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Exploring South Africa's hidden marine parasite diversity: two new marine *Ergasilus* species (Copepoda: Cyclopoida: Ergasilidae) from the Evileye blaasop, *Amblyrhynchote honckenii* (Bloch).

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Abstract

Marine parasites remain understudied in South Africa with little information available on their diversity and the effects these parasites may have on their hosts. This is especially true for parasitic copepods within the family Ergasilidae. Among the four genera known in Africa, *Ergasilus* Nordmann, 1832 is the most speciose with 19 reported species. However, this represents only 12% (19/163) of the global diversity. Furthermore, only five known African species are reported from marine environments, and only one is reported from the South African coastline. Given the rich biodiversity along this coastline, a high marine parasite diversity could be expected from these shores. As a case study, the Evileye blaasop, *Amblyrhynchote honckenii* (Bloch), a marine and brackish fish species, was screened for parasites along the South African coastline. This resulted in the discovery of two species of *Ergasilus* new to science (*Ergasilus arenalbus* n. sp. and *Ergasilus chintensis* n. sp.), which makes them the second and third ergasilid species reported for tetraodontid pufferfishes worldwide. Although genetically distinct, the two newly described species clustered in the same subclade within the Ergasilidae based on 18S rDNA, 28S rDNA, and COI mtDNA phylogenies. The newly described species differ morphologically from each other, and their respective congeners based on the size and armature of the antenna; body segmentation; and general ornamentation throughout the entire body. The addition of these two new species from a single host species indicates that South Africa's marine fishes contain most probably a hidden parasitic copepod diversity that is worth exploring.

Keywords: Crustacea, Molecular, Marine Fish Parasite, Phylogenetics, Tetraodontid pufferfishes; 28S rDNA; COI mtDNA

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Introduction

Exploring diversity within marine ecosystems has become increasingly important in recent years, revealing a previously unnoticed level of species richness and genetic variation. This is particularly true for parasitic copepods within the family Ergasilidae Burmeister, 1835 (Boxshall and Defaye, 2008). Among the various genera in this family, *Ergasilus* Nordmann, 1832, stands out as one of the most speciose and widely distributed (Oldewage and van As, 1988; Oldewage and Avenant-Oldewage, 1993; Fikiye *et al*., 2023; Míč *et al*., 2023). However, the extent of this diversity remains largely unexplored in Africa (Killian and Avenant-Oldewage, 2013; Fikiye *et al*., 2023; Míč *et al*., 2023), with merely 19 reported species, 12 % (19/163), of the global diversity (Fikiye *et al*., 2023; WoRMS, 2024).

The lack of comprehensive studies in Africa limits our understanding of *Ergasilus* diversity, where unique environmental conditions and host communities may foster an even higher diversity of distinct *Ergasilus* species. While some investigations have provided insights into *Ergasilus* species in African freshwater systems (Oldewage and van As, 1988; Fikiye *et al*., 2023), marine or brackish environments in this region remain largely unexplored, hosting only five known species and a single species from the South African coastline (Fikiye *et al*., 2023; WoRMS, 2024). Additionally, the limited knowledge regarding their diversity and the lack of genetic data, compared to those of other well-studied organisms, hinder comprehensive genomic analyses, creating further challenges in gaining deeper insights into their phylogeny and biology (Fikiye *et al*., 2023; Míč *et al*., 2023).

The discovery of new *Ergasilus* species, especially in unexplored regions would aid in filling these crucial gaps and understanding these parasites' biogeography and evolution (Boxshall and Halsey, 2004; Song *et al*., 2008; Míč *et al*., 2023). Furthermore, marine regions across the

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Atlantic and Indian oceans represent hotspots for parasitic diversity due to their wide range of marine habitats (Everett *et al*., 2015; Miller *et al*., 2018). Hence, given the rich diversity of *Ergasilus* species described from the southern Atlantic and Indian Ocean regions (see Table 1), South Africa could provide an ideal setting to study marine *Ergasilus* species and their host associations, possibly yielding a hidden marine parasite diversity within these shores. Understanding the distribution and diversity of *Ergasilus* species across South Africa can provide valuable insights into evolutionary patterns, connectivity between populations, and the impact of environmental factors on parasite distribution (Boxshall and Halsey, 2004). Additionally, such comparisons can aid in identifying potential host-switching events and the emergence of novel host-parasite associations (Boxshall and Halsey, 2004; Fikiye *et al*., 2023; Míč *et al*., 2023).

This study aimed to start filling this gap by investigating the presence, diversity, and molecular characteristics of *Ergasilus* copepods associated with the Evileye blaasop, *Amblyrhynchote honckenii* (Bloch), along the South African coastline. Combining morphological examination and molecular analyses based on partial ribosomal RNA gene regions (18S and 28S), and one mitochondrial DNA gene region (COI), two new marine *Ergasilus* species were found and described. Revealing and documenting these new species enhances our understanding of the marine parasite diversity within this region, revealing new host-parasite interactions and evolutionary links.

Materials and methods

Sampling

As part of a larger study on the biodiversity of marine fish parasites in southern Africa, 25 *Amblyrhynchote honckenii* specimens were collected from two coastal localities. Using rod and

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reel, 15 specimens of *A. honckenii* (13 males and two females) were collected from the Breede River Estuary, Witsand (-34.397323; 20.837474) in November 2021 and 10 specimens (one male, eight females, and one juvenile) from the intertidal rocky shore at Chintsa East (-32.836538; 28.116997) in July 2022 (Fig. 1). Following capture, the fish were transported in aerated water containers to a nearby field station for dissection. The specimens were then identified, photographed, weighed, measured, and humanely killed using percussive stunning followed by pithing (Ethics committee approved standard operation procedure NWU-00267-17-A5). Ethical approval for this project was received from the AnimCare Ethics Committee of the North-West University with ethics number NWU-00565-19-A5. Permits for collecting *A. honckenii* were issued by Cape Nature, Western Cape Province and the South African Department of Agriculture, Forestry and Fisheries (permit no. CN44-87-18289 and RES2022-44, respectively).

Fish were identified using Smith Sea Fishes (Smith and Heemstra, 2012), with fish nomenclature following FishBase (Froese and Pauly, 2024) and Eschmeyer's Catalog of Fishes (Fricke *et al*., 2024). Host authorities are not included in the text or references.

Morphological analyses

Fish gills were removed and screened for parasites using a Zeiss Stemi 305 compact stereomicroscope (Zeiss, Oberkochen, Germany). Copepod specimens were removed from the gills and preserved in 80% ethanol for morphology and 96% for molecular analysis. Twelve selected specimens underwent morphological observations after being cleared in lactic acid, dissected, and temporarily mounted onto slides with glycerine. Photomicrographs of various body structures were captured using a Nikon Y-TV55 video camera mounted on a Nikon ECLIPSE Ni microscope (Nikon, Tokyo, Japan). Image analysis software, Image-Pro Express (Nikon, Japan),

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facilitated obtaining all necessary measurements for descriptive analyses. All measurements and terminology for describing body somites and cephalic appendages follow Boxshall and Montu's (1997) guidelines. Measurements are provided in text descriptions and tabular form, with text descriptions including average measurements followed by the range and number of specimens in parentheses. Table 2 presents metrical data as the mean, followed by the standard deviation, and the number of specimens examined. Measurements are in micrometres unless otherwise specified. Pencil drawings of specimens and dissected appendages were created using a drawing tube attached to a Nikon ECLIPSE Ni microscope (Nikon, Tokyo, Japan). Final digital illustrations were made with Adobe Photoshop version 23.0.1 software using a Wacom Intuos Pro tablet (Wacom, Saitama, Japan).

Furthermore, six adult specimens collected from the Breede River Estuary, Witsand, were used for scanning electron microscopy (SEM). SEM could not be performed on specimens from Chintsa East due to the limited availability of specimens. Each specimen selected for SEM observation was cleaned by lightly brushing the surface. Cleaned specimens were dehydrated, placed in hexamethyldisilisane (HMDS), mounted onto carbon tape, placed on aluminium stubs, and sputter-coated with carbon (Emscope TB500, Quorum Technologies, Puslinch, Ontario, USA), followed by 20 to 30 nm gold/palladium (Eiko IB2 ion coater, Eiko, Japan). Specimens were examined with a FEI Nova NanoSEM 450 scanning electron microscope (FEI, Hillsboro, Oregon, USA). Images were taken of various characteristic body structures to aid in the morphological description and for comparisons among species.

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Molecular analyses

Genomic DNA extraction was conducted using egg strings from two copepod specimens from the Breede River Estuary, Witsand, and one copepod specimen from Chintsa East. Extraction followed the Macherey-Nagel NucleoSpin® Tissue extraction kit protocol (GmbH and Co. KG, Sandton, South Africa), with an adapted four-hour pre-lysis period and adding 50% more buffer BE. Partial gene amplification targeted three gene regions: two ribosomal RNA gene regions (18S and 28S) and one mitochondrial DNA gene region (Cytochrome c oxidase I or COI), using primers (18SF, 18SR; 28SF, 28SR) prepared by Song *et al.* (2008) for 18S and 28S, and universal mitochondrial primers (LCO1490 and HCO2198) (Folmer *et al*., 1994) for COI (Table 3). Amplification reactions were conducted in 25 µL volumes, made up of 12.5 µL of DreamTaq PCR Master Mix (Thermo Fischer Scientific, Waltham, MA, USA), 1.25 µL of 10 µM of each primer, 3 µL of DNA product, and 7 µL of double distilled water. Thermocycling conditions followed adapted protocols established by Folmer *et al*. (1994) and Song *et al*. (2008). The PCR thermocycling profile followed adapted conditions: 94 °C for 5 min, followed by 40 amplification cycles of 95 °C for 30 s, 47 °C for 30 s and 72 °C for 1 min with a final extension at 72 °C for 7 min. Positive PCR products were verified via 1% agarose gel electrophoresis and then sent for purification and sequencing in both forward and reverse directions to Inqaba Biotechnical Industries (Pty) Ltd. (Pretoria, South Africa).

Sequences were assembled, aligned, edited, and trimmed using Geneious Prime version 2023.1.2 (Biomatters, Auckland, New Zealand). Additionally, the nucleotide Basic Local Alignment Search Tool (BLAST) was used to select *Paracyclopina nana* Smirnov, 1935 (Cyclopettidae Martínez Arbizu, 2000), as the outgroup of the study (Table 4). Considering the limited availability of COI sequences, unpublished sequences of *Ergasilus* species, sourced from

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the Barcode of Life Database (BOLD), were also included in the COI alignment (Table 4). Alignments for the novel sequences were generated and trimmed using default parameters of MAFFT version 7.4.9 (Katoh *et al*., 2002; Katoh and Standley, 2013). Genetic divergences among aligned specimens were calculated within Geneious Prime version 2023.1.2, presenting percentage similarities and differences in base numbers.

The optimal nucleotide substitution model for each dataset was estimated using the Akaike Information Criterion (AIC) in jModelTest 2.1.4 (Posada, 2008; Darriba *et al*., 2012). The general time-reversible model with invariant sites and gamma-distributed rate variation (GTR+I+G) was recommended for all datasets (18S, 28S, and COI). Phylogenetic analyses were performed using Maximum Likelihood (ML) and Bayesian Inference (BI) methods with this suggested model. BI analyses were conducted on the CIPRES Science Gateway version 3.3 (Miller *et al*., 2010) using MrBayes version 3.2.7a (Ronquist *et al*., 2012), with two independent Markov Chain Monte Carlo (MCMC) runs of four chains for 10 million generations, sampling every 1000 generations, and a burn-in of the first 25,000 generations. ML analyses were performed using PhyML version 3.0 (Guindon *et al*., 2010) on the ATGC bioinformatics platform, with model parameters estimated and 1000 bootstrap repetitions for nodal support. The resulting phylogenetic trees from BI and ML analyses were visualised using TreeViewer version 2.2.0 (Bianchini and Sánchez-Baracaldo, 2024).

Results

Two distinct gill-associated parasitic species, morphologically and molecularly differentiated, were obtained from subsets of 10–15 *A. honckenii* specimens, ranging from 95 to 185 mm in length and weighing 30 to 140 g. Both morphotypes were classified as *Ergasilus* (Ergasilidae) based on

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specific characteristics, such as body typically cyclopiform with clear segmentation, biramous legs IV with 2-segmented exopods and 3-segmented endopods, 6-segmented antennules, antennas featuring a single claw, and the absence of maxillipeds in females, following descriptions by Boxshall and Montu (1997) and Boxshall and Halsey (2004). Notably, only one morphotype was found and described from each location, highlighting the uniqueness of both morphotypes in their respective collection sites.

