varela et al. 2021), as well as coincided with previously inferred phylogenies consistent with those of Hernández-Orts et al. (2017) and Lisitsyna et al. (2019). A recent study explored the genetic diversity of *C. australe* specimens isolated from otariids of the northern hemisphere (United States of America and Mexico) and southern hemisphere (Argentina and Brazil), where the low level of genetic divergence found among specimens from the same species (Garcia-Valera et al. 2021), furthermore, to support the synonymy between *C. obtuscens* and *C. australe*, data from cox1 sequences were compared and a low genetic divergence (1.1–1.6%) was evidenced. which corresponds to the intraspecific level (Lisitsyna et al. 2019). Similarly, we obtained the genetic divergence between Peruvian sequences of *C. australe* and other registered in the American continent ranged from 1.3 to 3.8%. In addition, they recorded the presence of *C. australe* in Magellanic penguins in the southern hemisphere (Brazil) but with lower levels of infection than in otariid definitive hosts (Hernández-Orts et al. 2017a).

Genetic/molecular markers based on mitochondrial DNA allow discriminating morphologically indistinguishable species and linking the different developmental stages of a species (Hebert and Gregory 2005). Lisitsyna et al. (2018), demonstrated that *C. obtuscens* is synonymous with *C. australe* by morphological and molecular analysis using the cox1 marker, and showed that *C. australe* appears to be the only species of the genus *Corynosoma* that parasitizes pinnipeds in both hemispheres. Specimens of *Corynosoma* spp. have been frequently studied using the cox1 gene (García-Varela and Nadler 2006; García-Varela and Pérez-Ponce de León 2008; García-Varela et al. 2013; Hernández-Orts et al. 2017a, b; Lisitsyna et al. 2018; Sasaki et al. 2019; García-Varela et al. 2021), thus, we provide in this study the first consistent molecular data through analysis of the cox1 mtDNA sequence and identify *C. australe* in the two stages of the biological cycle. The paratenic hosts of the present study are not recorded in the diet of South American sea lions in the Peruvian Sea, which is basically composed of *Engraulis ringens*, *Normanichthys crockeri* y *Merluccius gayi* (Zavalaga et al. 1998; Arias-Schreiber 2000), however, *C. obtuscens* has been reported *M. gayi*, *Sarda chiliensis*, *Cilus gilberti* y *Cynoscion analis* in very low prevalence (Chero et al. 2014a; Chero et al. 2014b; Chero et al. 2016; Minaya et al. 2016) for the central

Peruvian Sea. In addition, a study of the parasitic community in *Isacia conceptionis* reported *C. obtuscens* (now C. *australe*) as one of the species with the highest prevalence and mean abundance (Iannacone et al. 2015). In the present study, we recorded *C. australe* with a higher prevalence in *P. humeralis* but *C. variegatus* presented the highest abundance and mean intensity. The results obtained contribute to improve the knowledge in different biological aspects such as the mapping of the definitive and paratenic host association, tropic ecology, occurrence, and systematic position of *C. australe*, considering account the wide range of commercial fish present in the Peruvian sea, there is a possibility that corynosomiasis, considered a minor parasitic zoonosis, occurs in Peru.

Declarations

Acknowledgments The present study is supported by Faculty of Biological Sciences, National University of San Marcos, Peru. The authors extend their appreciations to members of Biomedical Sciences Research Institute,Universidad Ricardo Palma, Peru, Laboratory of Parasitology in helping to complete this study.

Author contribution Aarón Mondragón-Martínez (AMM), Rosa Martínez-Rojas (RMR) and Eduardo A. Pulido-Murillo (EDPM): designed the study. AMM, RMM, Martín Dávila-Rios (MDR) and Estrellita Rojas De-Los-Santos (ERS): field work. MDR, Miguel Dávila-Robles (MDR) and Juan C. Ramos-Gorbeña (JCRG): performed laboratory analyses. Lidia Cruz-Neyra (LCN), RMR and J.R Sanchez-Venegas (JRSV): performed statistical analyses. EDPM and Enrique Garcia-Candela (EGC): performed bioinformatics analyses. AMM, EDPM and EGC: prepared figures 1 - 3 and tables 1 - 2. AMM, RMR, MDR and LCN: wrote the first draft of the manuscript. All authors revised the manuscript. All authors read and approved the final version of the manuscript.

