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Additional description and molecular characterization of *Naobranchia lizae* (Krøyer, 1863) and *Naobranchia variabilis* Brian, 1924 (Copepoda: Lernaeopodidae) from the Mexican Pacific

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Abstract
Members of the copepod family Lernaeopodidae are parasites of chondrichthyan and actinopterygian fishes, with the genus *Naobranchia* Hesse, 1863 being one of the most diverse groups parasitizing the gills of marine fishes. The genus currently comprises 21 species; however, molecular data for most species remain unavailable or poorly validated. In this study, copepod specimens were collected from the gills of *Mugil cephalus* Linnaeus, 1758 in Teacapán, Sinaloa, and from *Aluterus monoceros* Linnaeus, 1758 in Puerto Ángel, Oaxaca, along the Mexican coast of the eastern tropical Pacific. Based on morphological examination, these specimens were identified as *Naobranchia lizae* (Krøyer, 1863) and *Naobranchia variabilis* Brian, 1924, respectively. Morphological features of both species were documented through detailed drawings and photographs. In addition, a fragment of the mitochondrial cytochrome c oxidase subunit I (*cox*1) and two nuclear ribosomal DNA markers (18S and 28S) were generated for both taxa, representing the first well-documented molecular data for the genus *Naobranchia*. Phylogenetic analysis of *cox*1 placed *N. lizae* and *N. variabilis* in the same clade with an unpublished sequence of *Naobranchia vermiformis* Rangnekar, 1956 (ON023684), forming a well-supported monophyletic group. The genetic distances between species of *Naobranchia* range from 13 to 19%, consistent with interspecific levels reported for other lernaeopodids. Our findings provide evidence supporting the presence of *N. lizae* and *N. variabilis* in the Mexican Pacific, establishing a reliable morphological and molecular reference to support future ecological, biogeographical, and systematic studies of Lernaeopodidae.

Keywords *Cox*1 · Crustacea · Fish · Genetic · Parasite · Phylogeny

Introduction

Lernaeopodidae Milne Edwards (1840) is a diverse family of parasitic copepods commonly found on marine fishes, notable for pronounced sexual dimorphism among its species (Boxshall and Halsey 2004; Boxshall 2005). The bodies of adult females are modified such that they scarcely resemble the typical crustacean form, with a large, fleshy, unsegmented trunks and well-developed maxillae. These maxillae are modified into a pair of cylindrical, unsegmented appendages, with jointed tips that bear a chitinous structure known as the bulla, which enables the parasite to attach permanently to its host. In contrast, adult males are relatively small and use their strong antennae to attach themselves to the female (Boxshall and Halsey 2004).

Lernaeopodidae comprises over 300 species under 48 genera (Walter and Boxshall 2021). The genus *Naobranchia* Hesse

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(1863) currently comprises 21 species. Members of this genus are distinct in lacking a bulla; instead, their maxillae are ribbon-like and form a loop that encircles the gill filaments of the host, securing attachment. Morphology-based identification of species of *Naobranchia* is often difficult because characters of the oral appendages are of limited diagnostic value, and species descriptions for several taxa are vague or incomplete. Consequently, species delimitation has relied mainly on body proportions, trunk shape, and position and arrangement of the egg sacs (Madinabeitia and Nagasawa 2011). However, body proportions may be unreliable due to the contractile nature of the cephalothorax (Hamza et al. 2015).

Naobranchia lizae (Krøyer, 1863) and *Naobranchia variabilis* Brian 1924 are both widely distributed in the Pacific and Atlantic Oceans. Whereas *N. lizae* has been reported mainly from mugilid fishes, *N. variabilis* has been found primarily on tetraodontiforms, although records also include other fish orders (Causey 1960; Kabata 1968; Luque and Farfán 1990; Knoff et al. 1994; Roubal and Graham 1999; Baker et al. 2005; Hamza et al. 2015; Kacem et al. 2015). Both species share the presence of egg sacs distributed along the lateral margins of the trunk but differ in trunk shape, being longer than wide in *N. lizae* and wider than long in *N. variabilis* (Hamza et al. 2015).

Genetic data for the Lernaeopodidae remains scarce (Montes et al. 2017, 2022; Ohtsuka et al. 2020; Hasegawa et al. 2022; Erasmus et al. 2023). To date, almost no DNA sequences have been published for species of *Naobranchia*, despite their ecological significance as gill parasites of marine fishes. In this study, we provide the morphological characterization together with the first DNA sequences for specimens identified as *N. lizae* and *N. variabilis*, based on material collected from the Mexican Pacific. Of these two species, only *N. lizae* had been previously reported in the region, but without morphological details to confirm its identification and without voucher specimens deposited in scientific collections. This contribution provides a taxonomic reference that supports future ecological, biogeographical, and systematic studies of parasitic copepods.

