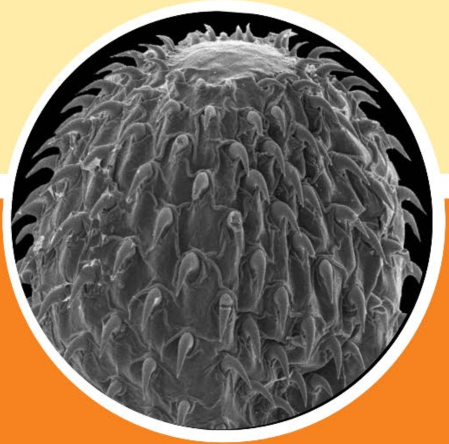
Versión Impresa:
ISSN 1816-0719

Versión en Línea:
ISSN 1994-9073

Versión CD-ROM:
ISSN 1994-9081

The Biologist
(Lima)

VOL. 23, JAN-JUL 2025, Suplemento Especial 2



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AUSPICIADO POR:

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ESCUELA PROFESIONAL DE BIOLOGÍA,
FACULTAD DE CIENCIAS NATURALES Y MATEMÁTICAS,
UNIVERSIDAD NACIONAL FERERICO VILLAREAL

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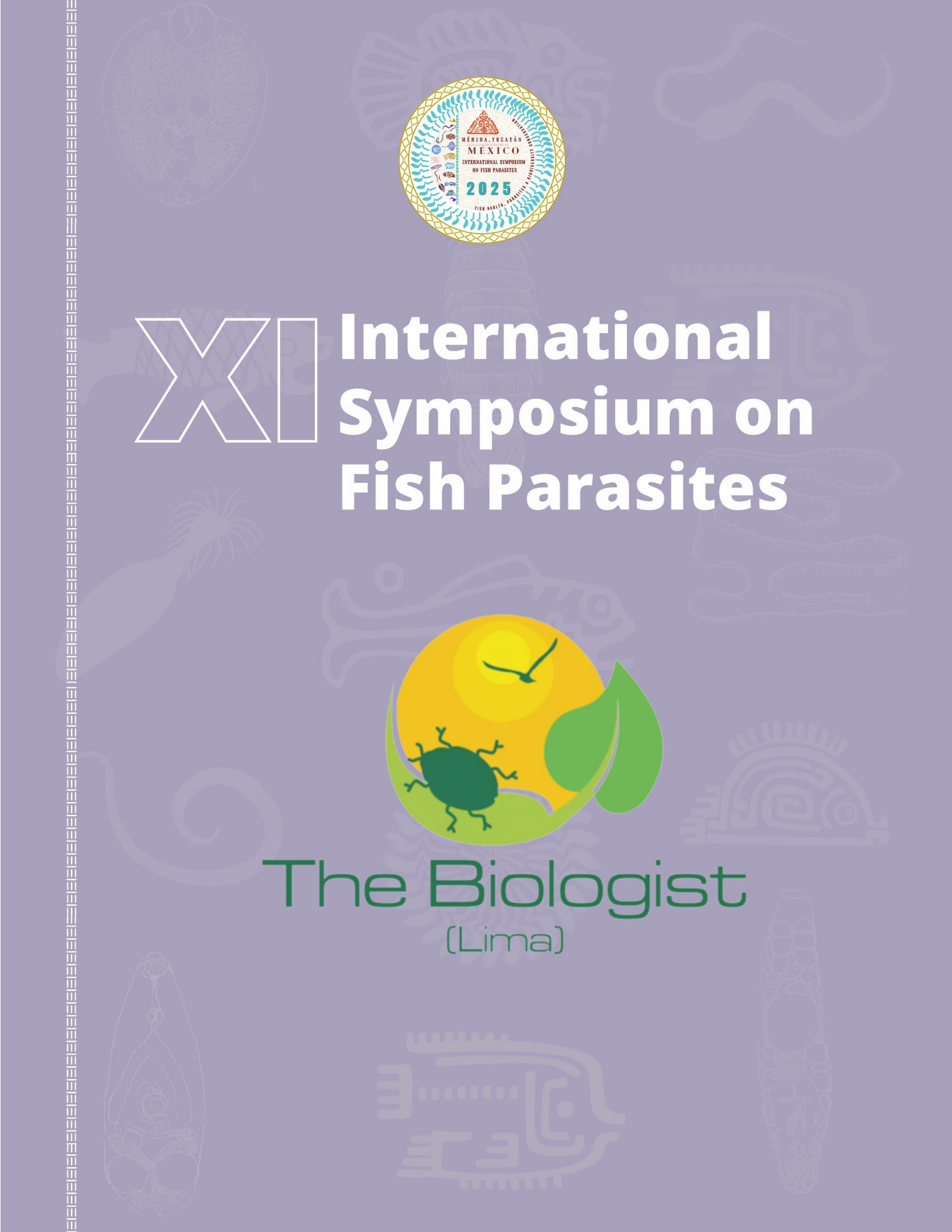