Funding We want to thank UNMSM for financing the project with internal funds with R.R. 05753-R-21 and code B21102151 and Universidad Ricardo Palma (URP) for financing.

Data availability The obtained sequences are deposited in GenBank under the accession numbers MZ920052-MZ920067.

Ethics approval This study was performed in agreement with the recommendations of all applicable institutional, national and international guidelines for the care and use of animals. The responsible conduct of the research was approved by the university council N° 0689-2020 of the “Universidad Ricardo Palma”.

Consent to participate Not applicable.

Consent for publication All the authors provided their consent for the publication of this manuscript.

Conflicts of interest The authors declare that they have no competing interests.

References

1. Acosta M, Tantaleán M, Serrano-Martínez E (2015) Identificación de parásitos gastrointestinales por coproscopía en carnívoros silvestres del Zoológico Parque de las Leyendas, Lima, Perú. Rev investig vet Perú 26(2): 282-290
2. Arias-Schreiber M (2000) Los lobos marinos y su relación con la abundancia de la anchoveta peruana durante 1979-2000. Bol Institit Mar Perú 19 (1-2): 133-138
3. Aznar FJ, Hernández-Orts J, Suárez AA, García-Varela M, Raga JA, Cappozzo HL (2012) Assessing hostparasite specificity through coprological analysis: a case study with species of *Corynosoma* (Acanthocephala: Polymorphidae) from marine mammals. J Helminthol 86: 156–164
4. Cabrera R, Coronado C, Ampuero S (1994) Parásitos de Otáridos de la costa peruana y su importancia sanitaria. Bol de Lima 16 (91-96): 77- 80
5. Cabrera R, Rojas R, Davalos M (1999) *Corynosoma obtuscens* Lincicome, 1943 (Acanthocephala: Polymorphidae) in *Canis familiaris* de la Ciudad de Chincha, Peru. Parasitol Día 23: 59–62
6. Castro M, Martínez R (2004) Proceso del desarrollo de *Corynosoma obtuscens* (Acanthocephala: Polymorphidae) en *Canis familiaris* y su posible implicancia en salud publica. Parasitol Latinoam 59: 26–30
7. Chero J, Cruces C, Iannacone J, Sáez G, Alvariño L, Rodríguez C, Rodríguez H, Tuesta E, Pacheco A, Huamani N (2014a) Índices parasitológicos de la merluza peruana *Merluccius gayi peruanus* (Ginsburg, 1954) (Perciformes: Merlucciidae) adquiridos del terminal pesquero de Ventanilla, Callao, Perú. Neotrop Helminthol 8:1
8. Chero J, Iannacone J, Cruces C, Sáez G, Alvariño L (2014b) Comunidad de metazoos parásitos de la corvina *Cilus gilberti* (Abbott, 1899) (Perciformes: Sciaenidae) en la zona costera de Chorrillos, Lima, Perú. Neotrop Helminthol 8:1
9. Chero J, Sáez G, Iannacone J, Cruces C, Alvariño L, Luque J (2016) Ecología comunitaria de metazoos parásitos del bonito *Sarda chiliensis* Cuvier, 1832 (Perciformes: Scombridae) de la costa peruana. Rev investig vet Perú 27(3): 539-555
10. Chirichigno N, Cornejo RM (2001) Catálogo comentado de los peces marinos del Perú. Callao, Perú: Institit del Mar del Perú
11. Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O (2008) Phylogeny. fr: robust phylogenetic analysis for the non-specialist. Nucleic acids res 36(suppl 2): 465-469
12. Folmer O, Black M, Hoeh W, Lutz R, Vrijenhoek R (1994) DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. Mol Mar Biol Biotechnol 3: 294–299
13. García-Varela M, Nadler SA (2006) Phylogenetic relationships among Syndermata inferred from nuclear and mitochondrial gene sequences. Mol Phylogenet Evol 40: 61–72