Taxonomy

Ergasilus arenalbus* n. sp.*: Fig. 2–5

ZooBank LSID: urn:lsid:zoobank.org:act:4B5580B2-C5BA-4B8E-99C3-14E9BBF32D3D

Type host: *Amblyrhynchote honckenii* (Bloch) (Tetraodontiformes: Tetraodontidae).

Type locality: Breede River Estuary, Witsand (-34.397323; 20.837474), Western Cape Province, South Africa.

Site on host: Gill filaments.

Prevalence of infection: 67% (10 of 15 pufferfish).

Type material: 151 *Ergasilus* specimens (adult females) were collected. Only adult females were examined: Six were used for SEM; two for dissection; 12 for morphology; and two egg strings were used for DNA extraction. The hologenophores (NMB P 1044–NMB P 1045), holotype (NMB P 1042) and 11 paratypes (NMB P 1043) were deposited in the parasitological collections of the National Museum, Bloemfontein, South Africa; the remaining specimens are in the possession of the Water Research Group, North-West University, Potchefstroom, South Africa.

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Representative DNA sequences: GenBank accession numbers and numbers of bases (bp) are given as follows: 18S: 1,333 and 1,344 bp long sequences of two specimens, accession numbers: PQ451954 and PQ451956; 28S: 668 and 664 bp long sequences of two specimens, accession numbers: PQ451957 and PQ451958; and COI: 701 bp long sequence of one specimen, accession number: PQ439339.

Etymology: The species name "*arenalbus*" is derived from "arena alba" meaning white sand (English) or wit sand (Afrikaans) in Latin. This refers to "Witsand" the name of the type locality of this species.

Description

Adult female description (based on 12 specimens). Body length (measured from the anterior margin of cephalosome to posterior margin of caudal rami) 1182 (959–1,370; n = 12). Body comprises prosome, urosome, and caudal rami. Prosome 5-segmented, composed of cephalosome and four free pedigerous somites. Cephalothorax composed of cephalosome and first pedigerous somite; cephalosome separated dorsally from previous somite by flexible cuticle (Figs. 2A; 5A). Cephalosome slightly shorter than wide, 336 (272–414; n = 12) long by 387 (316–460; n = 12) wide, oval to trapezoidal, with antennules and antenna visible in dorsal view. Cephalic ornamentation comprising of anterior circular eyespot and inverted T-shaped mark of thickened chitin situated medially on dorsal side (Figs. 2A, B). Paired sensory pores and papillae observed anterior to eyespot with numerous sensory papillae and pores scattered over dorsal surface of cephalosome. Rostrum well-developed, with truncated posterior margin. All pedigerous somites wider than long and progressively smaller. Paired sensory papillae observed mid-dorsally on segments two to five. First pedigerous somite 176 (129–218; n = 12) long by 358 (297-428; n=12)

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wide; second pedigerous somite 107 (82–154; n = 12) long by 274 (241–334; n = 12) wide; third pedigerous somite 105 (78–138; n = 12) long by 212 (163–268; n = 12) wide; fourth pedigerous somite 61 (44–82; n = 12) long by 140 (127–169; n = 12) wide.

Urosome comprising reduced fifth pedigerous somite, genital double somite, and three free abdominal somites (Fig. 3A). Reduced fifth pedigerous somite 31 (20–39; n = 12) long by 80 (72–114; n = 12) wide. Genital double-somite longer than wide, 135 (120–152; n = 12) long by 109 (100–130; n = 12) wide (Figs. 3A; 5C), bearing a pair of multiseriate egg sacs dorsally (Figs. 2A; 4A), measuring 1269 (989–1662; n = 12) long by 256 (222–340; n = 12) wide (Figs. 2A; 4A; 5C). Abdomen three-segmented; first abdominal somite widest, 43 (36–56; n = 12) long by 73 (64–92; n = 12) wide; second abdominal somite shorter, 31 (23–40; n = 12) long by 63 (55–67; n = 12) wide; third somite (= anal somite) incised dorsoventrally (= anal opening or anus) forming attachment for caudal rami, 28 (22–32; n = 12) long by 63 (59–68; n = 12) wide, ornamented with pair of pores on dorsal side; each pore located laterally to anal opening and carrying bristle (Figs. 3A; 4E; 5C). All abdominal somites with posterior row of ventral spinules (Figs. 4E; 5C).

Caudal rami slightly elongated, 30 (26–33; n = 12) long by 24 (22–28; n = 12) wide, with four setae (Fig. 3A). Innermost seta (IV) longest 282 (226–308; n = 12), followed by shortest seta (III) 28 (20–39; n = 12), and two longer setae (II and I) 77 (60–87; n = 12), and 92 (83–99; n = 12), respectively (Fig. 3A).

Antennule 6-segmented, armed with long and short setae (Fig. 2E). Setal formula from proximal to distal segments given as 3–12–6–2–3–8 (total 34). Antenna 4-segmented (Figs. 2D; 4B) comprising coxobasis, 174 (110–196; n = 12) long by 95 (73–114; n = 12) wide; and three-segmented endopod; armed with curved terminal claw (Figs. 2D; 4B). First endopod segment longest 339 (288–366; n = 12), followed by second endopod segment 196 (152–215; n = 12), and

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small third endopod segment 28 (24–40; n = 12). Prominent spine observed on anterior second endopod segment (Figs. 2D; 4B; 5D). Terminal claw pointed and smooth 161 (127–186; n = 12), with fossa on concave margin.

Mouth positioned ventrally on cephalosome. Labrum with internal teeth; teeth arranged in an arch. Mandible armed with three blades (anterior, medial, and posterior blades); anterior blade thinner and shorter than others, ornamented along anterior margin; medial and posterior blades, both with teeth on opposite margin. Maxillule armed with two unequal setae; innermost seta shortest; ornamented with 1 pore and multiple spinules; pore lacking bristle (Fig. 2C). Maxilla 2-segmented, comprising syncoxa (= first segment) and basis (= second segment); syncoxa broad, with two distal pores; basis ornamented with multiple spinules on posterior margin. Labium broad, unornamented; mid-region produced posteriorly, with truncated posterior margin.

Swimming legs I to IV; each comprising coxa, basis, and 2 segmented rami (i.e. exopod, endopod). Rami of all legs 3-segmented, except 2-segmented exopod of leg IV. Segments distinct, typical with similar basic morphology as in other species of *Ergasilus*. Armature on rami as Roman and Arabic numerals indicating spines and plumose setae, respectively, in Table 5.

Leg I (Fig. 3C). Coxa ornamented with spinules on outer margin. Basis armed with bare outer seta, ornamented with spinules on both sides; posterior margin protrudes posteriorly forming one spinous process; spines located between rami (Figs. 3C; 4C). Exopod 3-segmented; first endopodal segment with distal spine, ornamented with patch of spinules on outer margin; spinules located just above distal spine; and bristles along outer margin; second exopodal segment with 1 plumose seta, unornamented; third exopodal segment armed with 2 serrated spines (inner and outer spine); inner spine about 2.0 times longer than outer spine; and 5 plumose setae. Endopod 3-segmented; all segments with spinules along inner margin; first and second endopodal segment,

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each with 1 plumose seta on inner margin; third endopodal segment armed with 2 serrated spines (inner and outer spine); inner spine about 2.0 times longer than outer spine; and 4 plumose setae.

Leg II (Fig. 3D). Coxa ornamented with spinules on outer margin. Basis armed with bare outer seta, ornamented with spinules on both sides. Exopod 3-segmented; first exopodal segment with distal spine, ornamented with patch of spinules on outer margin; spinules located just above distal spine; and bristles along inner margin; second exopodal segment armed with 1 plumose seta; third exopodal segment with simple spine (or non-serrated) and 5 plumose setae. Endopod 3-segmented; first and second endopodal segments with 1 and 2 plumose setae, respectively; third endopodal segment with serrated spine and 5 plumose setae. Leg III with the same armament and ornamentation described for Leg II.

Leg IV (Fig. 3E). Coxa ornamented with spinules on both sides. Basis armed with bare outer seta, with spinules scattered across surface. Exopod 2-segmented; first exopodal segment armed with distal spine, ornamented with spinules and bristles on outer and inner margin, respectively; second exopodal segment with 1 spine and 5 plumose setae. Endopod 3-segmented, all segments lacking ornaments on both margins; first and second endopodal segment with 1 and 2 plumose setae, respectively; third endopodal segment with 1 serrated spine and 3 plumose setae.

Leg V (Fig. 3F) with single ramus. Ramus 2-segmented; proximal segment rectangular, without any armaments or ornaments; distal segment about 3.0 times longer than previous segment, with spinules scattered across surface, armed with 2 bare setae.

Intercoxal sclerites and interpodal plates of all legs, present (Figs. 2A; 3B; 4D). Intercoxal sclerites unornamented, with both ends directed posteriorly. Interpodal plates present; first to third plate with spinules; fourth plate absent (Figs. 2A; 3B).

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Remarks

The detailed morphological description of *E. arenalbus* n. sp. sheds light on its distinctiveness among the recognised species of *Ergasilus* worldwide. With 163 valid species known, comparisons were only made with other marine *Ergasilus* species from the southern Atlantic and Indian Ocean regions. Among the 17 marine species from these regions (Table 1), *E. arenalbus* n. sp. stands out in several key morphological aspects, notably in size; armature of the antenna; the segmentation in the body (free *vs* fused prosome somites); and general ornamentation throughout the entire body. Firstly, its larger body size, with a length averaging 1182 µm, sets it apart from species such as *E. atafonensis* Amado & Rocha, 1996, *E. bahiensis* Amado & Rocha, 1996, *E. caraguatatubensis* Amado & Rocha, 1996, *E. ilani* Oldewage & van As, 1988, *E. myctarothes* Wilson, 1913, *E. parvitergum* Ho, Jayarajan & Radhakrishnan, 1992, *E. rostralis* Ho, Jayarajan & Radhakrishnan, 1992, and *E. uniseriatus* Ho, Jayarajan & Radhakrishnan, 1992 which typically have a smaller total length, below 1054 µm. Conversely, *E. felichthys* (Pearse, 1947) and *E. youngi* Tavares & Luque, 2005 present larger body sizes, approximately 1400 µm, emphasising the distinctive size range of the newly described species. The segmentation of the body, particularly the free versus fused prosome somites, is another distinguishing factor. For instance, *E. arenalbus* n. sp. shows variations in abdominal somite dimensions, contrasting with the more uniform structures seen in species like *E. atafonensis*. This variability extends to cephalosome characteristics, with *E. caraguatatubensis* exhibiting an inflated shape absent in *E. arenalbus* n. sp. The spine-setae formulae on the swimming legs of *E. arenalbus* n. sp. further differentiate it, particularly when compared to all other marine congeners, except for *E. lizae* Krøyer, 1863. *Ergasilus atafonensis*, *E. bahiensis*, *E. myctarothes*, *E. parvitergum*, and *E. xenomelanirisi* Carvalho, 1955, have a spine on the outer margin of the second exopodite of leg I, which is absent in the new species. In addition,

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E. ilani lacks a certain number of armaments that are common on the legs of the species in the group, for example, spines and setae on the first segments of the exopod and endopod respectively. In *E. caraguatatubensis*, *E. felichthys*, *E. foresti* Boxshall, Araujo & Montu, 2002, *E. ilani*, *E. parvitergum*, and *E. youngi*, leg V is extremely reduced and is represented by one or two setae. While the setae formula of the antennule is also a clear distinguishing factor, species like *E. ilani*, *E. rostralis*, and *E. uniseriatus* were further excluded due to their antennules being described as only 5-segmented, unlike the 6-segmented antennules observed in the other *Ergasilus* species. Although *E. arenalbus* n. sp. morphologically resembles *E. lizae* in many aspects, it differs notably in the armature of the antenna, with *E. arenalbus* n. sp. exhibiting a single spine on the anterior second endopod segment, unlike *E. lizae*. Additionally, a distinctive feature of the new species is the spine projections on the posterior margin of the basis of the first leg, a characteristic absent in all other species examined. This comprehensive morphological analysis of *E. arenalbus* n. sp. provides a clear understanding of its unique features within the *Ergasilus* genus, emphasising size, body segmentation, appendage armature, and ornamentation as crucial factors in species differentiation.