XI International Symposium on Fish Parasites

The Biologist
(Lima)

XI International Symposium on Fish Parasites
"Fish Health, Parasites and Biodiversity Conservation"

ISFP XI-2025

January 20th-24th, 2025.
Centro Cultural Universitario
Universidad Autónoma de Yucatán

Mérida, Yucatán, México

The Biologist (Lima), 2025, Vol. 23, jan-jul.
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por las fotografías utilizadas en las portadas.

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XI International Symposium on fish Parasites
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ISFP XI-2025

ISSN Versión Impresa: 1816-0719, ISSN Versión En línea 1994-9073, ISSN Versión CD-ROM 1994-9081

La Revista The Biologist (Lima) se terminó de diagramar electrónicamente el 10 de enero de 2025

Dirección:
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Página Web: https://revistas.unfv.edu.pe/index.php/rtb
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Revista The Biologist (Lima)

Volumen 23, Suplemento Especial 1, 2025

La Revista The Biologist (Lima) [Biologist (Lima)] publicada por la Escuela Profesional de Biología, Facultad de Ciencias Naturales y Matemática de la Universidad Nacional Federico Villarreal (EPBFCCNM- UNFV), es una publicación de periodicidad semestral (se publica en enero y julio) y todos sus artículos son arbitrados por pares académicos y en forma anónima, tiene como objetivo publicar la producción científica en todos los aspectos de la investigación biológica, salud y de ciencias ambientales en trabajos de investigación originales y revisión de tópicos de importancia biológica, en salud y en ciencias ambientales. El contenido de la revista está dirigido a especialistas e investigadores. Los artículos sometidos deben ser originales e inéditos y no deben estar simultáneamente sometidos para publicación en otra revista. El proceso editorial se desarrolla en varias fases, una evaluación preliminar por el comité editorial y luego a pares académicos externos, cuya decisión definirá la aceptación o no de la publicación. La Revista The Biologist (Lima) requiere a los autores que cedan la propiedad de sus derechos de autor, para que su artículo sea reproducidos, publicados y transmitidos públicamente en cualquier forma o medio con fines exclusivamente científicos y sin fines de lucro. La información que contiene la Revista es de responsabilidad exclusiva de los autores que la proporcionan y no compromete la posición de EPB-FCCNM-UNFV o de los editores.

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Keynote speakers

Isabel Blasco-Costa
Natural History Museum of Geneva, Switzerland
Parasite biodiversity and eco-evolution in aquatic systems

Chelsea Wood
School of Aquatic and Fishery Science, University of Washington, U.S.A.
Parasite ecology in marine and freshwater ecosystems, and parasite conservation

Gabriela Tomas Jerônimo
Faculdade de Ciências Agrárias, Universidade Federal do Amazonas, Brazil.
Fish Parasites and aquaculture

Anindo Choudhury
St. Norbert College, De Pere, Wisconsin, U.S.A.
Historical biogeography of freshwater fish parasites

Víctor Vidal-Martínez
Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional Unidad Mérida, Mexico
Environmental parasitology

Keynote speaker

VIDAL-MARTÍNEZ V.M.