Materials and methods

Lernaeopodid specimens were collected from *Mugil cephalus* Linnaeus (1758) (Mugilidae), captured in Teacapán, Sinaloa (8 August 2024), and from *Aluterus monoceros* Linnaeus (1758) (Monacanthidae), captured in Puerto Ángel, Oaxaca (8 July 2023). Both localities are situated on the Pacific coast of Mexico. In each case, fish were obtained from local fishermen. Gills were excised, examined under a dissecting microscope, and attached copepods were removed with forceps and preserved in 96% ethanol.

Morphological analysis

For morphological analyses, copepods were cleared in 85% lactic acid for a few minutes, dissected, and examined under a Leica DMLB microscope. Line drawings were prepared using a drawing tube. Specimens were identified using the specialized literature available for the genus (e.g., Krøyer 1863; Leigh-Sharpe 1926; Kabata 1968; Knoff et al. 1994; Hamza et al. 2015). For scanning electron microscopy (SEM), six specimens from each host/locality were dehydrated through a graded ethanol series, critical point dried with CO_2, and sputter-coated with a gold–palladium mixture. Observations were made using a Hitachi SUI510 10 kV microscope at the Laboratorio Nacional de la Biodiversidad (LANABIO), Instituto de Biología, Universidad Nacional Autónoma de México (IB-UNAM). Voucher specimens were deposited in the Colección Nacional de Crustaceos (CNCR) of the IB-UNAM, and in the Copepoda collection of the Instituto de Ciencias del Mar y Limnología, Unidad Académica Mazatlán (ICML-EMUCOP).

DNA extraction, sequencing, and phylogenetic analyses

Genomic DNA was extracted from two specimens per host-locality combination using the Bio Basic DNA Extraction Mini Kit, following the manufacturer's instructions. The mitochondrial cytochrome c oxidase subunit I (*cox*1) was amplified using primers LCO1490/HCO2198 (Folmer et al. 1994). The small subunit of the ribosomal DNA (18S rDNA) was amplified with primers 18SE/18SL (Hamby and Zimmer 1988; Hillis and Dixon 1991) and the large subunit of the ribosomal DNA (28S rDNA) with primers 536/391 (García-Varela and Nadler 2005; Smythe and Nadler 2006). Polymerase chain reactions (PCR) were performed in 15 µl total volume, consisting of 9.5 µl DNase-free H_2O, 3 µl 5 × reaction buffer, 0.2 µl of each primer, 0.1 µl MyTaq DNA polymerase (Bioline, catalogue number BIO-21105), and 2 µl DNA template. Thermal cycling conditions for *cox*1 amplification were: initial denaturation at 94 °C for 3 min; 35 cycles of 94 °C for 45 s, 46 °C for 45 s, and 72 °C for 1 min; followed by a final extension at 72 °C for 7 min. For 18S and 28S rDNA the same conditions were applied except for the annealing temperature, which was set to 52 °C. All molecular procedures were carried out at LANABIO. All DNA sequences generated in this study are available in GenBank (Table 1).

A phylogenetic hypothesis for the Lernaeopodidae was reconstructed to estimate the affinities of the genus *Naobranchia*. Given the limited availability of DNA sequences for both nuclear markers in GenBank, the phylogenetic analyses included only *cox*1 data. However, BLAST comparisons

Table 1 Metadata associated to *cox*1sequences used for phylogenetic analysis

Taxon	Host	Locality	GenBank *cox*1 acc. Num	References
Family Caligidae				
Alebion sp.	Unspecified	Australia	KM896948	Unpublished
Caligus fajerae	*Scomberomurus sierra*	Mexican Pacific	MF069191, MF069192	Morales-Serna et al. 2017
Caligus belones	Unspecified	Norway	AY861368	Øines and Heuch 2005
Family Lernaeopodidae				
Achtheres cf. *pimelodi*	Unspecified	NY, USA	OP829988, OP829981, OP830071, OP830339, OP830206, OP830116	Unpublished
Naobranchia lizae	*Mugil cephalus*	Sinaloa, Mexican Pacific	PX408593, PX408594	**This work**
Naobranchia variabilis	*Aluterus monoceros*	Oaxaca, Mexican Pacific	PX408591, PX408592	**This work**
Naobranchia vermiformis	Unspecified	India, Kerala	ON023684	Unpublished
Parabrachiella anisotremi	*Anisotremus scapularis*		KX815887, KX815888, KX815889	Montes et al. 2017
Parabrachiella auriculata	*Cilus gilberti*		KX815906, KX815907, KX815908	Montes et al. 2017
Parabrachiella exilis	*Mugil cephalus*	Chile	KY026072, KY026073	Montes et al. 2017
Parabrachiella fasciata	*Sciaena fasciata*	Antofagasta, Chile	MZ356552	Montes et al. 2022
Parabrachiella hugu	*Takifugu rubripes*	South Korea	KT030285	Unpublished
Parabrachiella merluccii		North Sea	KT208689	Raupach et al. 2015
Parabrachiella mugilis	*Chelon auratus*	Turkey	MZ356557	Montes et al. 2022
Pseudocharopinus bicaudatus	*Squalus acutipinnis*	Canary Islands	MZ848417	Dippenaar et al. 2021
Pseudocharopinus pteromylaei	*Aetomylaeus bovinus*	Canary Islands	MZ695834	Dippenaar et al. 2021
Salmincola carpionis	*Salvelinus curilus*	Russia	OQ843998	Shedko et al. 2023
	Salvelinus malma	Russia	OQ844018	Shedko et al. 2023
Salmincola edwardsii	Unspecified	NY, USA	OP829914	Unpublished
	Oncorhynchus nerka	Russia	OQ355024, OQ355026, OQ355029	Katz et al. 2023
Tracheliastes maculatus	*Abramis brama*	Szczecin, Poland	PQ730002	Piasecki et al. 2025