Ergasilus chintensis* n. sp.*: Fig. 6–7

ZooBank LSID: urn:lsid:zoobank.org:act:E51F54EC-9CF7-47DA-B4B7-61DEC73B430F.

Type host: *Amblyrhynchote honckenii* (Bloch) (Tetraodontiformes: Tetraodontidae).

Type locality: Chintsa East (-32.836538; 28.116997), Eastern Cape Province, South Africa.

Site on host: Gill filaments.

Prevalence of infection: 20% (Two of 10 pufferfish observed).

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Type material: Two ergasilids (adult females) were collected. Only adult females were examined: two were used for morphology, and one egg string was used for DNA extraction. The hologenophore (NMB P 1047) and holotype (NMB P 1046) were deposited in the parasitological collections of the National Museum, Bloemfontein, South Africa.

Representative DNA sequences: GenBank accession numbers and numbers of bases (bp) are given as follows: 18S: 1,353 bp long sequence of one specimen, accession number: PQ451955; 28S: 668 bp long sequence of one specimen, accession number: PQ451959; and COI: 692 bp long sequence of one specimen, accession number: PQ439340.

Etymology: The species name "*chintensis*" is derived from Chintsa, representing the type locality of the species.

Description

Adult female description (based on 2 specimens). Body length (measured from the anterior margin of cephalosome to the posterior margin of caudal rami) 1035 (1,002–1,068; n = 2). Body comprises prosome, urosome, and caudal rami. Prosome composed of cephalosome, fused somites (first to third pedigerous somites), and fourth free somite (Fig. 6A). Cephalosome slightly shorter than wide, oval to trapezoidal, with antennules and antenna visible in dorsal view. Cephalic ornamentation comprising of anterior circular eyespot and an inverted T-structure of thickened chitin situated medially on dorsal side (Figs. 6A, B). Paired sensory pores and papillae observed anterior to eyespot with numerous sensory papillae and pores scattered over the dorsal surface of cephalosome. Rostrum well-developed, with truncated posterior margin. All pedigerous somites wider than long and progressively smaller. Second pedigerous somite 104 (98–110; n = 2) long by

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292 (287–297; n = 2) wide; third pedigerous somite 106 (99–113; n = 2) long by 224 (217–231; n = 2) wide; fourth pedigerous somite 40 (38–42; n = 2) long by 112 (110–114; n = 2) wide.

Urosome comprising reduced fifth pedigerous somite, non-pedigerous barrel-shaped genital double somite, and three free abdominal somites (Fig. 7A). Reduced fifth pedigerous somite 14 (10–18; n = 2) long by 83 (72–94; n = 2) wide. Genital double-somite longer, 113 (110–115; n = 2), than wide, 88 (86–90; n = 2) (Fig. 7A), bearing a pair of multiseriate egg sacs dorsally, measuring 1098 (1101–1095; n = 2) long by 190 (192–188; n = 2) wide (Fig. 6A). Abdomen three-segmented, first abdominal somite widest, 28 (24–32; n = 2) long by 53 (51–55; n = 2) wide, second abdominal somite shorter, 23 (20–25; n = 2) long by 50 (49–51; n = 2) wide; third somite (= anal somite) incised dorsoventrally (= anal opening or anus) forming attachment for caudal rami, 21 (17–25; n = 2) long by 46 (45–47; n = 2) wide (Fig. 7A). All abdominal somites with posterior row of ventral spinules.

Caudal rami slightly elongated, 23 (22–25; n = 2) long by 18 (17–18; n = 2) wide, with four setae (Fig. 7A). Innermost seta (IV) longest 184 (182–186; n = 2), followed by shortest seta (III) 24 (23–24; n = 2), and two longer setae (II and I) 55 (54–56; n = 2), and 59 (57–60; n = 2), respectively (Fig. 7A). Two sensory pores on posterior ventral margins on each ramus.

Antennule 6-segmented, armed with long and short setae (Fig. 6D). Setal formula from proximal to distal segments given as 3–10–6–3–2–6 (total 30). Antenna 4-segmented, comprising of coxobasis, 99 (97–101; n = 2) long by 61 (58–65; n = 2) wide; and three-segmented endopod, armed with curved terminal claw (Fig. 6E). First endopod segment longest 182 (181–184; n = 2), followed by second endopod segment 110 (108–112; n = 2), and small third endopod segment 14 (13–15; n = 2). Two spines observed on second endopod segment. Terminal claw pointed and smooth 83 (81–85; n = 2), with fossa on inner margin (Fig. 6E).

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Mouth positioned ventrally on cephalosome. Mandible armed with three blades (anterior, medial, and posterior blades); anterior blade thinner and shorter than others, ornamented along anterior margin; medial and posterior blades, both with teeth on opposite margin (Fig. 6C). Maxillule armed with two bare setae. Maxilla 2-segmented, comprising syncoxa (= first segment) and basis (= second segment); syncoxa broad with large maxillary pore; basis distally ornamented with numerous teeth on convex margin. Labium broad, unornamented; mid-region produced posteriorly, with rounded posterior margin.

Swimming legs I to IV; each comprising coxa, basis and 2 segmented rami (i.e. exopod, endopod). Rami of all legs 3-segmented, except 2-segmented exopod of leg IV. Segments distinct, typical with similar basic morphology as in other species of *Ergasilus*. Armature on rami as follows (Roman and Arabic numerals indicating spines and plumose setae, respectively) in Table 6.

Leg I (Fig. 7C). Coxa ornamented with spinules on outer margin. Basis lacking outer setae, ornamented with spinules on inner margin. Exopod 3-segmented; first segment with small outer spine; second segment with 1 inner plumose seta, lacking spine; third segment with small spine on outer corner, longer apical spine; both spines with serrated margins; and 5 plumose setae. Endopod 3-segmented; first and second segment each with 1 plumose seta; third segment with 4 plumose setae and 2 distal serrated spines.

Leg II (Fig. 7D). Coxa ornamented with spinules on outer margin. Basis with outer seta and pore, ornamented with multiple spinules on inner margin. Exopod 3-segmented; first segment with small outer spine; second segment with 1 plumose seta, lacking spine; third segment with small spine on outer corner and 6 plumose setae. Endopod 3-segmented; first segment with 1 plumose seta; second segment with 2 plumose setae; third segment with 4 plumose setae and 1

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distal serrated spine (Fig. 7D). Leg III (Fig. 7D) with same ornamentation and armament described for leg 2.

Leg IV (Fig. 7E). Coxa ornamented with spinules on outer margin. Basis with outer seta, ornamented with multiple spinules on inner margin. Exopod 2-segmented; first segment with small outer spine; second segment with small spine on outer corner and 4 plumose setae. Endopod 3-segmented; first segment with 1 plumose seta; second segment with 2 plumose setae; third segment with 3 plumose setae and 1 distal serrated spine.

Leg V (Fig. 7F) with single ramus. Ramus 2 -segmented: proximal segment rectangular, without any armaments or ornaments; distal segment about 2.5 times longer than previous segment, with spinules scattered across surface, bearing 2 setae (lateral and inner setae); lateral seta plumose.

Intercoxal sclerites of all legs, present (Figs. 6A; 7B); each sclerite with both ends directed Bposteriorly. Interpodal plates of leg I to III ornamented with spinules; fourth plate absent (Fig. 7B).

Remarks

The detailed description of *E. chintensis* n. sp. highlights its unique characteristics among *Ergasilus* species worldwide, especially compared to marine congeners from these geographic regions. Notably, similar to *E. arenalbus* n. sp., its body size averaging 1,035 µm sets it apart from both larger species like *E. felichthys* and *E. youngi*, ranging around 1,400 µm, and also from species with smaller sizes below 1054 µm, such as *E. atafonensis*, *E. bahiensis*, *E. caraguatatubensis*, *E. ilani*, *E. myctarothes*, *E. parvitergum*, *E. rostralis*, and *E. uniseriatus*. Similarities emerge due to their shared size range when comparing the two newly described South

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African species; however, subtle proportional variations in body segments and appendages are key to their differentiation upon closer examination. Additionally, *E. chintensis* n. sp. displays a more intricate armature on its antenna segments than *E. arenalbus* n. sp., where the second endopod segment in this species shows two developed spines rather than just one as present in *E. arenalbus* n. sp. The most striking feature of *E. chintensis* n. sp. is its body segmentation, characterised by a fused 2-segmented prosome. This completely contrasts with the free prosome somites observed not only in *E. arenalbus* n. sp. but also concerning all the other compared marine ergasilid species. *Ergasilus caraguatatubensis* also exhibits a fused prosome structure, although, to a lesser degree than *E. chintensis* n. sp. The antennule setae formula also contributes to this distinction, with *E. chintensis* n. sp. differing from *E. ilani*, *E. rostralis*, and *E. uniseriatus* in antennule segmentation (6-segmented vs 5-segmented). These distinguishing features collectively characterise *E. chintensis* n. sp. within the *Ergasilus* genus, highlighting body segmentation, appendage armature, and ornamentation as key characteristics for species differentiation.

Molecular characterisation and phylogenetic position of African marine Ergasilus species

The molecular analyses revealed distinct genetic profiles for the newly described *Ergasilus* species. This study successfully generated a total of eight sequences. For *E. arenalbus* n. sp., five sequences were produced: two 18S, two 28S, and one COI sequence. For *E. chintensis* n. sp., three sequences were obtained: one 18S, one 28S, and one COI sequence. Nucleotide comparisons of the two new species against the partial 18S rDNA, 28S rDNA, and COI mtDNA gene sequences of the genus *Ergasilus* were performed, as detailed in Tables 7, 8, and 9, respectively. Both Maximum Likelihood (ML) and Bayesian Inference (BI) analyses were conducted on the partial 18S rDNA, 28S rDNA, and COI gene alignments, producing phylogenetic trees with congruent

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topologies. Thus, only the ML tree of the 28S and COI gene regions are presented (Fig. 8 and Fig. 9, respectively).

The 18S phylogenetic analyses yielded a final alignment consisting of 1,354 bases. The 18S sequences exhibited no interspecific variability (0 bp difference) since no differences were found among the 18S rDNA sequences of *E. arenalbus* n. sp. and *E. chintensis* n. sp. (Table 7). The analysis revealed *E. scalaris* Markevich, 1940, as the most genetically distant species from *E. arenalbus* n. sp. (33 bp/ 2.48%) and *E. chintensis* n. sp. (35 bp/ 2.59%) (Table 7). The lowest interspecific differences (1.13–1.18%) were observed between the new species and *E. sieboldi* von Nordmann, 1832 (Table 7).

The 28S phylogenetic analysis produced a final alignment of 682 bases. These 28S sequences displayed minor interspecific variability (6 bp) among the 28S rDNA sequences of *E. arenalbus* n. sp. and *E. chintensis* n. sp. (Table 8). The analysis showed *E. parasarsi* Míč, Řehulková & Seifertová, 2023, and *E. yaluzangbus* Kuang & Qian, 1985, as the most genetically distant species from *E. arenalbus* n. sp. (71 bp/10.70%) and *E. chintensis* n. sp. (72 bp/10.68%), respectively (Table 8). The smallest interspecific differences (5.39–5.60%) were noted between the new species and *E. wilsoni* Markevich, 1933 (Table 8). ML and BI analyses using rDNA alignment that included partial 28S sequences of Ergasilidae produced trees with consistent topologies and similar nodal support values. Consistent with previous phylogenetic studies on ergasilids (Song *et al*., 2008; Santacruz *et al*., 2020; Fikiye *et al.*, 2023; Míč *et al*., 2023, 2024), the analyses identified five well-supported polyphyletic *Ergasilus* groups (Fig. 8): (A) The African freshwater *Ergasilus* species, (B) the *Sinergasilus* Yin, 1949, species and the *E. anchoratus* Markevich, 1946, group, (C) the Asian *Ergasilus* species and the *Neoergasilus japonicus* (Harada, 1930) group, (D) the recently described *Dermoergasilus madagascarensis* Mic, Rehulkova,

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Simkova, Razanabolana & Seifertova, 2024, and *E. sieboldi* group, and (E) the *Paraergasilus* Markevich, 1937, species and the *E. wilsoni* group (Fig. 8). Despite forming a distinct subclade (F), the newly described species still clustered within the larger clade that includes subclade (A) comprising African freshwater species, along with non-African species like *E. yaluzangbus* and *E. peregrinus* Heller, 1865 (Fig. 8).