Laboratorio de Patología Acuática, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional (CINVESTAV–IPN) Unidad Mérida, Carretera antigua a Progreso Km. 6, 97310 Mérida, Yucatán, México

Víctor Manuel Vidal-Martínez is a Research Professor in the Department of Sea Resources of CINVESTAV Mérida, Mexico from which he was Director from 2022 to 2024. He received his bachelor's degree as a biologist from the National University of Mexico (1988, México), his MSc in Marine Biology from Cinvestav-IPN Mérida (1990, México), and his PhD in Biological Sciences from the University of Exeter (1995, UK). His research focuses on parasite taxonomy, community ecology and environmental indicators. He is author of more than 110 peer-reviewed publications, 8 book chapters and 2 books. Many of these papers are related to the use of parasites as bioindicators of environmental health, and to diseases in wild and farmed aquatic organisms. He has supervised 9 PhD, 14 MSc and 12 undergraduate students. He was also Member and Vice-President of the Aquatic Animal Health Standards Commission of the World Organisation for Animal Health (OIE) (France; 2009-2015). He is member of the Mexican National Research System (SNI) Level 3 (Mexico; 1992-present). Recently (November, 2024) he has been appointed by the Mexican Government as Director General of the Mexican Institute for Research on Sustainable Fisheries and Aquaculture.

Keynote speaker

JERÔNIMO G.T.

Faculty of Agricultural Sciences, Federal University of Amazonas (UFAM), Amazonas, Brazil

Dr. Gabriela Tomas Jerônimo is Brazilian, with a degree in Aquaculture Engineering, a Master's, and a PhD in Aquaculture and Fisheries Resources. Her academic and professional trajectory is marked by a strong commitment to research and teaching, especially in the field of pathology and health of aquatic organisms. With extensive experience in aquaculture health, Dr. Jerônimo focuses her research on diseases affecting aquatic organisms and the development of strategies for the prevention and control of pathologies in aquaculture systems. In recent years, she has conducted research with an emphasis on parasites of Amazonian fish, identifying pathogenic agents, investigating their potential as bioindicators of environmental quality, and evaluating dietary supplementation with immunostimulants, phytotherapeutics, and food additives to improve performance, health, and hematological and immunological parameters in animals exposed to adversity or experimental challenges. Her scientific output includes publications in high-impact journals, as well as books and chapters that serve as references for researchers and professionals in the aquaculture sector. Gabriela is also an active professor in higher education, sharing her knowledge on aquaculture health, microbial ecology, and sustainability in the production of aquatic organisms. As a researcher, she has significantly contributed to the advancement of aquaculture, merging science and practice to promote the health and well-being of aquatic organisms, with direct impacts on environmental sustainability and the economic development of the sector.

Keynote speaker

BLASCO-COSTA I.

Department of Invertebrates, Natural History Museum of Geneva, Geneva, Switzerland.

Isabel Blasco-Costa is originally from Spain, where she conducted her studies and PhD. She obtained a European Marie Skłodowska-Curie scholarship that took her to work in New Zealand and Czech Republic before stablishing as an independent researcher at the Natural History Museum in Geneva, Switzerland, where she is now the curator-in-chief of the Invertebrates collection. Isabel has a sound and long-standing interest in biodiversity of parasitic organisms and the evolutionary and ecological drivers of host-parasite associations. She combines classical taxonomy and phylogenetic methods with population genomics and ecology to investigate how life cycle strategies, transmission modes and ecological processes influence the genetic make-up of parasite species, their distribution and biogeographic patterns, and ultimately species diversification.

Keynote speaker

CHOUDHURY A.

Division of Natural Sciences, St. Norbert College, De Pere, Wisconsin, USA

Anindo Choudhury is a professor of Biology and Environmental Science at St. NorbertCollege in the United States. Anindo's research is focused on the Diversity, Systematics, Biogeography and Biology of freshwater fish parasites. Anindo earned his bachelor's degree in Zoology from India, and his master's and PhD degrees in Canada. He was an NSERC post-doctoral fellow at the University of Toronto, and a research associate at the USGS National Wildlife Health Center in Madison, U.S.A., before taking up a faculty position at St. Norbert College. Anindo is currently President Elect of the American Society of Parasitologists. Anindo's research spans a wide geographic range, from the systematics and biogeography of fish parasites in the north temperate regions to the fish parasites in Central America, including more recently, invasive species in the Panama Canal. This research, facilitated by on-going collaborations with scientists in the U.S., Canada, the Czech Republic, Mexico, India, Panama and the Philippines, has helped develop a deeper, yet always incomplete, understanding of contemporary and historical processes the shape fish-parasite associations.