of nuclear markers were conducted using the server of the National Center for Biotechnology Information (https://blast.ncbi.nlm.nih.gov/Blast) to assess sequence similarity with available lernaeopodid sequences. Mitochondrial *cox*1 DNA sequences were aligned with homologous sequences of Lernaeopodidae available in GenBank (Table 1), mainly corresponding to the dataset previously analyzed by Piasecki et al. (2025). Also included was the only previously available sequence identified as representative of the genus *Naobranchia*, specifically *Naobranchia vermiformis* Rangnekar (1956), although, to the best of our knowledge, the sequence is not linked to a published article or to a voucher specimen deposited in a scientific collection. As outgroup, one species of *Alebion* and two species of *Caligus* were selected, based on previous phylogenetic analyses (Bernot et al. 2021). Pairwise sequence alignment was conducted online with MAFFT (Katoh et al. 2019). The *cox*1 matrix comprised 36 terminals and 625 aligned nucleotides. Phylogenetic inference was performed under parsimony in TNT (Goloboff et al. 2008) and under maximum likelihood (ML) in IQ-TREE (Nguyen et al. 2015). For the parsimony analysis, a heuristic search (traditional search) with 2000 replicates, random addition of terminals, and tree bisection and regrafting (TBR) perturbation algorithm was conducted; gaps were codified as missing data. Jackknife support values were obtained with 1000 pseudoreplicates. For the ML analyses, the best-fit model (K3Pu + F + I + G4) was chosen according to Bayesian Information Criterion, suggested by ModelFinder (Kalyaanamoorthy et al. 2017) as implemented in IQ-Tree3 (Nguyen et al. 2015; Chernomor et al. 2016). Pairwise genetic distances within the newly generated *cox*1 sequences were estimated under the Kimura 2-parameter model (K2P; Kimura 1980) in the software Mesquite (Maddison and Maddison 2023).

Results

Morphological study

Copepod specimens collected from *M. cephalus* in Teacapán, Sinaloa, were identified as *N. lizae* based on the redescription

by Knoff et al. (1994). Specimens obtained from *A. monoceros* in Puerto Ángel, Oaxaca, were identified as *N. variabilis* following Kabata (1968) and Hamza et al. (2015). Morphological features of voucher specimens are described and illustrated to support the newly generated DNA sequence data.

Family: Lernaeopodidae Milne Edwards, 1840.

Genus: *Naobranchia* Hesse, 1863.

Naobranchia lizae (Krøyer, 1863).

Material examined: 10 ovigerous females for measurements of the total body length; four of these dissected for observation of cephalothoracic appendages.

Voucher material: four ovigerous females deposited in CNCR (38,374); 16 ovigerous females deposited in ICML-EMUCOP (080824–01 and 080824–02).

GenBank accession numbers: *cox*1: PX408593 and PX408594; 18S PX867596; 28S PX503689.