COI sequences were aligned using invertebrate mitochondrial translation, resulting in an alignment length of 700 bases. The sequences included GenBank and BOLD sequences submitted from Canada (Table 4). These results displayed substantial interspecific variability (43 bp) among the COI sequences of *E. arenalbus* n. sp. and *E. chintensis* n. sp. and more than 110 bases from all other *Ergasilus* congeners (Table 9). The analysis showed *E. mirabilis* Oldewage & van As, 1987, and *E. lizae* as the most genetically distant species from *E. arenalbus* n. sp. (139 bp/ 20.06%) and *E. chintensis* n. sp. (134 bp/ 20.36%), respectively (Table 9). The smallest interspecific differences (19.07–19.59%) were noted between the new species and *E. wilsoni* (Table 9). Similar to the 28S tree topology, the novel sequences of *E. arenalbus* n. sp. and *E. chintensis* n. sp. formed the same subclade (F), within the larger clade that includes subclade (A) comprising African freshwater species, *E. mirabilis*, and the morphologically similar marine species *E. lizae*, which is also found within the Indian Ocean (Fig. 9).

Based on these analyses this study proposes the existence of a sixth clade (F) consisting of African marine *Ergasilus* species (Figs. 8, 9). However, this proposition remains speculative as their precise phylogenetic placement within Ergasilidae remains unresolved due to low support values and limited molecular data, concerning marine ergasilids.

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Discussion

The discovery of two new *Ergasilus* species, *E. arenalbus* n. sp. and *E. chintensis* n. sp., from the Evileye blaasop, *Amblyrhynchote honckenii*, significantly enhances our understanding of marine parasite diversity in South Africa. These findings highlight the underexplored nature of marine parasites in this region, particularly within the genus *Ergasilus*, known for its rich diversity in global freshwater and marine environments (Boxshall and Defaye, 2008; Fikiye *et al*., 2023; Míč *et al*., 2023). To date, only a limited number of *Ergasilus* species have been reported from African marine environments, with only five documented, including just one from South Africa (Fikiye *et al*., 2023; WoRMS, 2024). Moreover, despite *Ergasilus* being found in a wide range of fish host families (see Table 1), only a single species, *E. colomesus* Thatcher & Boeger, 1983, has been described from the family Tetraodontidae Bonaparte, 1832 (Thatcher and Boeger, 1983) in the Amazon River, Brazil.

The addition of *E. arenalbus* n. sp. and *E. chintensis* n. sp. not only introduces new host records but also suggests a higher hidden diversity of *Ergasilus* within South Africa's coastal region and the Tetraodontidae family. This hints at a potentially broader copepod diversity and novel host-parasite relationships yet to be explored, aligning with global trends revealing extensive species diversity in under-studied marine ecosystems (Boxshall and Defaye, 2008). The presence of these new species along the South African coastline highlights the region's rich marine biodiversity and emphasises the importance of investigating lesser-known areas and hosts for hidden parasite diversity.

Taxonomically, detailed morphological examinations of these species, focusing on size, body segmentation, appendage armature, and ornamentation, provide crucial insights into their distinctiveness from known congeners. Integrating traditional morphological taxonomy with

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molecular techniques has been instrumental in characterising these new *Ergasilus* species. Molecular analyses alongside morphological assessments confirm the uniqueness of these species with greater accuracy (Míč *et al*., 2024; Walter and Boxshall, 2024). This integration is valuable as morphological characters alone often yield conflicting results in distinguishing new species and understanding their placement within Ergasilidae lineages (Míč *et al*., 2024; Walter and Boxshall, 2024).

The nomenclatural history of ergasilids emphasises the significant challenge of formulating generic diagnoses that effectively distinguish species. This complexity is evidenced by the synonymisation of 33 *Ergasilus* species either with other previously described *Ergasilus* species or with species from different genera within the Ergasilidae family (Walter and Boxshall, 2024). Moreover, genera such as *Acusicola* Cressey, in Cressey & Collette, 1970, *Dermoergasilus* Ho & Do, 1982, *Neoergasilus* Yin, 1956, *Paraergasilus*, and *Sinergasilus*, have consistently been confirmed as monophyletic (Song *et al*., 2008; Santacruz *et al*., 2020; Kvach *et al*., 2021; Míč *et al*., 2023, 2024). However, these genera render *Ergasilus* polyphyletic, with certain species, like *E. anchoratus*, *E. sieboldi*, and *E. wilsoni*, showing closer relationships to *Sinergasilus*, *Dermoergasilus*, and *Paraergasilus*, respectively (Figs. 8, 9).

Phylogenetics pose significant challenges that hinder comprehensive genomic analyses of *Ergasilus* species, creating obstacles in gaining deeper insights into their biology. The limited knowledge regarding their diversity and the lack of genetic data, compared to those of other well-studied organisms, are major contributing factors. Previous studies (Song *et al*., 2008; Santacruz *et al*., 2020; Kvach *et al*., 2021; Míč *et al*., 2023, 2024) have attempted to overcome these challenges through molecular characterisation using ribosomal RNA (rRNA) genes, particularly the 18S and 28S rDNA regions. However, the effectiveness of these markers in species-level

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differentiation has been variable (Míč *et al*., 2023, 2024). The 18S rDNA region of the present study has shown minimal or even zero variation (0–2.59%) in some cases, making it unsuitable for distinguishing between closely related species. This is consistent with findings from earlier studies, which reported that the 18S rRNA gene is highly conserved and not suitable for identification at lower taxonomic levels (Taniguchi *et al*., 2004; Huys *et al*., 2006; Tang *et al*., 2012; Marrone *et al*., 2013). This lack of variation reinforces the limitations of the 18S rDNA marker for species-level differentiation within this genus.

In contrast, the 28S rDNA analyses have proven more effective in distinguishing between species (Song *et al*., 2008; Santacruz *et al*., 2020; Kvach *et al*., 2021; Míč *et al*., 2023, 2024). The present study supports these findings to an extent, revealing higher, albeit minor interspecific divergence (6 bp between *E. arenalbus* n. sp. and *E. chintensis* n. sp.). The analysis also identified other *Ergasilus* species as genetically distant from the newly described taxa, highlighting the potential of 28S rDNA in elucidating phylogenetic relationships within the family Ergasilidae. However, despite its relative effectiveness, the genetic variation observed in the 28S rDNA is still limited, with little variation (0.90–10.70%), compared to other markers, raising questions about its adequacy for reliable species identification.

The COI gene, a widely used barcode for species-level differentiation (Tang *et al*., 2012; Baek *et al*., 2016; Mayor *et al*., 2017; Míč *et al*., 2023, 2024), demonstrated high resolution at the species level for the *Ergasilus* species described in this study and indicated significant interspecific variability. The COI analyses revealed substantial differences (43 bp) among the COI sequences of *E. arenalbus* n. sp. and *E. chintensis* n. sp., as well as notable variation from other *Ergasilus* congeners. This suggests that the COI gene may be a more suitable marker for species-level differentiation in this group. However, it is important to note that the limited availability of only

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four other *Ergasilus* COI sequences (see Fig. 9 and Table 9) means that drawing definitive conclusions from these results is premature. While COI shows promise for more precise species identification, further research is needed to expand the dataset and validate its effectiveness across a broader range of *Ergasilus* species. Moving forward, prioritising the COI gene in future studies may provide a clearer understanding of the diversity and evolutionary relationships within the family Ergasilidae.

The phylogenetic relationships of ergasilid copepods remain largely unclear, with only 11% (31 out of 277) of the known species with any molecular data available (Míč *et al*., 2023, 2024; Walter and Boxshall, 2024). Limited studies have examined the genetic characteristics of African *Ergasilus* species (Fikiye *et al*., 2023, Míč *et al*., 2023), and no genetic studies exist for the characterisation of marine species. Notably, the present study provides the first marine sequences for this genus. The only available brackish sequences are for *Ergasilus wilsoni* and *Ergasilus sieboldi* (Walter and Boxshall, 2024), both of which are primarily associated with freshwater environments rather than being strictly marine or brackish. *Ergasilus wilsoni* and *E. sieboldi* can inhabit fresh or brackish waters, while recognised as typical freshwater species found in the Palearctic region, particularly in rivers and lakes (Kvach *et al*., 2021), distinguishing them from the newly discovered *Ergasilus* species, as close relationships among ergasilids may be influenced by the geographical origin of the species or the endemism of their hosts (Míč *et al*., 2023). This means that parasite distribution is closely linked to the geographic distribution of their hosts (Morand and Guégan, 2000), suggesting potential coevolution between parasites and hosts. The discovery of two genetically similar species from the same host species suggests that the two newly identified *Ergasilus* species associated with pufferfish along the South African coast reflect coevolutionary patterns and host-specific endemism. These findings are consistent with

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conclusions drawn from previous phylogenetic studies (Song *et al*., 2008; Santacruz *et al*., 2020; Kvach *et al*., 2021; Oliveira *et al*., 2021). Therefore, the geographic separation between *E. sieboldi* and *E. wilsoni* from the newly discovered species further highlights the critical need for more comprehensive genetic data on marine *Ergasilus* species to enhance our understanding of their diversity, evolutionary relationships, and distribution patterns.

Conclusion

The discovery and descriptions of *E. arenalbus* n. sp. and *E. chintensis* n. sp. in association with the Evileye blaasop represent a significant advance in our understanding of marine parasite diversity in South Africa. These results highlight the rich marine ecosystems of the region and emphasise the importance of investigating under-explored areas to uncover the hidden biodiversity. Furthermore, the new *Ergasilus* sequences and phylogenetic analyses presented in this study provide the first insight into the phylogenetic relationships of marine *Ergasilus* species within the South Atlantic and Indian Ocean regions. Alongside the studies by Míč *et al*. (2023, 2024) and Fikiye *et al*. (2023), this research also offers a further understanding of the African clade lineage, making the molecular data presented here the first to elucidate the phylogenetic relationships of this genus in African and marine systems. Our phylogenetic analysis suggests that African marine ergasilids form a distinct monophyletic lineage separate from freshwater species, proposing the recognition of a sixth clade (F) for African marine *Ergasilus* species (Figs. 8, 9). Nonetheless, due to low support values and the scarcity of molecular data for marine ergasilids, their exact phylogenetic placement within the family Ergasilidae remains unresolved. Further studies that integrate both morphological and molecular data are essential to elucidate these relationships.

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K.A. Hadfield: Methodology, Funding acquisition, Writing – review & editing.

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Table 1. Updated information for all marine species of *Ergasilus* Nordmann, 1832 described within the South Atlantic and Indian oceans, with information on host species, host families, distribution, and available GenBank data. Information from the present study is represented in bold. Abbreviations: **Syn** – synonym; **TH** – type host; **TLOC** – type locality.