Keynote speaker

WOOD C.L.

School of Aquatic and Fishery Sciences, University of Washington

Chelsea Wood is an Associate Professor in the School of Aquatic and Fishery Sciences at the University of Washington, as well as her department's Associate Director and Graduate Program Coordinator. Her research addresses the question: is the world wormier than it used to be? That is, she is interested in the historical ecology of parasitism. She uses multiple techniques to resurrect information on parasite populations of the past, supplying historical context that can reveal whether and why the abundance of parasites is changing through time. She received her bachelor's degree from Dartmouth College and her PhD from Stanford University and she completed postdocs at the University of Michigan and the University of Colorado before starting her current position in Seattle.

Thematic areas

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9. ACANTHOCEPHALA WORKSHOP

1. KEYNOTE SPEAKERS

KEYNOTE SPEAKERS

1. THE METAZOAN PARASITE COMMUNITIES OF FLOUNDERS AS INDICATORS OF CHEMICAL POLLUTION IN THE SOUTHERN GULF OF MEXICO: TAXONOMIC AND TRAIT-BASED APPROACHES. Vidal-Martínez V.M. Laboratorio de Patología Acuática, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional (CINVESTAV–IPN) Unidad Mérida, Carretera antigua a Progreso Km. 6, 97310 Mérida, Yucatán, México
2. MOLECULES FOR PARASITE DIVERSITY: ARE WE MISSING THE BOAT?. Blasco-Costa I. Department of Invertebrates, Natural History Museum of Geneva, Geneva, Switzerland
3. HISTORICAL BIOGEOGRAPHY OF FRESHWATER FISH PARASITES. Choudhury A. Division of Natural Sciences, St. Norbert College, De Pere, Wisconsin, USA
4. IS THE WORLD WORMIER THAN IT USED TO BE? ANSWERS FROM A NEW SUB-DISCIPLINE: THE HISTORICAL ECOLOGY OF PARASITISM. Wood C.L. School of Aquatic and Fishery Sciences, University of Washington
5. FISH PARASITES AND AQUACULTURE: AN EXPERIENCE FROM BRAZIL, A TROPICAL COUNTRY. Jerônimo G.T. Faculty of Agricultural Sciences, Federal University of Amazonas (UFAM), Amazonas, Brazil

THE METAZOAN PARASITE COMMUNITIES OF FLOUNDERS AS INDICATORS OF CHEMICAL POLLUTION IN THE SOUTHERN GULF OF MEXICO: TAXONOMIC AND TRAIT-BASED APPROACHES

Vidal-Martínez V.M.

Laboratorio de Patología Acuática, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional (CINVESTAV–IPN) Unidad Mérida, Carretera antigua a Progreso Km. 6, 97310 Mérida, Yucatán, México
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Metazoan parasite species composition changes with an increase in geographical distance, but not their functional traits. We compared the performance of the taxonomy and functional traits of metazoan parasites as bioindicators of chemical pollution along the continental shelf of the South Gulf of Mexico (sGOM). Parasites were obtained from Syacium gunteri and Syacium papillosum, together with hydrocarbons, heavy metals and physicochemical variables from water and sediments during 12 oceanographic cruises. We compared regions without oil extraction: Veracruz-Tamaulipas (VT) and Yucatan shelf (YS) and one with it, north-western end of YS to Coatzacoalcos, Veracruz (NYV). In addition to taxonomy, the trait-based approach community-weighted means (CWM) was performed. Species richness was compared between regions using rarefaction curves, and the taxonomic and trait composition between regions were compared using multivariate analyses. The relationships between taxonomy, traits and environmental variables were tested using BIOENV. We identified 57 species and body tegument, transmission, feeding mode, life stage and attachment organs as informative traits. By rarefaction, VT and YS had higher species richness than NYV for both hosts, but there were questionable values due to the small fish sample size. Except for YS, significant parasite community variability was detected by PERMANOVA using taxonomy and CWM for all regions, hosts and interactions. The same group of larval species was detected by SIMPER for regions and hosts, suggesting low functional turnover. BIOENV showed that polyaromatic hydrocarbons explained most of the variability. Taxonomy and functional traits produced similar explained variance, but the latter saved time analysis and financial resources.