14. García-Varela M, Pérez-Ponce de León G (2008) Validating the systematic position of *Profilicollis* Meyer, 1931 and *Hexaglandula* Petrochenko, 1950 (Acanthocephala: Polymorphidae) using cytochrome c oxidase (cox 1). J Parasitol 94: 212–217
15. García-Varela M, Masper A, Crespo EA, Hernández-Orts JS (2021) Genetic diversity and phylogeography of *Corynosoma australe* Johnston, 1937 (Acanthocephala: Polymorphidae), an endoparasite of otariids from the Americas in the northern and southern hemispheres. Parasitol Int 80: 102205
16. Hebert PD, Gregory TR (2005) The promise of DNA barcoding for taxonomy. Syst Biol 54: 852–859
17. Hernandez-Orts JS, Brandão M, Georgieva S, Raga JA, Crespo EA, Luque JL, Aznar F J (2017a) From mammals back to birds: Host-switch of the acanthocephalan *Corynosoma australe* from pinnipeds to the Magellanic penguin *Spheniscus magellanicus*. PLoS One, 12(10): e0183809
18. Hernández-Orts JS, Smales LR, Pinacho-Pinacho CD, García-Varela M, Presswell B (2017b) Novel morphological and molecular data for *Corynosoma hannae* Zdzitowiecki, 1984 (Acanthocephala: Polymorphidae) from teleosts, fish-eating birds and pinnipeds from New Zealand, Parasitol Int 66: 905–916
19. Hernández-Orts JS, Alama-Bermejo G, García NA, Crespo EA, Montero FE, Raga JA, Aznar FJ (2019a) Acanthocephalans from marine fishes from Patagonia, Argentina. J Parasitol 105(1): 162-169
20. Hernández-Orts JS, Montero FE, García NA, Crespo EA, Raga JA, García-Varela M, Aznar FJ (2019b) Transmission of *Corynosoma australe* (Acanthocephala: Polymorphidae) from fishes to South American sea lions *Otaria flavescens* in Patagonia, Argentina. Parasitol res 118(2): 433-440
21. Iannacone J, Alvariño L, Chero J, Sáez G (2015) Comunidad Parasitaria de Cabinza *Isacia conceptionis* (Cuvier & Valenciennes, 1830) (Perciformes: Haemulidae) en la Zona de Chorrillos, Lima, Perú. Rev de Investig Vet del Perú 26(1): 96-110
22. Ionita M, Varela MG, Lyons ET, Spraker TR, Tolliver SC (2008) Hookworms (*Uncinaria lucasi*) and acanthocephalans (*Corynosoma* spp. and *Bolbosoma* spp.) found in dead northern fur seals (*Callorhinus ursinus*) on St. Paul Island, Alaska in 2007. Parasitol Res 103: 1025–1029
23. Kumar S, Stecher G, Li M, Knyaz C, Tamura K (2018) MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol biol evol 35(6): 1547
24. Laskowski Z, Zdzitowiecki K (2005) The helminth fauna of some notothenioid fishes collected from the shelf of argentine islands, West Antarctica, Polar Res 26: 315–324
25. Minaya D, Chero J, Sáez G, Rodriguez L, Sandoval M, Alvariño L, Iannacone J (2016) Comunidad de parásitos de “Cachema” *Cynoscion analis* (Jenyns, 1842) (Perciformes: Sciaenidae) en el Pacífico Oriental. Neotrop Helminthol 10(1)
26. Muñoz G, Olmos V (2008) Revisión bibliográfica de especies endoparásitas y hospedadoras de sistemas acuáticos de Chile. Rev biol mar oceanogr 43(2): 173-245
27. Lisitsyna OI, Kudlai O, Spraker TR, Kuzmina TA (2018) New records on acanthocephalans from California sea lions *Zalophus californianus* (Pinnipedia: Otariidae) from California, USA. Vestn Zool 52: 181–192.