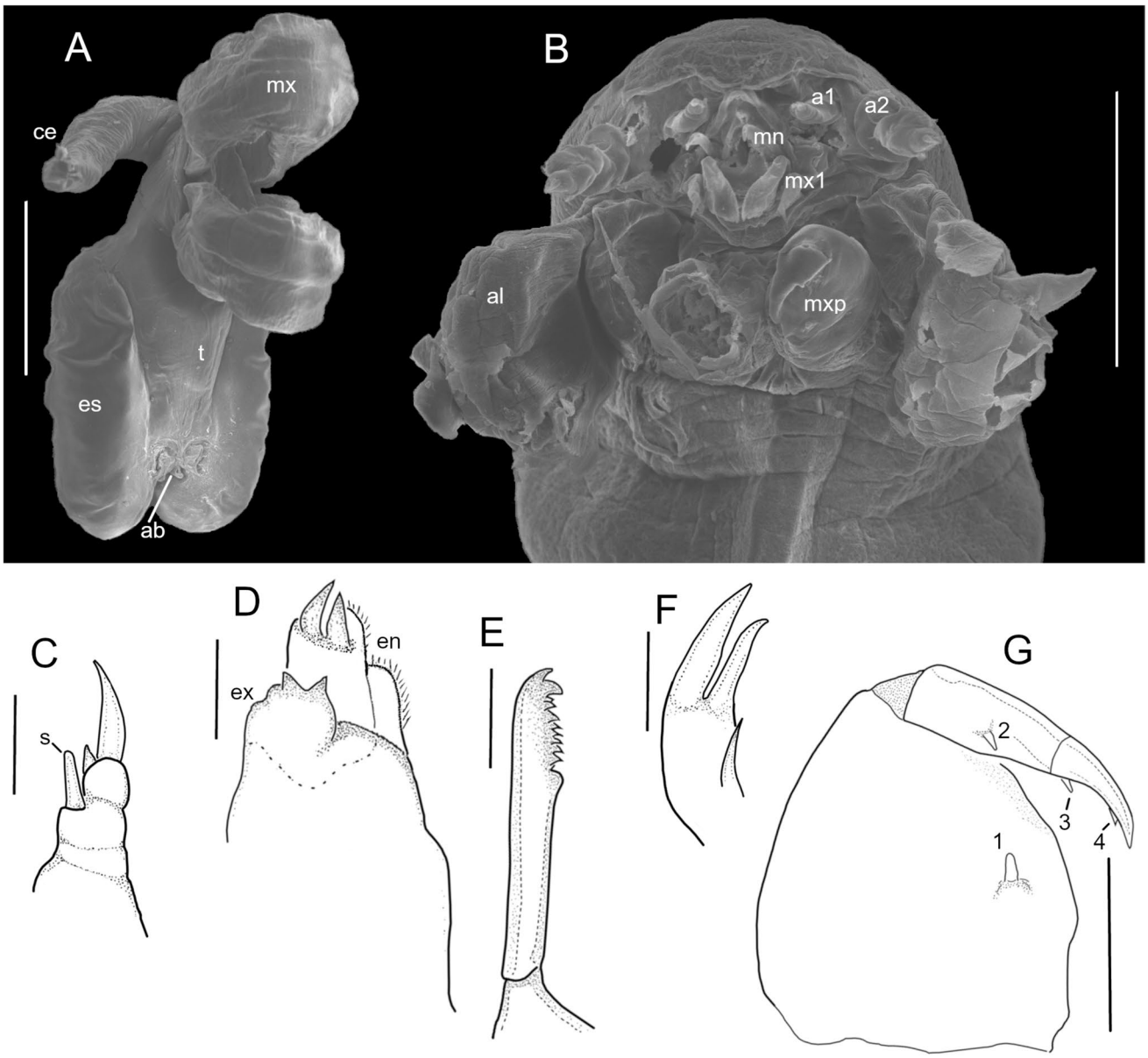

Fig. 1 *Naobranchia lizae*, adult female. **A** Habitus showing cephalothorax (ce), maxilla (mx), trunk (t), egg sac (es), and abdomen (ab); **B** head with antennule (a1), antenna (a2), mandible (mn), maxillule (mx1), maxilliped (mxp), and adhesive lobes (al); **C** antennule showing solus (s); **D** antenna showing exopod (ex) and endopod (en); **E** mandible; **F** maxillule; **G** maxilliped indicating stout spine (1), papilliform seta (2), digitiform seta (3), and accessory tines (4). Scale bars A = 1 mm, B = 100 µm, C–F = 10 µm, G = 25 µm

Adult female morphology. Body (Figs. 1A and 3A) 4.3–5.2 mm long (average, 4.7 mm), measured from tip of cephalothorax to posterior margin of abdomen. Cephalothorax subcylindrical, slightly wider posteriorly. Head small, bearing oral cone and mouthparts; paired adhesive (corrugated) lobes located lateral to maxillipeds and protrude beyond cephalothorax margins (Fig. 1B). Trunk subrectangular, longer than wide. Egg sacs extending along entire lateral margins of trunk, from anterior margin to beyond tip of abdomen (Figs. 1A and 3A). Abdomen poorly defined, at posterior trunk margin between the egg sacs, with median anal slit and minute paired caudal rami.

Antennule (Fig. 1C) lateral to mouth tube (Fig. 1B), 4-segmented; first 2 segments stout, unarmed; third segment bearing a medial digitiform process (solus) reaching tip of fourth segment; fourth segment with long spiniform process and small tubercle-like process. Antenna (Fig. 1D) biramous; endopod indistinctly 2-segmented; first segment longer, distal segment with two spiniform setae; exopod 1-segmented, bearing two short spiniform setae.

Mandible (Fig. 1E) with 10 teeth. Maxillule (Fig. 1F) biramous; exopod consisting of one seta; endopod with two long apical setae. Maxillae (Fig. 1A) at base of cephalothorax, ribbon-like, separate from each other, forming a flattened band encircling host gill filament. Maxilliped (Fig. 1G) corpus robust, 1-segmented, myxa with one stout spine; subchela with papilliform seta at midlength, and distal digitiform seta; claw gently curved, with accessory tines.

Host: *Mugil cephalus* Linnaeus, 1758 (Mugiliformes: Mugilidae).

Locality: off Teacapan, Sinaloa (northwestern Mexican Pacific).