MOLECULES FOR PARASITE DIVERSITY: ARE WE MISSING THE BOAT?

Blasco-Costa I.

Department of Invertebrates, Natural History Museum of Geneva, Geneva, Switzerland.

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Since the onset of molecular methods, a variety of molecular approaches have been employed to detect genetic variation in a quest to stablish relationships among taxa, assess species diversity, spatial distribution of genetic variants and matching life cycle stages. Based on a review of the literature, I will discuss the trends on the use of approaches for molecular data generation and of molecular markers in the last decades. In the process, I will identify early genome-wide molecular approaches that have lacked assimilation in the field of parasitology, or that are doing so at a slow pace. I will discuss the consequences of missing out on these tools for our understanding of parasite diversity. Through a series of examples, I argue that it is time to embrace novel approaches that allow characterization of multiple loci across the genome to study parasite diversity. These approaches provide a wealth of data upon which to ground our conclusions, while allowing to compare to existing sequence data in repositories. Thus, prior information generated over the last three decades on classical ribosomal and mitochondrial markers is still useful and should be complemented with novel, more comprehensive datasets. While the classic sanger sequencing approach continues to be practical and sufficient in many cases, I recommend incorporating genome-wide approaches in a series of specific cases.

HISTORICAL BIOGEOGRAPHY OF FRESHWATER FISH PARASITES

Choudhury A.

Division of Natural Sciences, St. Norbert College, De Pere, Wisconsin, USA

Anindo.Choudhury@snc.edu

The North American continent, comprising Mexico, USA and Canada, is home to a rich and diverse assemblage of some 1200 fishes in its inland waters. This fauna comprises families showing various combinations of endemism, vicariant Holarctic distribution, marine derivation, and continental colonization as part of the Great American Biotic Interchange (GABI). The parasite fauna of North American freshwater fishes is likewise rich and diverse. Here, I explore the historical biogeography of these enduring host-parasite associations in the tradition of parascript studies and drawing on on-going research in the Pacific Northwest and Panama. Patterns of associations of the core helminth fauna (emphasis on trematodes, cestodes and nematodes) in selected groups of fishes are examined/reviewed. Results suggest that: a) hypotheses of the historical biogeography of earlier branching Holarctic fish families (sturgeons, salmonids) are largely consistent with the biogeography of their parasite faunas; b) more recent clades such as percids and cyprinids show considerable deviation from this pattern; c) catostomids and ictalurids harbor a well-established core helminth fauna consistent with their biogeographical affinities; d) there is increasing evidence of localized radiation and host-shifting in the southern transitional regions; and e) the historical colonization of North American freshwater environments from marine environments by ancestors of species-rich host groups such as Centrarchidae (sunfishes and basses) allow us to develop testable hypotheses of parasite relationships. I will conclude with thoughts about future directions.

IS THE WORLD WORMIER THAN IT USED TO BE? ANSWERS FROM A NEW SUB-DISCIPLINE: THE HISTORICAL ECOLOGY OF PARASITISM

Wood C.L.

School of Aquatic and Fishery Sciences, University of Washington

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Many disease ecologists and conservation biologists believe that the world is wormier than it used to be – that is, that parasites are increasing in abundance through time. This argument is intuitively appealing. Ecologists typically see parasitic infections, through their association with disease, as a negative endpoint, and are accustomed to attributing negative outcomes to human interference in the environment, so it slots neatly into our worldview that habitat destruction, biodiversity loss, and climate change should have the collateral consequence of causing outbreaks of parasites. But surprisingly, the hypothesis that parasites are increasing in abundance through time remains entirely untested for the vast majority of wildlife parasite species. Historical data on parasites are nearly impossible to find, which leaves no baseline against which to compare contemporary parasite burdens. If we want to know whether the world is wormier than it used to be, there is only one major research avenue that will lead to an answer: parasitological examination of specimens preserved in natural history collections. Natural history specimens are “parasite time capsules” that give ecologists the opportunity to test whether infectious disease is on the rise and to identify the driving forces. In this talk, I will discuss the potential of this approach and present some of its recent insights. I anticipate that parasitological examination of natural history specimens will facilitate major advances in a new sub-discipline – the historical ecology of parasitism – and will finally answer the question: is the world wormier than it used to be?