Species	Host Family	Host Species	Distribution	Ocean	18S	28S	COI	References
***E. arenalbus* n. sp. Present study**	**Tetraodontidae**	**TH: *Amblyrhynchote honckenii* (Bloch)**	**TLOC: Witsand, Breede River Estuary, South Africa**	**South Atlantic**	✓	✓	✓	**Present study**
E. atafonensis Amado and Rocha, 1996	Mugilidae	**TH:** *Mugil curema* Valenciennes, 1836 *M. liza* Valenciennes, 1836; *M. rubrioculus* Harrison, Nirchio, Oliveira, Ron and Gaviria, 2007; *M. trichodon* Poey, 1875	**TLOC:** Rio de Janeiro, Brazil Sergipe, Brazil; Rio Grande do Sul, Brazil; São Paulo, Brazil; Santos, Brazil; Maranhão, Brazil; Bahia, Brazil	South Atlantic	-	-	-	Amado and Rocha, 1996
E. bahiensis Amado and Rocha, 1996	Mugilidae Ariidae	**TH:** *Mugil curema* Valenciennes, 1836 *Sciades herzbergii* (Bloch, 1794)	**TLOC:** Bahia, Brazil Caeté estuary, Brazil; Ajuruteua beach, Brazil	South Atlantic	-	-	-	Amado and Rocha, 1996; Dos Santos, 2021
E. caraguatatubensis Amado and Rocha, 1996	Mugilidae	**TH:** *Mugil curema* Valenciennes, 1836 *M. liza* Valenciennes, 1836; *M. rubrioculus* Harrison, Nirchio, Oliveira, Ron and Gaviria, 2007	**TLOC:** Caraguatatuba, Brazil São Paulo, Brazil; Cananeia, Brazil; Rio de Janeiro, Brazil; Maranhão, Brazil	South Atlantic	-	-	-	Amado and Rocha, 1996

***E. chintensis* n. sp. Present study**	**Tetraodontidae**	**TH: *Amblyrhynchote honckenii* (Bloch)**	**TLOC: Chintsa East, South Africa**	**Indian**	✓	✓	✓	**Present study**
E. cyanopictus Carvalho, 1962	Mugilidae	**TH:** *Mugil cephalus* Linnaeus, 1758	**TLOC:** Rio Nóbrega, Brazil	South Atlantic	-	-	-	Carvalho, 1962
E. felichthys (Pearse, 1947) **Syn:** *E. elongatus* Thomsen, 1949	Polyodontidae Ariidae	**TH:** *Bagre marinus* (Mitchill, 1815) *Ariopsis felis* (Linnaeus, 1766); *Genidens barbus* (Lacepède, 1803); *Polyodon spathula* (Walbaum, 1792)	**TLOC**: Beaufort, USA Uruguay; Mobile Bay, USA; St. Louis Bay, USA; Tallapoosa River, USA; Colyell Bay, USA	North Atlantic South Atlantic Gulf of Mexico	-	-	-	Pearse, 1947; Thomsen, 1949; Johnson and Rogers, 1972
E. foresti Boxshall, Araujo and Montu, 2002	-	Free-living (Plankton nets)	**TLOC:** Piau River estuary, Brazil; Grande do Sul, Brazil	South Atlantic	-	-	-	Boxshall *et al*. (2002)
E. ilani Oldewage and van As, 1988	Mugilidae	**TH:** *Mugil cephalus* Linnaeus, 1758	**TLOC:** Sodwana estuary, Sodwana Bay, KZN, SA	Indian	-	-	-	Oldewage and van As, 1988
E. lizae Krøyer, 1863 **Syn:** *E. nanus* Beneden, 1870	Mugilidae Anguillidae Bagridae Cochleae Cyprinodontidae Fundulidae Oxudercidae Sparidae	**TH:** *Mugil liza* Valenciennes, 1836 *Anguilla anguilla* (Linnaeus, 1758); *Acanthopagrus butcheri* (Munro, 1949); *A. australis* (Günther, 1859); *A. berda* (Fabricius, 1775); *Chelon auratus* (Risso, 1810); *C. ramada*	**TLOC:** New Orleans, USA Louisiana, USA; Brisbane River, Australia; Texas coast, USA; Georgia coast, USA; Israel; Rio Aconcagua, Chile; La Parguera, Puerto Rico; Melbourne, Australia; Lakes Entrance, Australia; Port	North Atlantic Pacific Caribbean Mediterranean Gulf of Mexico Indian	-	-	✓	Beneden, 1870; Byrnes, 1986; Kabata, 1992

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		(Risso, 1827); *C. saliens* (Risso, 1810); *Coptodon zillii* (Gervais, 1848); *Fundulus similis* (Baird and Girard, 1853); *F. heteroclitus* (Linnaeus, 1766); *Floridichthys carpio* (Günther, 1866); *M. cephalus* Linnaeus, 1758; *M. trichodon,* Poey, 1875; *Mystus gulio* (Hamilton, 1822); *Pseudapocryptes elongatus* (Cuvier, 1816); *Sarotherodon galilaeus* (Linnaeus, 1758); *Trachystoma petardi* (Castelnau, 1875)*;*	Lincoln, Australia; Coffs Harbour, Australia; Gladstone, Australia; Port Canning, India					
E. myctarothes Wilson, 1913	Sphyrnidae	**TH:** *Sphyrna zygaena* (Linnaeus, 1758)	**TLOC:** Indian Ocean islands	Indian	-	-	-	Wilson, 1913
E. pakistanicus Jafri, 1995	Mastacembelidae	**TH:** *Mastacembelus armatus* (Lacepède, 1800)	**TLOC:** Sindh, Pakistan	Indian	-	-	-	Jafri, 1995
E. parvitergum Ho, Jayarajan and Radhakrishnan, 1992	Cichlidae Carangidae	**TH:** *Etroplus suratensis* (Bloch, 1790); *Carangoides malabaricus* (Bloch and Schneider, 1801)	**TLOC:** Veli Lake, India	Indian	-	-	-	Ho *et al*. (1992)
E. polynemi Redkar, Rangnekar and Murti, 1952	Polynemidae	**TH:** *Eleutheronema tetradactylum* (Shaw, 1804)	**TLOC:** Maharashtra, Mumbai, India	Indian	-	-	-	Redkar *et al*. (1952)

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E. rostralis Ho, Jayarajan and Radhakrishnan, 1992	Mugilidae	**TH:** *Planiliza parsia* (Hamilton, 1822) *Osteomugil cunnesius* (Valenciennes, 1836); *P. tade* (Fabricius, 1775); *P. abu* (Heckel, 1843); *P. macrolepis* (Smith, 1846);	**TLOC:** Madras, India Mangalore, Pakistan; Veli Lake, India; Neendakara, India; Shatt Al-Arab River, India	Indian	-	-	-	Ho *et al*. (1992); El-Rashidy and Boxshall, 2002
E. uniseriatus Ho, Jayarajan and Radhakrishnan, 1992	Gobiidae Belonidae	**TH:** *Glossogobius giuris* (Hamilton, 1822) *Xenentodon cancila* (Hamilton, 1822)	**TLOC:** Veli Lake, India Karuvanoor River, India	Indian	-	-	-	Ho *et al*. (1992)
E. vembanadensis Thomas, 1993	Siluridae	**TH:** *Wallago attu* (Bloch and Schneider, 1801)	**TLOC:** Vembanad Lake, India	Indian	-	-	-	Thomas, 1993
E. xenomelanirisi Carvalho, 1955	Atherinopsidae	**TH:** *Atherinella brasiliensis* (Quoy and Gaimard, 1825)	**TLOC:** Cananéia, Brazil	South Atlantic	-	-	-	Carvalho, 1955
E. youngi Tavares and Luque, 2005	Ariidae	**TH:** *Aspistor luniscutis* (Valenciennes, 1840) *Sciades herzbergii* (Bloch, 1794)	**TLOC:** Angra dos Reis, Brazil Caeté estuary, Brazil	South Atlantic	-	-	-	Tavares and Luque, 2005; Dos Santos, 2021

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Table 2. Metrical information of the new species of *Ergasilus* Nordmann, 1832. Information is presented as the mean, followed by the standard deviation and the number of specimens examined. All measurements are in micrometres. Abbreviations: L – length; W – width.

Character	*Ergasilus arenalbus* n. sp.	*Ergasilus chintensis* n. sp.
Body (L)	1182 ± 137; 12	1035 ± 47; 2
Body (W)	408 ± 49; 12	424 ± 17; 2
Cephalothorax (L)	626 ± 93; 12	608 ± 5; 2
Cephalothorax (W)	397 ± 53; 12	417 ± 6; 2
Cephalosome (L)	336 ± 43; 12	Fused
Cephalosome (W)	387 ± 38; 12	Fused
First pedigerous somite (L)	176 ± 27; 12	Fused
First pedigerous somite (W)	358 ± 42; 12	Fused
Second pedigerous somite (L)	107 ± 24; 12	138 ± 6; 2
Second pedigerous somite (W)	274 ± 31; 12	292 ± 7; 2
Third pedigerous somite (L)	105 ± 18; 12	106 ± 10; 2
Third pedigerous somite (W)	212 ± 37; 12	224 ± 10; 2
Fourth pedigerous somite (L)	61 ± 9; 12	40 ± 3; 2
Fourth pedigerous somite (W)	140 ± 11; 12	112 ± 3; 2
Fifth pedigerous somite (L)	31 ± 6; 12	14 ± 6; 2
Fifth pedigerous somite (W)	80 ± 12; 12	83 ± 16; 2
Genital double somite (L)	135 ± 8; 12	113 ± 4; 2

Genital double somite (W)	109 ± 8; 12	88 ± 3; 2
First abdomen (L)	43 ± 6; 12	28 ± 6; 2
First abdomen (W)	73 ± 8; 12	53 ± 3; 2
Second abdomen (L)	31 ± 6; 12	23 ± 4; 2
Second abdomen (W)	63 ± 3; 12	50 ± 1; 2
Third abdomen (L)	28 ± 4; 12	21 ± 6; 2
Third abdomen (W)	63 ± 2; 12	46 ± 1; 2
Caudal rami (L)	30 ± 2; 12	25 ± 2; 2
Caudal rami (W)	24 ± 1; 12	18 ± 1; 2
Seta I (L)	92 ± 5; 12	61 ± 2; 2
Seta II (L)	77 ± 7; 12	55 ± 2; 2
Seta III (L)	28 ± 5; 12	24 ± 4; 2
Seta IV (L)	282 ±24; 12	183 ± 3; 2
Antennule (L)	121 ± 8; 12	98 ± 1; 2
Coxobasis (L)	174 ± 23; 12	102 ± 3; 2
Coxobasis (W)	95 ± 10; 12	65 ± 4; 2
First endopodal segment (L)	339 ± 25; 12	184 ± 2; 2
Second endopodal segment (L)	196 ± 15; 12	108 ± 3; 2
Third endopodal segment (L)	28 ± 4; 12	13 ± 2; 2
Claw (L)	161 ± 13; 12	86 ± 3; 2
Eggs (L)	1269 ± 257; 12	1101 ± 4; 2
Eggs (W)	256 ± 42; 12	193 ± 3; 2

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Table 3. List of primers used for DNA amplification of parasitic copepods with sequences and references, used to amplify partial 18S, 28S, and COI genes in this study.

Gene Regions	Primers	Sequences	Sources
18S	18SF	5′-AAG GTG TGM CCT ATC AAC T-3′	Song *et al*., 2008
	18SR	5′-TTA CTT CCT CTA AAC GCT C-3′	
28S	28SF	5′-ACA ACT GTG ATG CCC TTA G-3′	Song *et al*., 2008
	28SR	5′-TGG TCC GTG TTT CAA GAC G-3′	
COI	LCO1490 (F)	5′-GGTCAACAAATCATAAAGATATTGG-3′	Folmer *et al*., 1994
	HCO2198 (R)	5′-TAAACTTCAGGGTGACCAAAAAATCA-3′	

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Table 4. List of GenBank and Barcode of Life Database (BOLD) Ergasilidae sequences included in the phylogenetic analyses. The taxa in bold fonts are sequences generated from the present study. *Paracyclopina nana* (in the grey shade) was used as the outgroup.