Naobranchia variabilis Brian, 1924

Material examined: 10 ovigerous females for measurements of the total body length; four of these dissected for observation of cephalothoracic appendages.

Voucher material: 12 ovigerous females deposited in CNCR (38375); 29 ovigerous females deposited in ICML-EMUCOP (080723–01 to 080723–04).

GenBank accession numbers: *cox*1: PX408591 and PX408592; 18S PX867595; 28S PX503688.

Adult female morphology. Body (Figs. 2A and 3B) 3.2–4.7 mm long (average, 4.1 mm), measured from tip of cephalothorax to posterior margin of abdomen. Cephalothorax subcylindrical, slightly wider posteriorly. Head small, bearing oral cone and mouthparts; paired adhesive (corrugated) lobes are located lateral to maxillipeds and protrude beyond cephalothorax margins (Fig. 2B). Trunk with rounded corners, subquadrangular, slightly wider than long. Egg sacs extending along entire lateral margins of trunk, from anterior margin to beyond tip of abdomen (Figs. 2A and 3B). Abdomen situated at posterior margin of trunk between the egg sacs, with median anal slit and minute paired caudal rami.

Antennule (Fig. 2C) lateral to mouth tube (Fig. 2B), 4-segmented; first 2 segments stout, unarmed; third segment bearing a medial digitiform process (solus); fourth segment with long spiniform process and small tubercle-like process. Antenna (Fig. 2D) biramous; endopod indistinctly 2-segmented, distal segment with four short spiniform setae; exopod 1-segmented, bearing two small spiniform setae.

Mandible (Fig. 2E) with nine teeth. Maxillule (Fig. 2F) biramous; exopod consisting of one seta; endopod with two long apical setae. Maxillae (Fig. 2A) at base of cephalothorax, ribbon-like, separate from each other, forming a flattened band encircling host gill filament. Maxilliped (Fig. 2G) corpus robust, 1-segmented, myxal area with process opposing tip of claw and papilla on surface of segment; subchela with small spinous process proximally and distal digitiform seta; claw gently curved, with accessory tines.

Host: *Aluterus monoceros* Linnaeus, 1758 (Tetraodontiformes: Monacanthidae).

Locality: off Puerto Ángel, Oaxaca (Southern Mexican Pacific).

Phylogenetic analyses cox1

Parsimony analysis resulted in three optimal trees of 1404 steps, whereas the ML analysis yielded a single optimal tree with log likelihood –6507.876. Monophyly of *Naobranchia* was strongly inferred by both methods (parsimony jackknife = 92; ML bootstrap = 99), although most internal nodes received weak support under both approaches (Fig. 4). Within *Naobranchia*, interspecific genetic distances ranged from 13% (*N. lizae* vs. *N. vermiformis*) to 19% (*N. lizae/N. vermiformis* vs. *N. variabilis*). No intraspecific variation was detected, with the two *cox*1 sequences obtained for each of *N. lizae* and *N. variabilis* being identical.

BLAST similarity analyses of nuclear markers

BLAST analyses of the nuclear markers (18S and 28S) were conducted to assess sequence similarity with the limited reference data currently available in GenBank for Lernaeopodidae. Because sequences of *Naobranchia* are absent from public databases for these markers, the closest matches corresponded to representatives of other lernaeopodid genera. For the 28S gene, *N. variabilis* showed the highest similarity to *Lernaeopoda* sp. from Argentina (MN822001),