FISH PARASITES AND AQUACULTURE: AN EXPERIENCE FROM BRAZIL, A TROPICAL COUNTRY

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Aquaculture is recognized as an important ally in the promotion of food safety worldwide, and its production in Brazil contributes to this scenario, considering that it has shown a notable growth in the last years. However, with the expansion of production, the intensification of the aquaculture systems is inevitable, which increases the vulnerability to dissemination of infectious diseases among the animals, especially because pathogens such as parasites are present. The main parasites and the way in which these pathogens have interfered in the production of fish in Brazil, a vast territory with diverse biomes and ecosystems, will be the main point of this lecture. According to Brazilian experiences, it's been proved that the parasites respond to environmental changes, which facilitate secondary infections, affecting the zootechnical performance and also cause mortalities. Among the most important parasites to be considered in Brazilian fish farming, we could mention the following protozoa: trichodinids, *Chilodonella*, *Ichthyophthirius*, *Piscinoodinium* and *Epistylis*. We can also consider the monogenean helminths, the lerneids, ergasilids and branchiura crustaceans – such as *Dolops* and *Argulus* – as well as internal acanthocephalan parasites. Thus, the adopted preventive measures will be presented, as well as the efforts that have been employed by different research groups in Brazil in the development of new technologies for the control of parasitosis in farmed fishes.

Thematic areas

2. BIODIVERSITY SURVEYS

ORAL PRESENTATIONS

(Please note the name and institution shown in this list are those of the person presenting the talk, who may not be the first author; the complete author list including all institutional affiliations are shown with the full abstract)