28. Lisitsyna OI, Kudlai O, Spraker TR, Tkach VV, Smales LR, Kuzmina TA (2019) Morphological and molecular evidence for synonymy of *Corynosoma obtuscens* Lincicome, 1943 with *Corynosoma australe* Johnston, 1937 (Acanthocephala: Polymorphidae). Syst Parasitol 96(1): 95-110.
29. Naupay A, Castro J, Rojas V, Suarez D (2019) Helmintos gastrointestinales de *Otaria flavescens* Shaw 1800 (Mammalia: Otariidae) león marino sudamericano de la costa central del Perú. Neotrop Helminthol 13(2)
30. Noronha D (1988) *Corynosoma clementei* Giovannoni y Fernandes, 1965 y su sinónimo *Corynosoma seropedicus* Machado Filho, 1970, un parásito accidental de *Canis familiaris* L., 1758. Arq Flum Med Vet 3:119–120
31. Reiczigel J, Rózsa L (2005) Quantitative Parasitology 3.0 Budapest. Distributed by the authors
32. Ronquist F, Teslenko M, Van Der Mark P, Ayres DL, Darling A, Höhna S, Bret Larget, Liang Liu, Marc A Suchard, John P Huelsenbeck (2012) MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Syst biol 61(3): 539-542
33. Santos CP, Gibson DI, Tavares LE, Luque JL (2008) Checklist of Acanthocephala associated with the fishes of Brazil. Zootaxa 1938(1): 1-22
34. Sardella NH, Mattiucci S, Timi JT, Bastida RO, Rodrıguez DH, Nascetti G (2005) *Corynosoma australe* Johnston, 1937 and *C. cetaceum* Johnston & Best, 1942 (Acanthocephala: Polymorphidae) from marine mammals and fishes in Argentinian waters: allozyme markers and taxonomic status. Syst Parasitol 61: 143–156.
35. Sasaki M, Katahira H, Kobayashi M, Kuramochi T, Matsubara H, Nakao M (2019) Infection status of commercial fish with cystacanth larvae of the genus *Corynosoma* (Acanthocephala: Polymorphidae) in Hokkaido, Japan. Int J Food Microbiol 305: 108256
36. Sinisalo T, Valtonen ET (2003) *Corynosoma* acanthocephalans in their paratenic fish hosts in the northern Baltic Sea. Parasite 10:227–233
37. Tantaleán VM (1993) Algunos helmintos de mamíferos marinos del Perú y su importancia médica. Rev peru med trop 67-71
38. Tantaleán M, Sánchez L, Gómez L, Huiza A (2005) Acantocéfalos del Perú. Rev peru biol 12(1): 83-92
39. Valtonen ET, Niinimaa A (1983) Dispersion and frequency distribution of *Corynosomas* pp. (Acanthocephala) in the fish of the Bothnian Bay, Aquilo Ser. Zool 22: 1–11
40. Zavalaga C, Paredes R, Arias-Schreiber M (1998) Dieta del lobo fino *Arctocepbatus australis* y el lobo chusco *Otaria byronia* en la costa sur del Perú en febrero de 1998. Inf Prog Inst Mar Perú 79:3-16
41. Zdzitowiecki K (1984) Some antarctic acanthocephalans of the genus *Corynosoma* parasitizing Pinnipedia, with descriptions of three new species. Acta Parasitol 29: 359–377