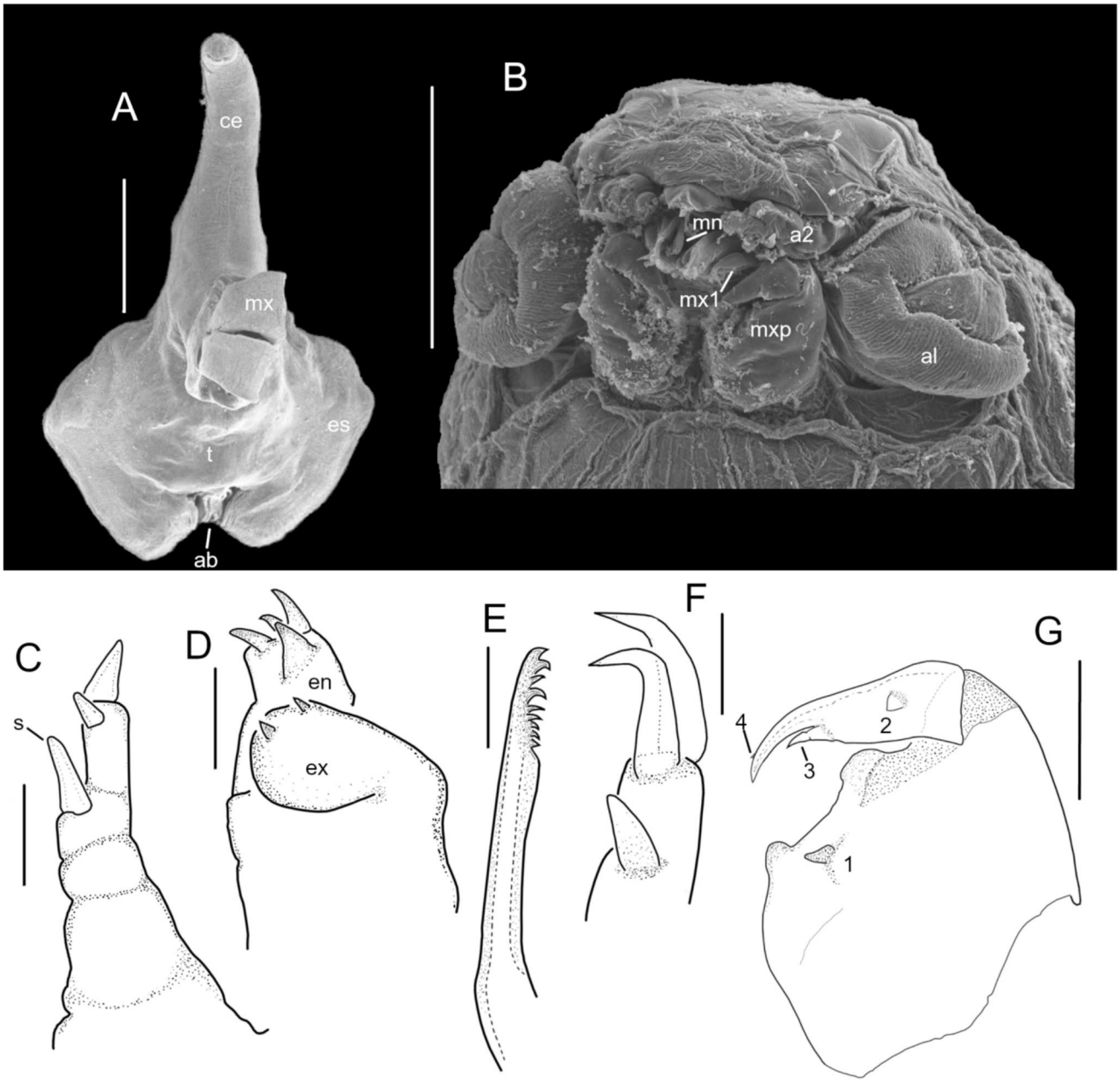

Fig. 2 *Naobranchia variabilis*, adult female. **A** Habitus showing cephalothorax (ce), maxilla (mx), trunk (t), egg sac (es), and abdomen (ab); **B** head with antenna (a2), mandible (mn), maxillule (mx1), maxilliped (mxp), and adhesive lobes (al); **C** antennule showing solus (s); **D** antenna showing exopod (ex) and endopod (en); **E** mandible; **F** maxillule; **G** maxilliped indicating papilla (1), spinous process (2), digitiform seta (3), and accessory tines (4). Scale bars A = 1 mm, B = 100 µm, C–F = 10 µm, G = 25 µm

whereas *N. lizae* matched an unidentified lernaeopodid from Chile (KX815911), with sequence similarities of 94% and 92%, respectively. For the 18S gene, the highest similarities were observed with *Tripaphylus elongatus* from South Africa (96%; FJ447460) and *Sphyrion lumpi* from Iceland (91%; MN986930).

Discussion

The identification of *N. lizae* and *N. variabilis* in this study was based on comparisons with the original descriptions and with subsequent detailed morphological accounts provided by Knoff et al. (1994) and Hamza et al. (2015), respectively.

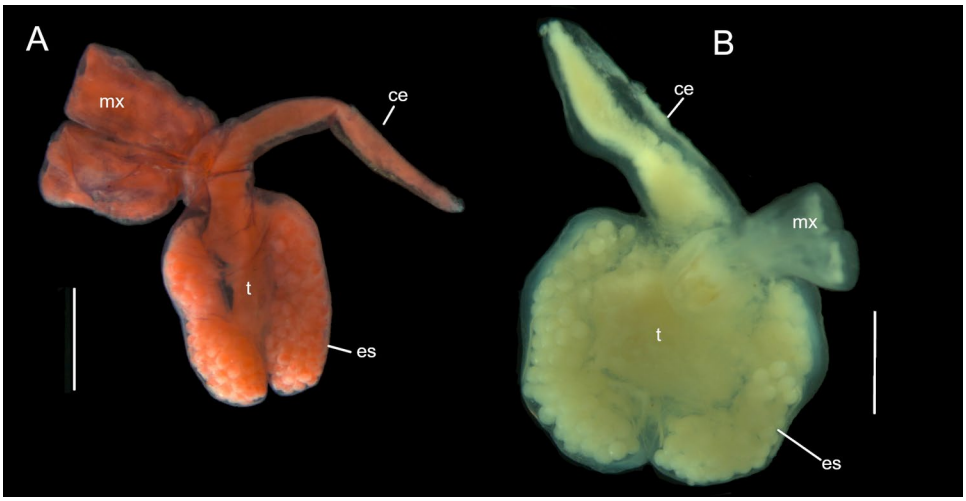

Fig. 3 Photographs of complete body of *Naobranchia lizae* (**A**) and *Naobranchia variabilis* (**B**) showing cephalothorax (ce), maxilla (mx), trunk (t), and egg sac (es). Scale bars 1 mm