1. FIRST SURVEY OF PLATYHELMINTH ECTOPARASITES FROM THE GILLS OF *Diplodus capensis* (SMITH) (TELEOSTEI: SPARIDAE) FROM THE COAST OF SOUTH AFRICA. Acosta A.A. et al. Water Research Group, Unit for Environmental Sciences and Management, Potchefstroom Campus, South Africa
2. IF YOU BUILD IT, THEY WILL COME: PARASITES AS BIODIVERSITY SURROGATES FOR HABITAT RESTORATION. Blakeslee A.M.H. et al. Department of Microbiology, Oregon State University, Corvallis, Oregon, USA
3. eDNA METABARCODING IN MYXOZOAN RESEARCH: NEW PERSPECTIVES. Fiala I. et al. Biology Centre, Czech Academy of Sciences, České Budějovice, Czech Republic
4. HAVING IMPACT ON MONITORING PARASITE DIVERSITY – FIRST EXPERIMENTAL RESULTS EVALUATING EDNA AS AN INTEGRATIVE TOOL FOR STUDYING FISH PARASITES. Hupalo K. et al. Department of Aquatic Ecology, University of Duisburg-Essen, Germany Centre for Water and Environmental Research, University of Duisburg-Essen, Germany
5. HISTORY, ADVANCES, AND PERSPECTIVES ON THE STUDY OF THE PARASITIC TRICHODINIDS ASSOCIATED WITH FISHES IN MEXICO. Islas Ortega A.G. et al. Facultad de Ciencias, Universidad Nacional Autónoma de México (UNAM), México
6. A REPORT OF FRESHWATER *Kudoa* sp. FROM THE HEART OF ARCTIC CHARR S*alvelinus alpinus* IN ICELAND. Kristmundsson Á. et al. Institute for Experimental Pathology at Keldur, University of Iceland, Iceland
7. GENETIC DIVERSITY OF THE ANISAKID NEMATODE *Contracaecum osculatum* sp. B OVER A TEMPORAL SCALE: A TOOL FOR UNDERSTANDING AND MONITORING A PARASITE SPECIES RESPONSE TO THE GLOBAL CHANGE OF THE ARCTIC MARINE ECOSYSTEM? Mattiucci S. et al. Department of Public Health and Infectious Diseases Sapienza-University of Rome Piazzale, Rome, Italy
8. PARASITES AND DIET OF THE INVASIVE FISH *Oncorhynchus mykiss* FROM LAKE CHUNGARÁ, NORTHERN CHILE: SPILLBACK EFFECT? Oliva M.E. et al. Instituto Ciencias Naturales Alexander von Humboldt, Universidad de Antofagasta, Chile
9. IS THE RICHNESS OF METAZOAN ENDOPARASITES HIGHER IN DEEP SEA FISHES THAN SHALLOW WATERS FISHES: THE CASE OF THE HUMBOLDT CURRENT SYSTEM AND ATACAMA TRENCH. Oliva M.E. et al. Instituto Ciencias Naturales Alexander von Humboldt, Universidad de Antofagasta, Chile
10. AN AMERICAN TAPEWORM OF THE BLACK BULLHEAD (*Ameiurus melas*) (SILURIFORMES: ICTALURIDAE) INVADES EUROPE. Oros M. et al. Institute of Parasitology, Slovak Academy of Sciences, Košice, Slovakia
11. LINKING DIGENEANS IN FRESHWATER FISH TO THEIR SNAIL HOSTS IN PUERTO RICO. Perales-Macedo D.M.B. & Locke S.A. Departamento de Biología del Recinto Universitario de Mayagüez de la Universidad de Puerto Rico, Puerto Rico
12. TINY HOSTS, MIGHTY LOAD: THE PARASITE DIVERSITY OF *Chiloglanis pretoriae* AND *Amphilius uranoscopus* FROM THE LIMPOPO RIVER SYSTEM, SOUTH AFRICA. Přikrylová I. et al. Department of Biodiversity University of Limpopo, Sovenga, South Africa
13. MONOGENEAN DIVERSITY ON NORTH AMERICAN CATOSTOMIDS (CYPRINIFORMES): FIRST INSIGHTS INTO THE PHYLOGENY OF THE PSEUDOMURRAYTREMATIDAE. Řehulková E. et al. Department of Botany and Zoology, Faculty of Science, Masaryk University, Brno, Czech Republic
14. YOURS, MINE AND OURS: GYRODACTYLIDS INFECTING THE FISH COMMUNITY IN AN ENCLOSED NEOTROPICAL LAKE. Rubio Godoy M. et al. Instituto de Ecología, A.C., México
15. UNSEEN AND UNCOUNTED: THE HIDDEN GAPS IN FISH PARASITE DETECTION. Shamsi S. Gulbali Institute, Charles Sturt University, Australia
16. POLLUTION'S RIPPLE EFFECT: UNRAVELING PESTICIDE INFLUENCE ON FISH PARASITE DIVERSITY IN SOUTH AFRICA'S COASTAL ECOSYSTEMS. Van Der Spuy L. et al. Water Research Group, North-West University, South Africa
17. THE ROLE OF MARINE PROTECTED AREAS IN THE CONSERVATION OF PARASITE DIVERSITY: METAZOAN PARASITE COMMUNITY COMPOSITION OF *Diplodus capensis* (SMITH) (TELEOSTEI, SPARIDAE) AS A CASE STUDY. Welicky R.L. et al. Water Research Group, North-West University, South Africa

POSTER PRESENTATIONS

(Please note the name and institution shown in this list are those of the person presenting the poster, who may not be the first author; the complete author list including all institutional affiliations are shown with the full abstract)