Figures

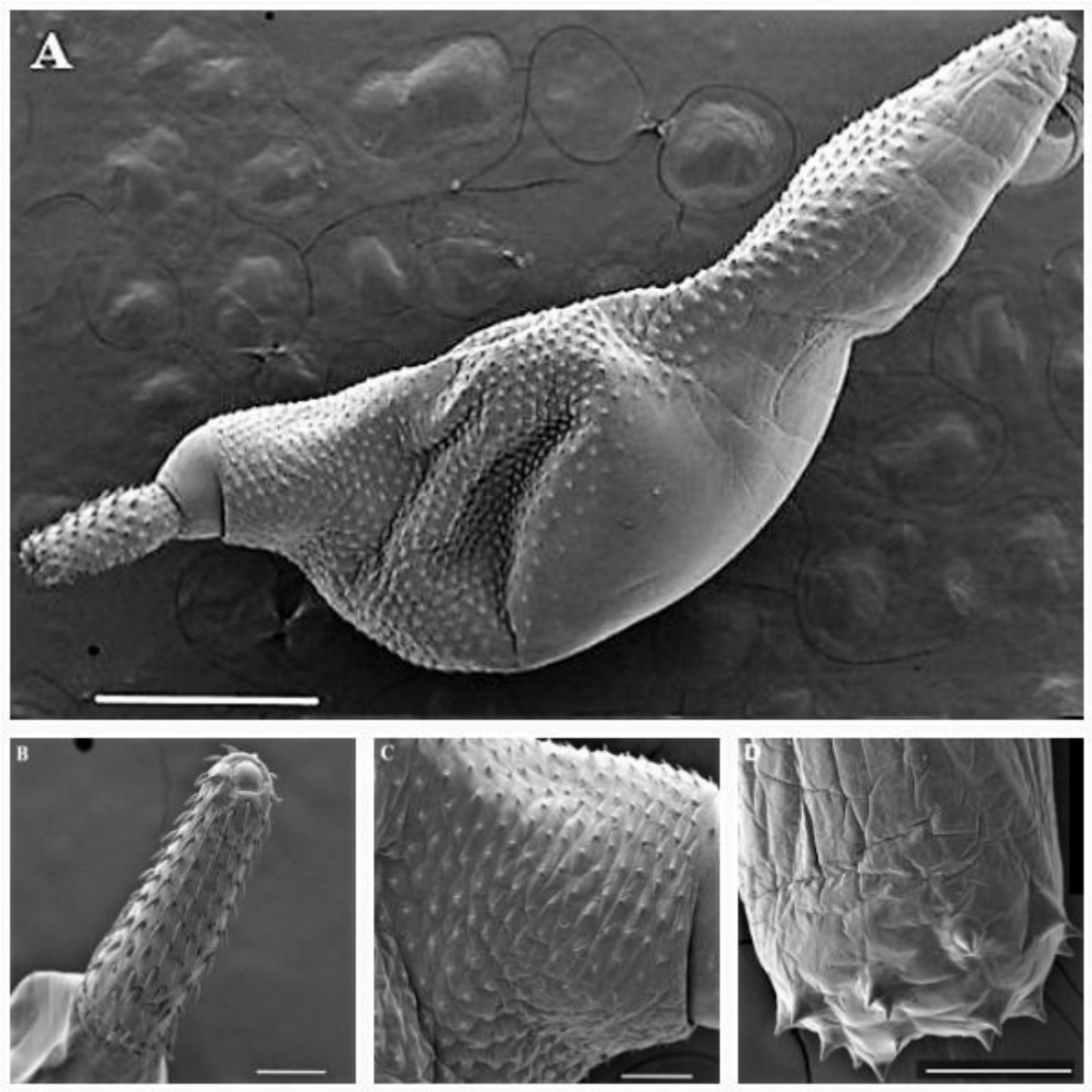

Figure 1

Scanning electron micrographs of cystacanths larvae of *Corynosoma australe* from fish. (A) Cystacanth larvae lateral view; (B) Cystacanth proboscis armature; (C) Tegumental spines; (D) Posterior end of male showing genital spines, lateral view. Scale bars 500 µm (A); 100 µm (B); 100 µm (C); 100 µm (D).