Our specimens closely matched these redescriptions, and no morphological differences were noted. *Naobranchia lizae* was redescribed by Knoff et al. (1994) from *Mugil liza* Valenciennes in Cuvier & Valenciennes (1836) (as *Mugil platanus*) collected off Rio de Janeiro, Brazil (southwestern Atlantic). That work provided a comprehensive account of the species, addressing limitations of the original description by Krøyer (1863), which lacked morphological detail and was based on specimens found attached to *M. liza* from New Orleans, USA (northwestern Atlantic). Wilson (1915) also confirmed *N. lizae* on *M. cephalus* in the northwestern Atlantic, and Causey (1960) reported the species on *M. cephalus* from Mazatlán, a locality in the northwestern Mexican Pacific close to our sampling site. *Mugil liza* inhabits most of the western Atlantic, from Florida to Argentina, whereas *M. cephalus* sensu lato is a globally distributed complex of cryptic species (Viet Tran et al. 2017; Froese and Pauly 2025). The occurrence of *N. lizae* in Brazil and the Mexican Pacific is consistent with the broad distribution of its hosts.

Naobranchia variabilis was originally described from *Lagocephalus laevigatus* (Linnaeus 1766) (Tetraodontidae) off the coast of Mauritania (Brian 1924). Subsequent detailed morphological accounts were provided by Kabata (1968), based on specimens from *Marilyna pleurosticta* (Gunther 1872) (Tetraodontidae) from Queensland, Australia, and later by Hamza et al. (2015) from *Balistes capriscus* Gmelin (1789) (Balistidae) collected off the Algerian coast (Mediterranean). Reports of *N. variabilis* have thus been associated with tetraodontiform hosts across widely separated regions of the Atlantic and Indo-Pacific. Our specimens from *A. monoceros* in the eastern Pacific are morphologically consistent with these previous descriptions. The molecular data generated in this study represent the first sequences attributed to this taxon and provide a baseline for future comparisons. However, given the considerable geographic distance from the type locality and previous suggestions that *N. variabilis* may represent a complex of closely related species (Hamza et al. 2015), our identification should be regarded as the best available under the current taxonomic framework. Additional molecular data from specimens collected across the reported range of the species, particularly from the type region, will be necessary to determine whether the eastern Pacific population corresponds to *N. variabilis* sensu stricto or represents a distinct, closely related lineage.

A readily visible morphological feature shared by *N. lizae* and *N. variabilis* is the position of the egg sacs, which extend along the entire lateral margins of the trunk. This condition is also found in six congeners, *Naobranchia wilsoni* Nigrelli (1933), *Naobranchia spinosa* Pearse (1952), *Naobranchia vermiformis*, *Naobranchia polynemi* Tripathi (1962), *Naobranchia pritchardae* Kensley & Grindley (1973), and *Naobranchia kabatana* Dippenaar & Jordaan 2008 (Dippenaar and Jordaan 2008; Hamza et al. 2015). In contrast, the remaining species of *Naobranchia* bear egg sacs only posteriorly or posterolaterally, making lateral egg sac extension a useful character for recognizing a subset of species within the genus.

The level of genetic divergence estimated among the species of *Naobranchia* in our dataset (13 to 19% %) falls within the range reported for other lernaeopodids. Montes et al. (2017) reported *cox*1 divergences ranging from 9 to 16% among species of *Parabrachiella*, including a 9% distance between two morphologically similar species infecting the same host. Erasmus et al. (2023) found interspecific divergences exceeding 20% among lernaeopodid species. In contrast, Hasegawa et al. (2022) documented intraspecific variation between 0% and 0.67%. These comparisons suggest that *cox*1 might be a reliable marker for the identification of species of *Naobranchia*, although further sampling is required to assess genetic variability across the genus.