Taxon	Host	Locality	GenBank Accession Numbers			References
			18S	28S	COI	
Acusicola margulisae	*Amphilophus citrinellus*; *Parachromis managuensis*; *Oreochromis* sp.; *Poecilia exicana*	Nicaragua	MN852694 MN852695	MN852849 MN852850	MN854868 MN854869	Santacruz *et al.* (2022)
Dermoergasilus madagascarensis	*Paretroplus*; *polyactis*	Madagascar	PP115568 -	PP115569 -	PP117931 PP117932	Míč *et al.* (2024)
Ergasilus anchoratus	*Pseudobagrus fulvidraco*	China	DQ107564	DQ107528	-	Song *et al.* (2008)
***Ergasilus arenalbus* n. sp.**	***Amblyrhynchote honckenii***	**South Africa**	**PQ451954 PQ451956**	**PQ451957 PQ451958**	**PQ439339 -**	**Present study**
***Ergasilus auritus*	*Gasterosteus aculeatus*	Canada	-	-	ECTCR091 -14	BOLD
Ergasilus briani	*Misgurnus anguillicaudatus*	China	DQ107572	DQ107532	-	Song *et al.* (2008)
Ergasilus caparti	*Neolamprologus brichardi*	Burundi	OQ407469	OQ407474	-	Míč *et al.* (2023)
***Ergasilus chintensis* n. sp.**	***Amblyrhynchote honckenii***	**South Africa**	**PQ451955**	**PQ451959**	**PQ439340**	**Present study**

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Ergasilus hypomesi	*Acanthogobius hasta*	China	DQ107573	DQ107539	-	Song *et al.* (2008)
***Ergasilus lizae*	*Fundulus diaphanus*	Canada	-	-	ECTCR024-14	BOLD
Ergasilus macrodactylus	*Gnathochromis permaxillaris*	Burundi	OQ407465	OQ407470	-	Míč *et al.* (2023)
Ergasilus megacheir	*Simochromis diagramma*	Burundi	OQ407466	OQ407471	-	Míč *et al.* (2023)
Ergasilus mirabilis	*Clarias gariepinus*	South Africa Zambia	OR449753 OR449754	OR449755 OR449756	OR448769 OR448770	Fikiye *et al.* (2023)
Ergasilus parasarsi	*Simochromis diagramma*	Burundi	OQ407467	OQ407473	-	Míč *et al.* (2023)
Ergasilus parvus	*Spathodus erythrodon*	Burundi	OQ407468	OQ407472	-	Míč *et al.* (2023)
Ergasilus parasiluri	*Tachysurus fulvidraco*	China	DQ107567	DQ107536	-	Song *et al.* (2008)
Ergasilus peregrinus	*Siniperca chuatsi*	China	DQ107577	DQ107531	-	Song *et al.* (2008)
Ergasilus scalaris	*Tachysurus dumerili*	China	DQ107565	DQ107538	-	Song *et al.* (2008)
Ergasilus sieboldi	*Perca fluviatilis*; *Sparus aurata*	Czech Republic	MW810238	MW810242	-	Kvach *et al.* (2021)
Ergasilus tumidus	*Acanthorhodeus taenianalis*	China	DQ107569 DQ107570	DQ107533 DQ107534	- -	Song *et al.* (2008)

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Ergasilus wilsoni	Free-living	South Korea	KR048765	KR048843	KR049036	Baek *et al.* (2016)
Ergasilus yaluzangbus	*Gymnocypris stewartii*	China	DQ107578	DQ107540	-	Song *et al.* (2008)
Neoergasilus japonicus	*Lepomis gibbosus*	Czech Republic	MH167970 MW810236	MH167968 MW810240	- -	Ondračková *et al.* (2019)
	Scardinius erythrophthalmus	USA	- -	- -	MZ964935 MZ964938	Kvach *et al.* (2021) Vasquez *et al.* (2021)
Paraergasilus brevidigitus	*Cyprinus carpio*	China	DQ107576	DQ107530	-	Song *et al.* (2008)
Paraergasilus longidigitus	*Abramis brama*; *Perca fluviatilis*; *Scardinius erythrophthalmu*	Czech Republic	MW810239	MW810243	-	Kvach *et al.* (2021)
Paraergasilus medius	*Ctenopharyngodon idellus*	China	DQ107574	DQ107529	-	Song *et al.* (2008)
Sinergasilus major	*Ctenopharyngodon Idella* *Silurus glanis*	China Hungary	DQ107558 -	- MZ047815	- -	Song *et al.* (2008) Dos Santos *et al.* (2021)
Sinergasilus polycolpus	*Hypophthalmichthys molitrix*	China	DQ107563	DQ107525	-	Song *et al.* (2008)

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Sinergasilus undulatus	*Cyprinus carpio*	China	DQ107561 -	DQ107526 -	- MW080644	Song *et al.* (2008) Hua *et al.* (2021)
***Thersitina gastorostei*	*Gasterosteus aculeatus*	Canada	-	-	ECTCR063 -14	BOLD
Paracyclopina nana	Free-living	Korea	- FJ214952	- FJ214952	EU877959 -	Ki *et al.* (2009) Ki *et al.* (2011)

**Taxon from the Barcode of Life Database (BOLD)

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Table 5. Spine-setae formula on swimming legs of *Ergasilus arenalbus* n. sp. Number of spines in Roman numerals, number of setae in Arabic numerals.

	Coxa	Basis	Exopod	Endopod
Leg I	0-0	I-1	I-0; 0-1; II-5	0-1; 0-1; II-4
Leg II	0-0	0-1	I-0; 0-1; I-6	0-1; 0-2; I-4
Leg III	0-0	0-1	I-0; 0-1; I-6	0-1; 0-2; I-4
Leg IV	0-0	0-1	I-0; I-5	0-1; 0-2; I-3

Table 6. Spine-setae formula on swimming legs of *Ergasilus chintensis* n. sp. Number of spines in Roman numerals, number of setae in Arabic numerals.

	Coxa	**Basis**	**Exopod**	**Endopod**
Leg I	0-0	0-0	I-0; 0-1; II-5	0-1; 0-1; II-4
Leg II	0-0	0-1	I-0; 0-1; I-6	0-1; 0-2; I-4
Leg III	0-0	0-1	I-0; 0-1; I-6	0-1; 0-2; I-4
Leg IV	0-0	0-1	I-0; I-4	0-1; 0-2; I-3

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Table 7. Nucleotide comparison of the partial 18S rDNA sequences of the genus *Ergasilus* Nordman, 1832, based on 1,354 bp-long alignment.

	Number of bases/ residues which are not identical																		
	E. arenalbus	*E. chintensis*	*E. caparti*	*E. parvus*	*E. macrodactylus*	*E. megacheir*	*E. parasarsi*	*E. sieboldi*	*E. mirabilis*	*E. hypomesi*	*E. tumidus*	*E. briani*	*E. anchoratus*	*E. yaluzangbus*	*E. wilsoni*	*E. parasiluri*	*E. peregrinus*	*E. scalaris*	*P. nana*
E. arenalbus		0	14	14	14	15	15	15	15	19	23	23	25	26	26	27	31	33	99
E. chintensis	100		14	14	14	15	15	16	17	20	24	24	26	30	27	29	32	35	103
E. caparti	98.60	98.60		0	0	1	1	14	3	12	19	19	14	16	18	24	27	19	76
E. parvus	98.60	98.60	100		0	1	1	14	3	12	19	19	14	16	18	24	27	19	76
E. macrodactylus	98.60	98.60	100	100		1	1	14	3	12	19	19	14	16	18	24	27	19	76
E. megacheir	98.50	98.50	99.90	99.90	99.90		0	13	4	13	20	20	15	15	19	25	28	20	76
E. parasarsi	98.50	98.50	99.90	99.90	99.90	100		13	4	13	20	20	15	15	19	25	28	20	76
E. sieboldi	98.87	98.82	98.59	98.59	98.59	98.69	98.69		13	19	21	21	24	23	24	28	33	32	100
E. mirabilis	98.87	98.74	99.70	99.70	99.70	99.60	99.60	99.04		20	22	22	24	23	25	29	36	32	102
E. hypomesi	98.57	98.52	98.80	98.80	98.80	98.69	98.69	98.59	98.52		14	14	24	34	30	20	31	35	104
E. tumidus	98.27	98.23	98.09	98.09	98.09	97.99	97.99	98.45	98.37	98.96		4	31	36	30	20	36	41	106
E. briani	98.27	98.23	98.09	98.09	98.09	97.99	97.99	98.45	98.37	98.96	99.70		31	36	30	20	37	41	106

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E. anchoratus	98.12	98.08	98.59	98.59	98.59	98.49	98.49	98.22	98.22	98.22	97.71	97.71		37	37	34	39	28	105
E. yaluzangbus	98.05	97.78	98.39	98.39	98.39	98.49	98.49	98.30	98.30	97.49	97.34	97.34	97.26		33	39	39	45	103
E. wilsoni	98.05	98.00	98.19	98.19	98.19	98.09	98.09	98.22	98.15	97.78	97.78	97.78	97.26	97.56		38	42	49	108
E. parasiluri	97.98	97.86	97.59	97.59	97.59	97.49	97.49	97.93	97.86	98.52	98.52	98.52	97.49	97.12	97.19		42	44	110
E. peregrinus	97.67	97.63	97.29	97.29	97.29	97.19	97.19	97.56	97.34	97.71	97.34	97.26	97.11	97.12	96.89	96.89		50	107
E. scalaris	97.52	97.41	98.09	98.09	98.09	97.99	97.99	97.63	97.63	97.41	96.97	96.97	97.93	96.67	96.37	96.75	96.3		116
P. nana	92.58	92.39	92.38	92.38	92.38	92.38	92.38	92.61	92.47	92.32	92.17	92.17	92.25	92.39	92.02	91.88	92.1	91.4	

Percentage of basis/ residues which are identical

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Table 8. Nucleotide comparison of the partial 28S rDNA sequences of genus *Ergasilus* Nordman, 1832, based on 682 bp-long alignment.

	Number of bases/ residues which are not identical																		
	E. arenalbus	*E. chintensis*	*E. wilsoni*	*E. hypomesi*	*E. peregrinus*	*E. sieboldi*	*E. briani*	*E. tumidus*	*E. scalaris*	*E. parasiluri*	*E. caparti*	*E. megacheir*	*E. macrodactylus*	*E. anchoratus*	*E. parvus*	*E. mirabiis*	*E. parasarsi*	*E. yaluzangbus*	*P. nana*
E. arenalbus		6	37	37	38	48	50	54	55	55	61	62	63	66	68	69	70	71	176
E. chintensis	99.10		36	38	40	46	47	50	54	54	61	62	63	66	68	65	72	72	176
E. wilsoni	94.46	94.61		38	40	42	37	40	42	44	66	66	67	66	70	69	73	70	171
E. hypomesi	94.47	94.32	94.32		40	36	32	35	34	32	55	62	59	67	63	61	60	64	169
E. peregrinus	94.31	94.01	94.01	94.02		44	42	45	46	44	56	57	56	66	59	60	64	64	168
E. sieboldi	92.55	92.86	93.48	94.41	93.17		40	41	43	43	65	72	70	72	74	62	75	66	168
E. briani	92.53	92.97	94.47	95.22	93.72	93.8		19	22	18	65	67	64	77	68	64	69	75	169
E. tumidus	91.93	92.53	94.02	94.78	93.27	93.64	97.16		29	25	67	70	66	80	70	65	72	72	168
E. scalaris	91.77	91.92	93.71	94.92	93.11	93.32	96.71	95.67		8	71	74	71	79	73	76	72	70	173
E. parasiluri	91.77	91.92	93.41	95.22	93.41	93.32	97.31	96.26	98.80		70	73	70	80	70	70	69	72	167
E. caparti	90.67	90.67	89.91	91.59	91.44	89.83	90.08	89.77	89.14	89.30		14	13	78	17	32	18	73	180
E. megacheir	90.52	90.52	89.91	90.52	91.28	88.73	89.77	89.31	88.69	88.84	97.86		9	81	13	41	19	73	180
E. macrodactylus	90.37	90.37	89.76	90.98	91.44	89.05	90.23	89.92	89.14	89.30	98.01	98.62		81	6	43	15	71	177
E. anchoratus	90.13	90.13	90.13	90.00	90.13	88.82	88.51	88.06	88.19	88.04	88.07	87.61	87.61		85	84	85	95	180

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E. parvus	89.60	89.60	89.30	90.37	90.98	88.42	89.62	89.31	88.84	89.30	97.40	98.01	99.08	87.00		45	15	74	180
E. mirabilis	89.69	90.28	89.69	90.88	91.03	90.37	90.45	90.30	88.64	89.54	95.10	93.72	93.42	87.44	93.11		44	81	176
E. parasarsi	89.30	88.99	88.84	90.83	90.21	88.26	89.47	89.01	88.99	89.45	97.24	97.09	97.70	87.00	97.70	93.26		70	177
E. yaluzangbus	89.47	89.32	89.61	90.50	90.50	89.81	88.89	89.33	89.61	89.32	88.91	88.91	89.21	85.93	88.75	87.96	89.36		174
P. nana	74.00	74.00	74.74	75.07	75.18	74.27	75.07	75.22	74.45	75.33	72.85	72.85	73.30	73.45	72.85	74.04	73.30	74.37	

Percentage of basis/ residues which are identical

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Table 9. Nucleotide comparison of the mtDNA COI gene sequences of genus *Ergasilus* Nordman, 1832, based on 700 bp-long alignment.