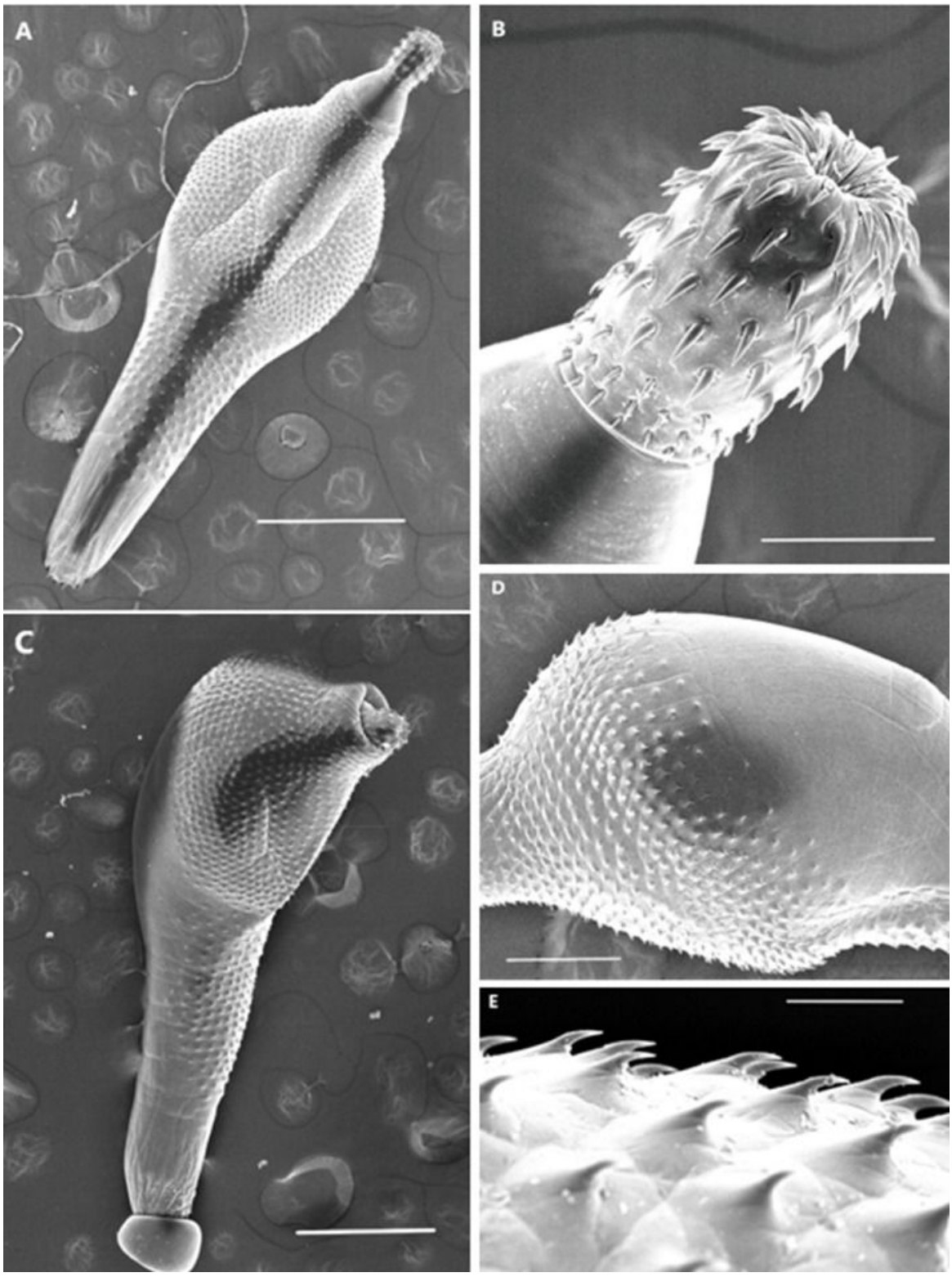

Figure 2

Scanning electron micrographs of *Corynosoma australe* from *Otaria byronia.* (A) Adult female, whole worm, ventral view; (B) Adult female proboscis; (C) Adult male, whole worm, lateral view; (D) Adult female showing trunk armature; (E) Somatic spine of male. Scale bars = 500 µm (A); 100 µm (B); 500 µm (C); 200 µm (D); 20 µm (E)