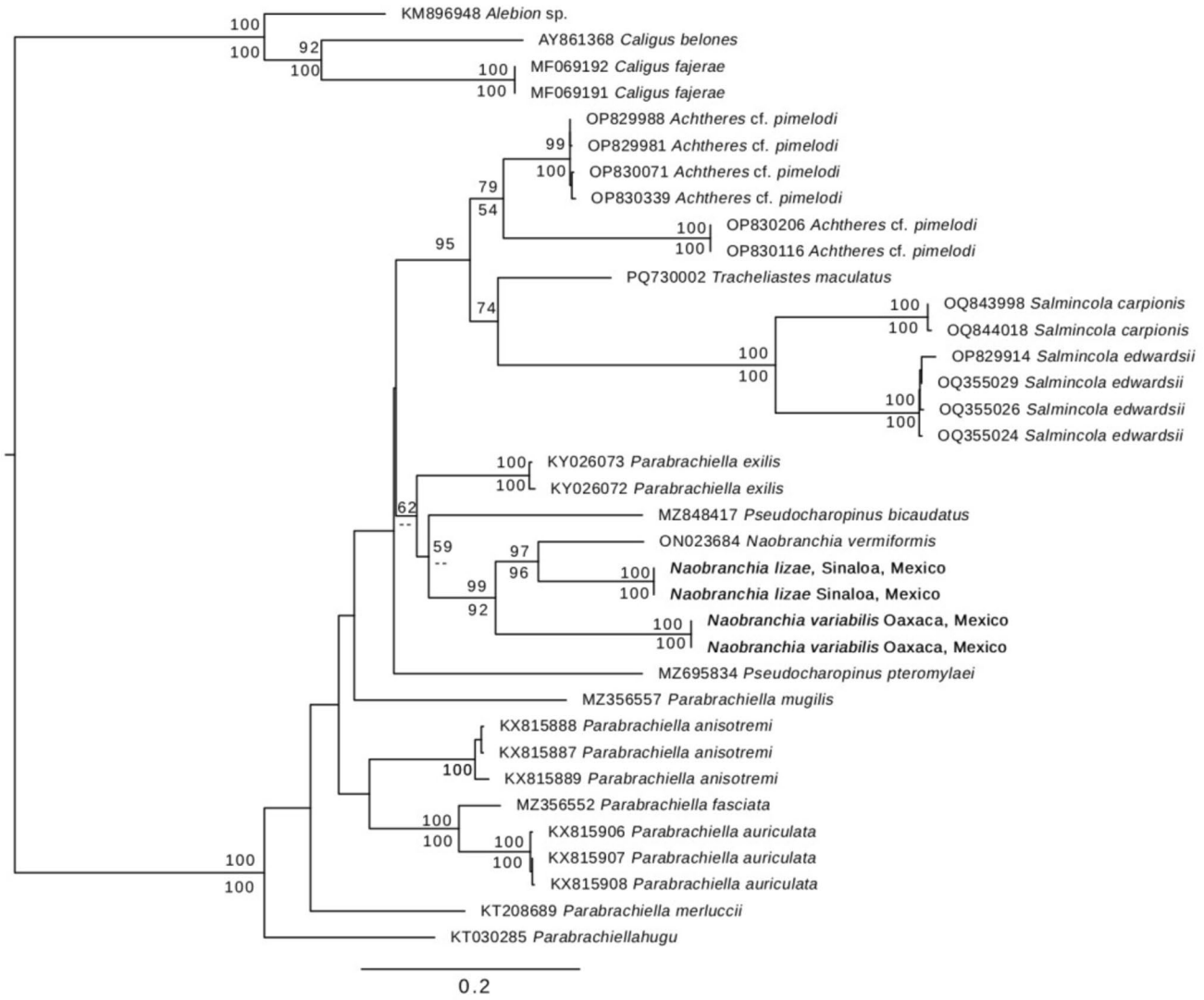

Fig. 4 Phylogenetic tree resulting from the Maximum Likelihood analysis of species of Lernaeopodidae based on *cox*1 sequences. Numbers above nodes indicate Maximum Likelihood bootstrap values and number under the nodes indicate parsimony Jackknife values. In bold, samples of *Naobranchia lizae* and *Naobranchia variabilis* from Mexican Pacific

Considering the broad geographic ranges attributed to *N. lizae* and *N. variabilis*, future population-level genetic studies will be essential to determine whether these taxa represent single widely distributed species or complexes of closely related forms.

Conclusion

This study provides morphological documentation and DNA sequences of *Naobranchia lizae* and *N. variabilis* from the central eastern tropical Pacific, Mexico. These sequences represent the first well-documented molecular data for the genus *Naobranchia*. Our findings confirm the occurrence of *N. lizae* in the region and document specimens attributable to *N. variabilis* from the eastern Pacific, expanding the available records for the group. By combining morphological and molecular evidence, this work offers a reliable reference for future ecological, biogeographical, and evolutionary studies of Lernaeopodidae, which is particularly valuable given the limited molecular information currently available for the family.

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Declarations

Conflict of interest The authors declare no competing interests.

Ethical approval No animal testing was performed during this study.

Sampling and field studies No special permits were required for the acquisition of fish from artisanal fisheries. This study complies with the Convention on Biological Diversity (CBD) and the Nagoya Protocol.

Data availability All data supporting the findings of this study are included in the article. DNA sequences generated in this study have been deposited in GenBank.

Author contribution GTC performed sampling, investigation, data analysis, and drafted the manuscript. FRE contributed to sampling and resources. AOF proposed the study, provided resources, assisted with data analysis, and revised the manuscript. SG prepared drawings and assisted with revision. FNMS conceptualized the study, conducted sampling and investigation, prepared drawings, and wrote the original manuscript.

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