Number of bases/ residues which are not identical							
	E. arenalbus	*E. chintensis*	*E. wilsoni*	*E. auritus*	*E. lizae*	*E. mirabilis*	*P. nana*
E. arenalbus		43	111	119	128	139	177
E. chintensis	93.78		114	123	134	137	179
E. wilsoni	80.93	80.41		111	114	122	146
E. auritus	81.91	81.31	80.93		133	141	177
E. lizae	80.55	79.64	80.41	79.79		130	181
E. mirabilis	79.94	80.17	79.04	78.57	80.24		184
P. nana	74.46	74.36	74.91	73.10	72.49	73.45	
Percentage of basis/ residues which are identical							

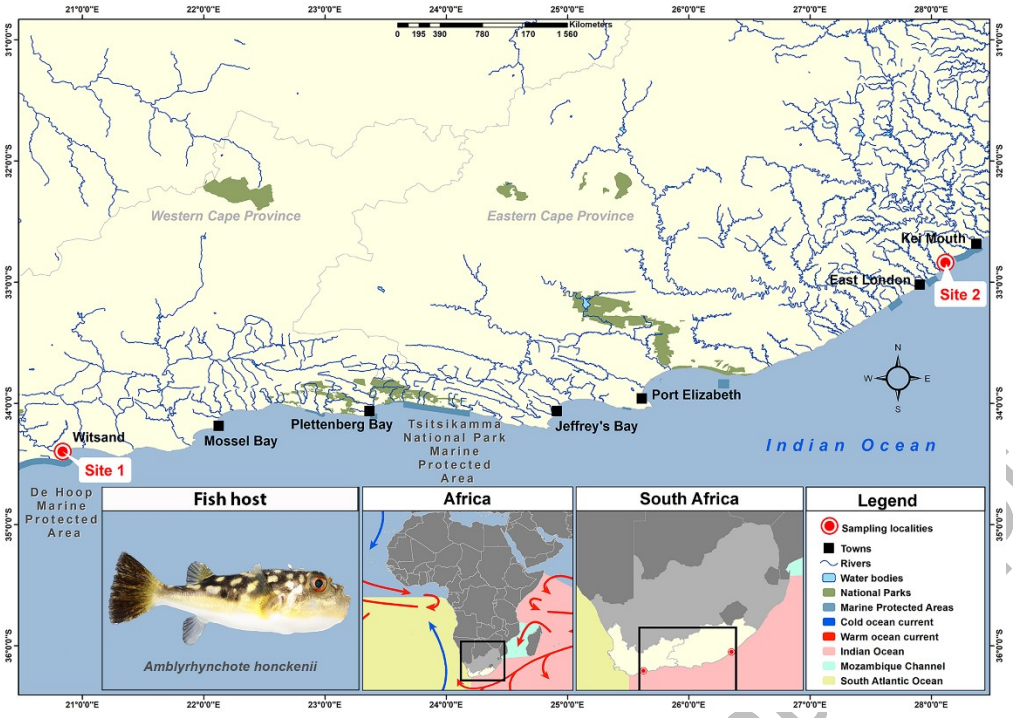

Figure 1. Map indicating the sampling localities of specimens of *Amblyrhynchote honckenii* (Bloch).

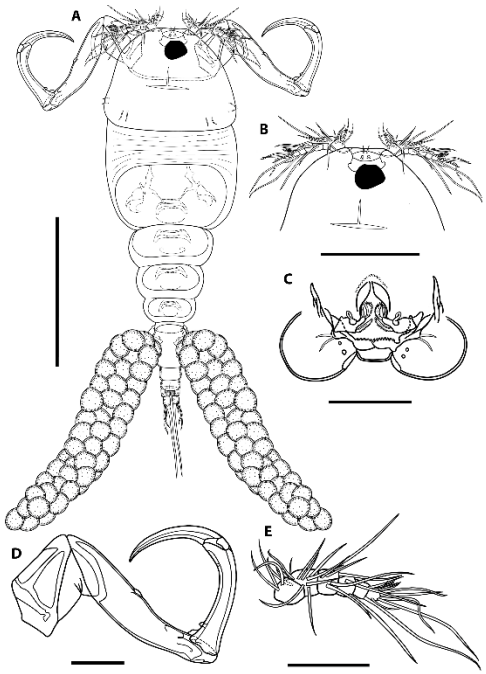

Figure 2. Illustrations of adult female of *Ergasilus arenalbus* n. sp: **A** – entire specimen, dorsal view; **B** – detail of cephalosome, dorsal view; **C** – mouth, mandible, maxillule, and maxilla; **D** – antenna; **E** –antennule. Scale bars: **A** – 500 µm; **B** – 250 µm; **C**–**E** – 100 µm.

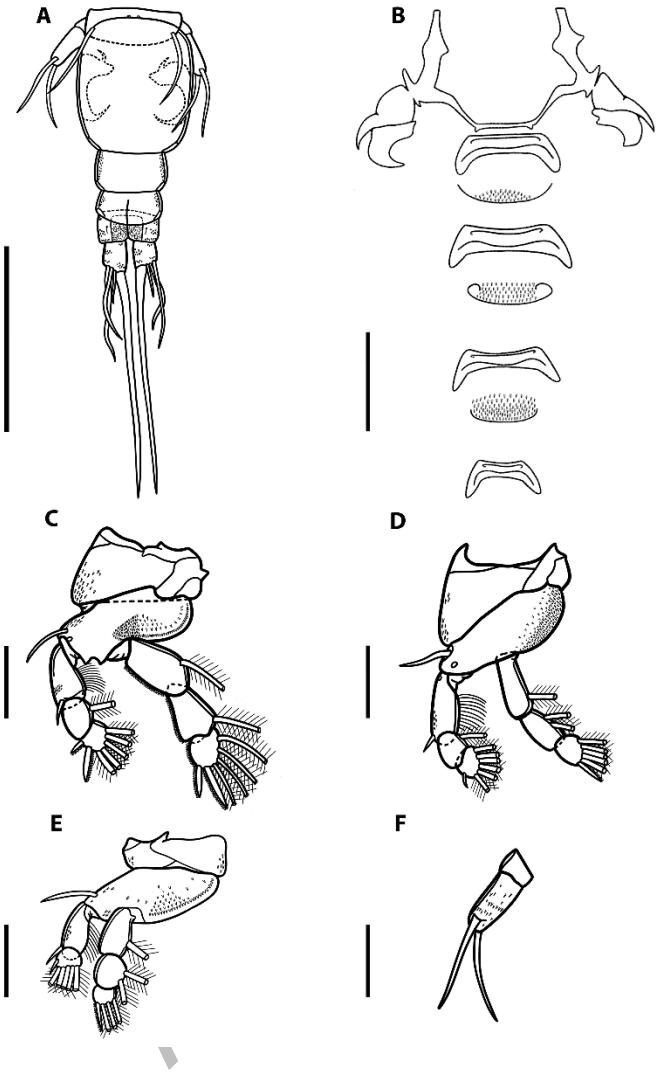

Figure 3. Illustrations of adult female of *Ergasilus arenalbus* n. sp: **A** – urosome, dorsal view; **B** – intercoxal sclerites and interpodal plates; **C** – leg 1; **D** – leg 2 and leg 3; **E** – leg 4; **F** – leg 5. Scale bars: **A** – 200 µm**; B** – 100 µm; **C**–**F** – 50 µm.

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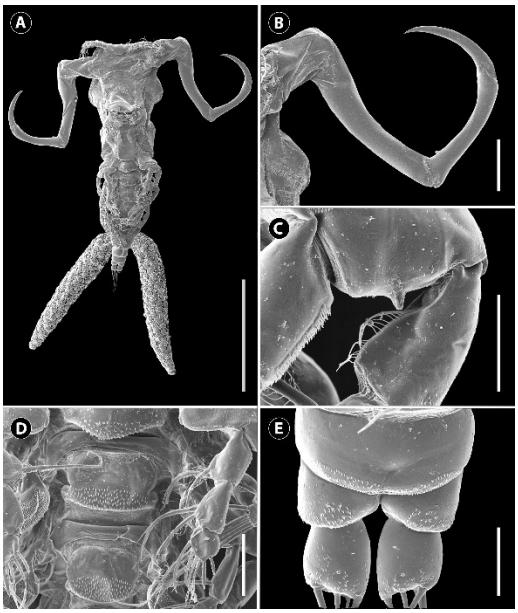

Figure 4. Scanning electron microscope photomicrographs of adult female *Ergasilus arenalbus* n. sp. showing features from the ventral and dorsal view: **A** – entire specimen; **B** – antenna; **C** – base of first leg; **D** – ventral view of interpodal plates; **E** – dorsal view of ornamentation on caudal rami. Scale bars: **A** – 500 µm; **B** – 100 µm; **C**–**E** – 25 µm.

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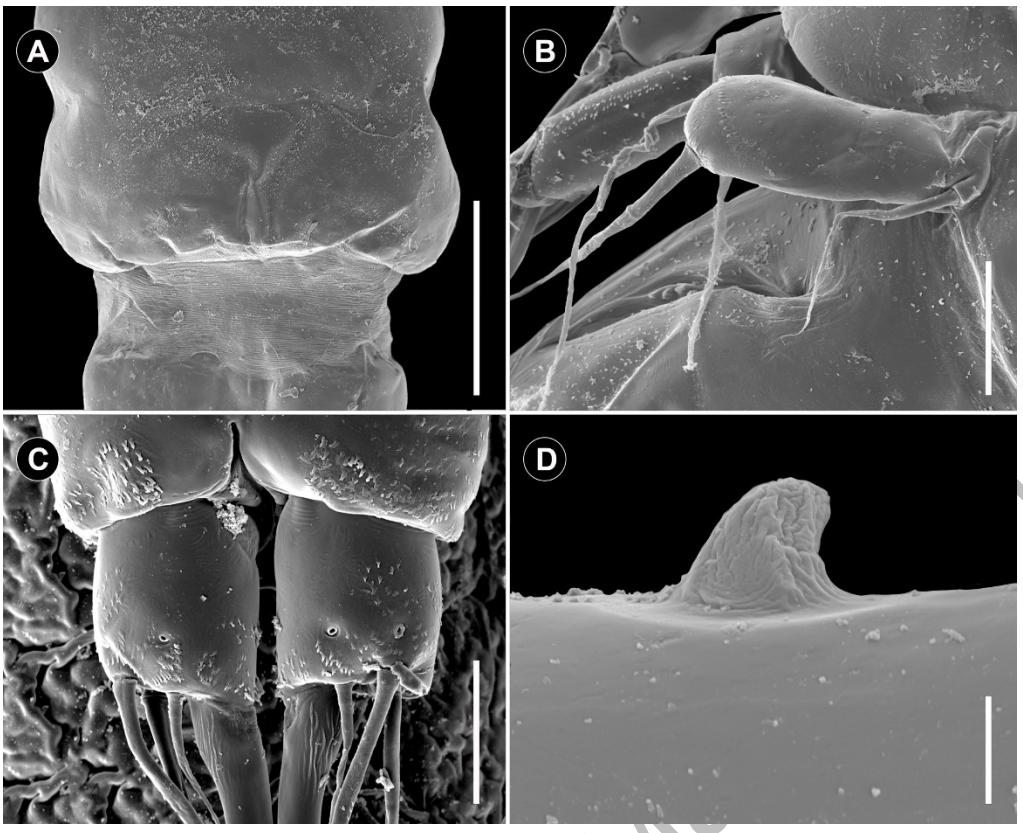

Figure 5. Scanning electron microscope photomicrographs of adult female *Ergasilus arenalbus* n. sp showing features from the ventral and dorsal view: **A** – detail of the cuticular membrane of cephalothorax; **B** – leg 5; **C** – ventral view of detail of the caudal rami; **D** – detail of the spine of the third antennal segment. Scale bars: **A** – 150 µm; **B** – 25 µm; **C** – 20 µm; **D** – 5 µm.