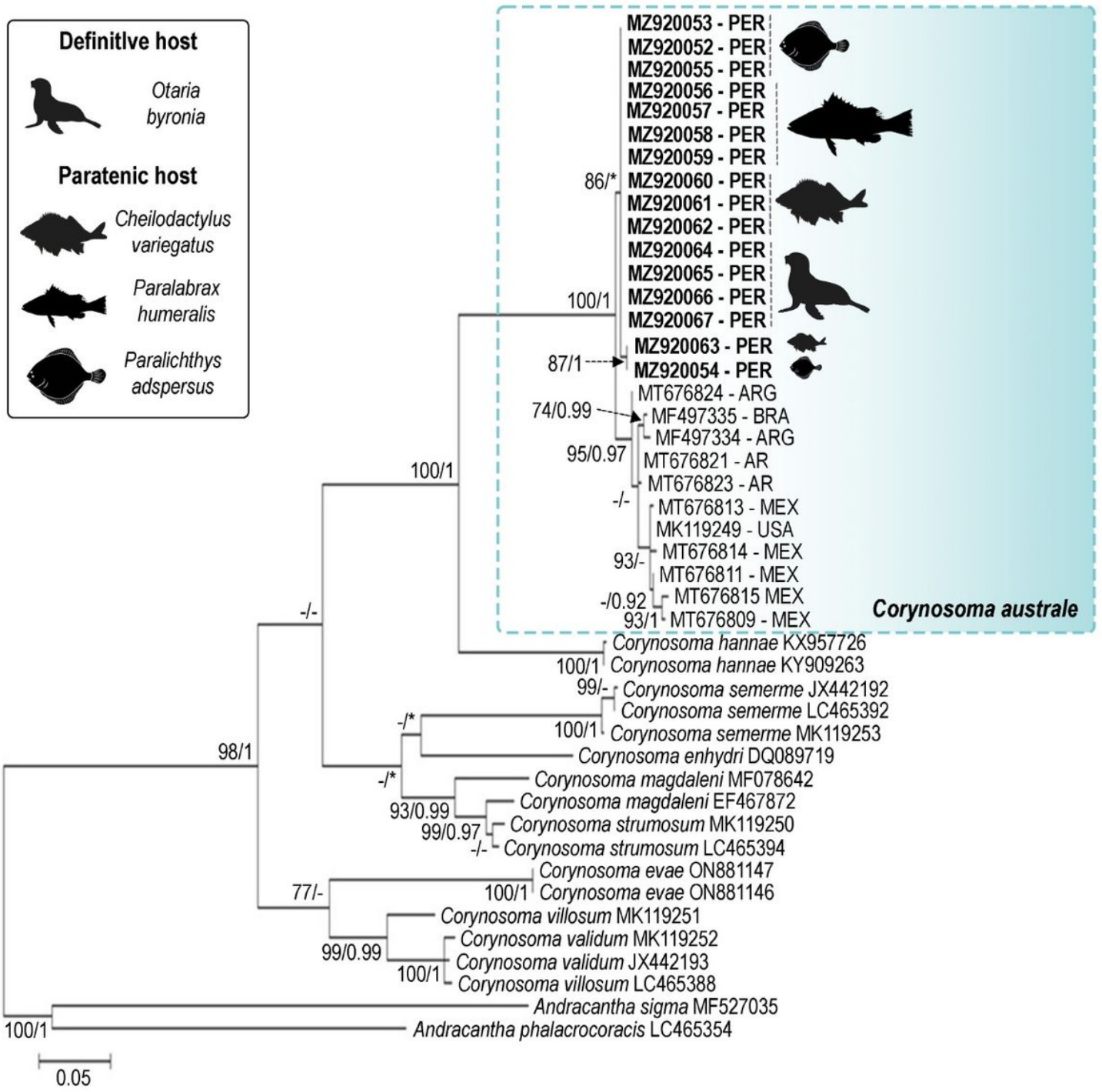

Figure 3

Phylogenetic relationships inferred from maximum likelihood (ML) and Bayesian inference (BI) analyses for the *cox*1 data set. Newly generated sequences are indicated by bold typeface. Nodal support is indicated as ML/BI; values < 0.90 (BI) and < 70 (ML) are indicated by a dash. Asterisks indicate clades that were no presente in tree obtained by BI. The scale-bar indicates the number of substitutions per site. Abbreviations: ARG, Argentina; BRA, Brazil; MEX, Mexico; PER, Peru; USA, United States of America.