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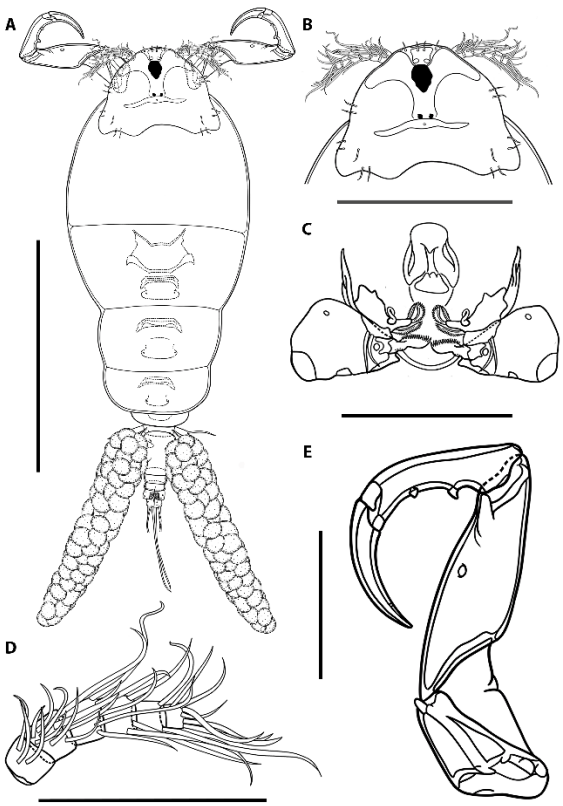

Figure 6. Illustrations of adult female of *Ergasilus chintensis* n. sp: **A** – entire specimen, dorsal view; **B** – detail of the cephalosome, dorsal view; **C** – mouth, mandible, maxillule, and maxilla; **D** – antennule; **E** –antenna. Scale bars: **A** – 500 µm; **B** – 250 µm; **C**–**E** – 100 µm.

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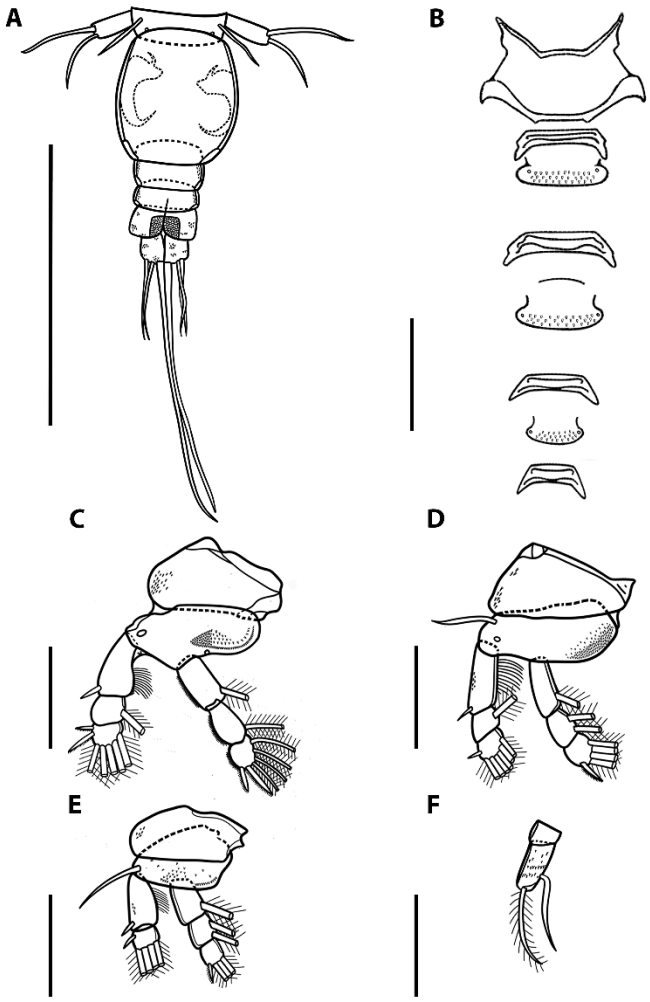

Figure 7. Illustrations of adult female of *Ergasilus chintensis* n. sp: **A** – urosome, dorsal view; **B** – intercoxal sclerites and interpodal plates; **C** – leg 1; **D** – leg 2 and leg 3; **E** – leg 4; **F** – leg 5. Scale bars: **A** – 200 μm; **B** – 100 μm; **C**–**F** – 50 μm.

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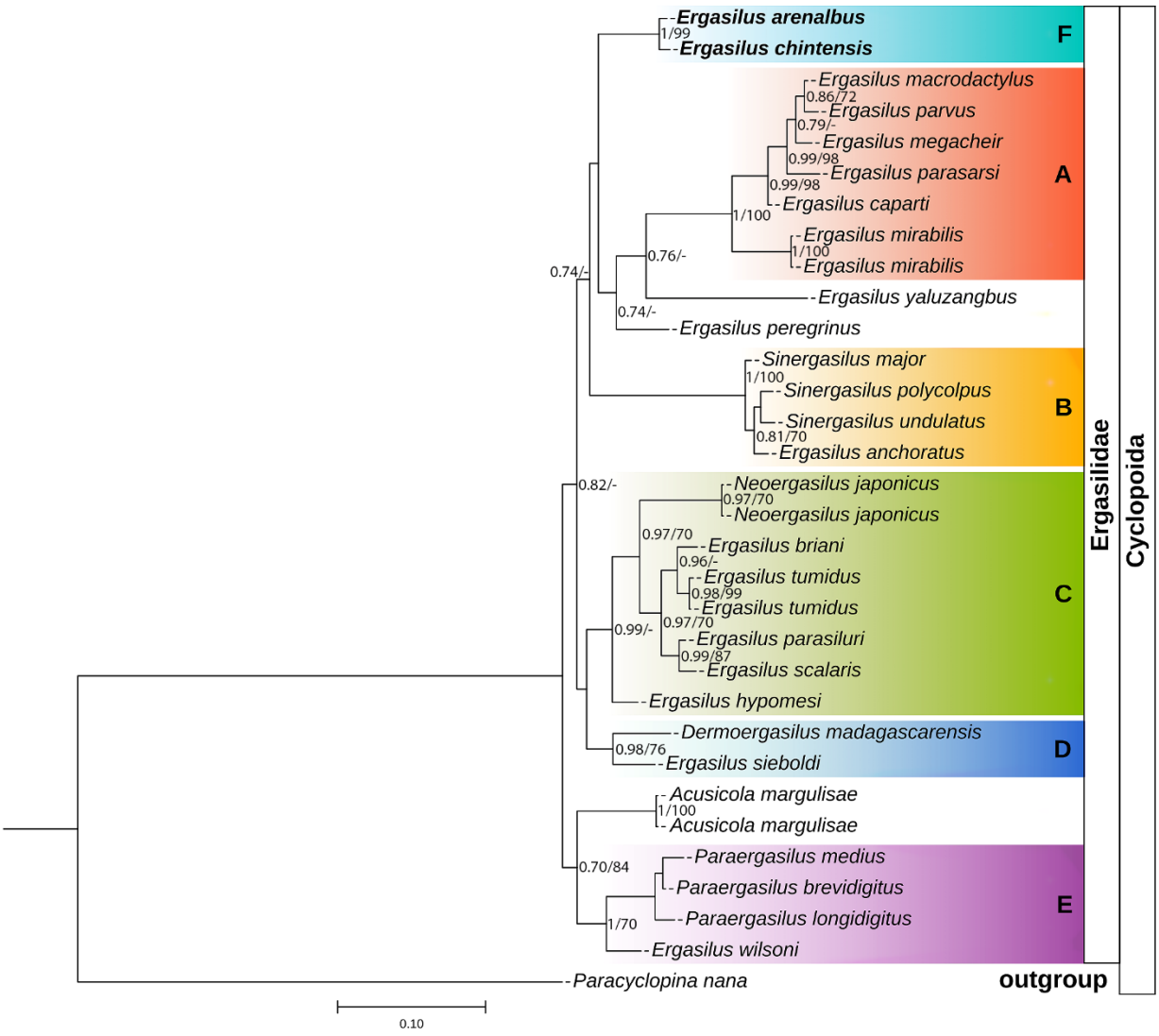

Figure 8. Phylogenetic tree of Ergasilidae copepods based on partial 28S rRNA gene alignments. Newly generated sequences for *Ergasilus arenalbus* n. sp. and *Ergasilus chintensis* n. sp. are provided in bold. Nodal support presented above or below branches for Bayesian Inference (>0.7) and Maximum Likelihood (>70%) analyses (BI/ML). Dashes indicate values below 0.7 and 70%, respectively. *Paracyclopina nana* Smirnov, 1935, was used as the outgroup.

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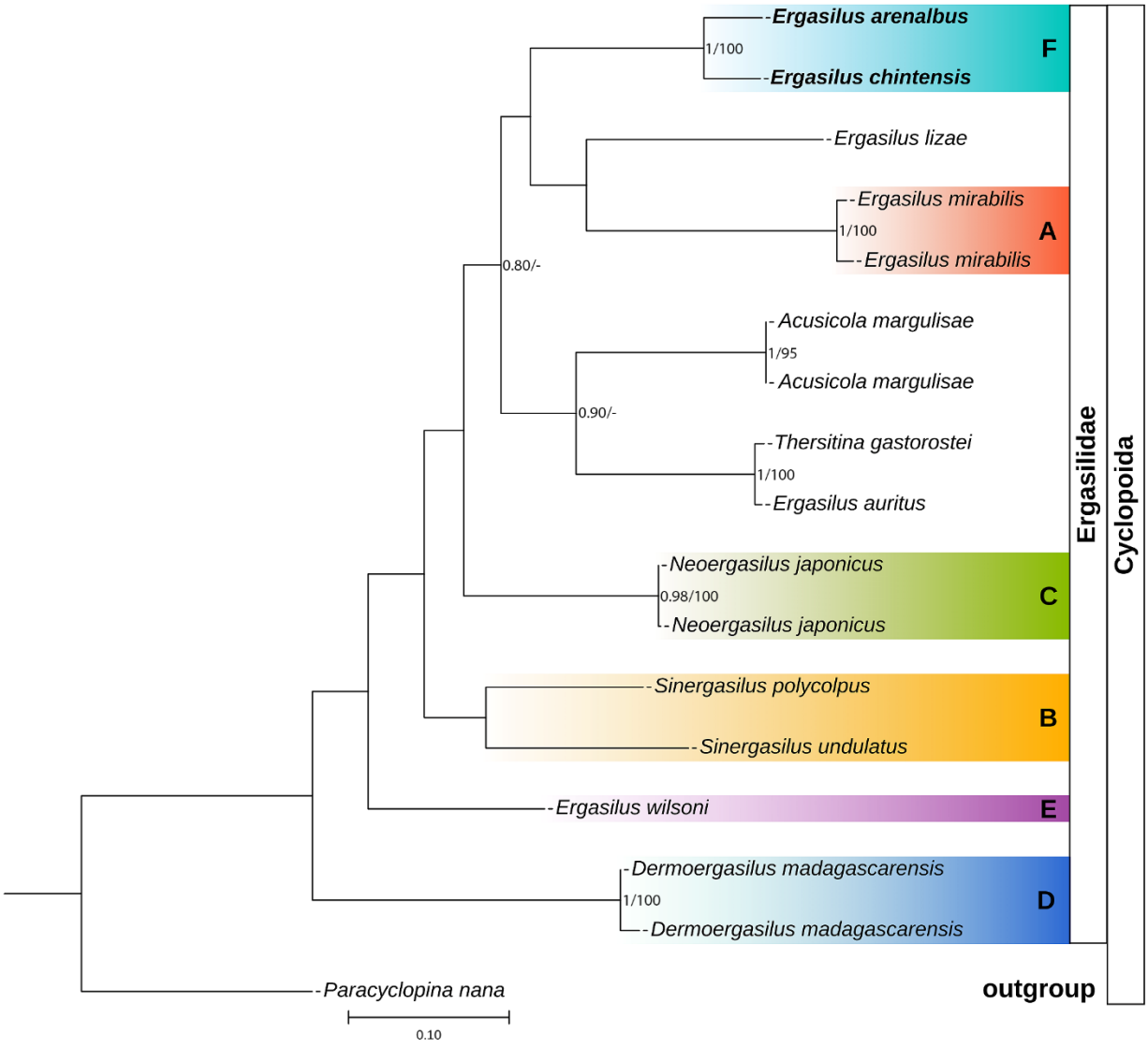

Figure 9. Phylogenetic tree of Ergasilidae copepods based on partial COI mtDNA gene alignments. Newly generated sequences for *Ergasilus arenalbus* n. sp. and *Ergasilus chintensis* n. sp. are provided in bold. Nodal support presented above or below branches for Bayesian Inference (>0.7) and Maximum Likelihood (>70%) analyses (BI/ML). Dashes indicate values below 0.7 and 70%, respectively. *Paracyclopina nana* Smirnov, 1935, was used as the outgroup.