1. LITTLE-KNOWN MEMBERS OF THE KELP FOREST: HELMINTH PARASITES OF THE GARIBALDI DAMSELFISH *Hypsypops rubicundus* (POMACENTRIDAE) FROM BAHÍA DE TODOS SANTOS, BAJA CALIFORNIA, MEXICO. Aguilar Aguilar R. et al. Laboratorio de Zoología Acuática, Facultad de Ciencias, Universidad Nacional Autónoma de México, Mexico
2. METAZOAN PARASITE FAUNA OF JUVENILES OF THE WHITE MULLET, *Mugil curema* (MUGILIDAE) IN COASTAL LAGOONS OF NORTHERN YUCATÁN PENINSULA, MEXICO. Andrade-Gómez L. et al. Laboratorio de Parasitología y Medicina de la Conservación, Escuela Nacional de Estudios Superiores Unidad Mérida Universidad Nacional Autónoma de México (UNAM), Mérida, Yucatán, Mexico
3. MORPHOLOGICAL AND MOLECULAR DESCRIPTION OF *Contracaecum quadripapillatum* LARVAE INFECTING NORTH AFRICAN CATFISH (*Clarias gariepinus*) FROM LAKE HULA, ISRAEL. Davidovich N. et al. Israeli Veterinary Services, Bet Dagan, Israel
4. METAZOAN PARASITES OF THE OCELLATED KILLIFISH *Floridichtys polyommus* THROUGHOUT ITS DISTRIBUTION RANGE IN THE YUCATÁN PENINSULA, MÉXICO. Espínola-Novelo J.F. et al. Laboratorio de Parasitología y Medicina de la Conservación, Escuela Nacional de Estudios Superiores Unidad Mérida, Universidad Nacional Autónoma de México (UNAM), México
5. COMMUNITIES OF METAZOAN PARASITES OF *Haemulon aurolineatum* FROM THE NORTH OF THE YUCATAN PENINSULA, MEXICO. García Teh J.G. et al. Laboratorio de Patología Acuática, Departamento de Recursos del Mar, Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Unidad Mérida, Yucatán, México
6. UPDATED RECORDS OF PARASITIC ISOPODS OF MARINE FISHES OF THE TROPICAL EASTERN PACIFIC. Grano Maldonado M. I. et al. Facultad de Ciencias del Mar, Universidad Autónoma de Sinaloa, Mazatlán, Sinaloa, México
7. METAZOAN PARASITES IN SNAPPERS (PERCIFORMES: LUTJANIDAE) FROM THE SOUTHERN GULF OF MEXICO AND MEXICAN CARIBBEAN. Hernández Olascoaga A. et al. Departamento de Sistemática y Ecología Acuática, El Colegio de la Frontera Sur, unidad Chetumal, Chetumal, Quintan Roo, México
8. NEGLECTED DIVERSITY OF CATSHARK PARASITES: UNVEILING THE PARASITE COMMUNITY OF ICELANDIC PENTANCHIDS. Dallarés, S. et al. Departamento de Biología Animal, de Biologia Vegetal i d’Ecologia, Universitat Autònoma de Barcelona, Barcelona, Spain
9. PARASITE BIOBLITZ: TRACKING HELMINTH LIFE CYCLES ACROSS A BROAD TAXONOMIC SCALE AND INTERCONNECTED ECOSYSTEMS. Hill Spanik K.M. et al. College of Charleston, Charleston, South Carolina, USA
10. EXPLORING PARASITE DIVERSITY ACROSS AN ECOLOGICAL GRADIENT USING ENVIRONMENTAL DNA METABARCODING. Hill Spanik K.M. et al. College of Charleston, Charleston, South Carolina, USA
11. METAZOAN PARASITES OF THE “LUMPTAIL SEAROBIN” *Prionotus stephanophrys* (LOCKINGTON, 1881) (PERCIFORMES: TRIGLIDAE) FROM THE MARINE COAST FROM PERU. Iannacone O.J.I. et al. Universidad Ricardo Palma, Lima-Perú
12. METAZOAN PARASITE GUILD COMMUNITY IN *Astronotus ocellatus, Cichla monoculus, Hoplas malabaricus* AND *Calophysus macropterus* IN SAN LORENZO, DATEM DEL MARAÑÓN (LORETO – PERU): ICHTHYOZOONOTIC RISK IN PERUVIAN AMAZONIA. Iannacone O.J.I. et al. Universidad Ricardo Palma, Lima-Perú
13. EXPLORING AFRICAN FRESHWATER FISH *Trypanosoma* WITH MOLECULAR AND MORPHOLOGICAL TOOLS. Le Roux C. et al. Water Research Group, Unit for Environmental Sciences and Management, North-West University, Potchefstroom, South Africa
14. TRYPANOSOMATIDS ASSOCIATES TO *Hypanus americanus* (Hildebrand & Schroeder, 1928) IN NORTH VERACRUZ, MEXICO. Luquín García C. et al. Posgrado en Manejo de Ecosistemas Marinos y Costeros, Facultad de Ciencias Biológicas y Agropecuarias región Poza Rica-Tuxpan, Universidad Veracruzana, Tuxpan de Rodríguez Cano, Veracruz, México
15. PARASITES OF STRANDING MARINE ORGANISMS BY THE HARMFUL ALGAE BLOOM PHENOMENON “RED TIDE” ON THE COASTS OF YUCATAN. May Sosa G.A. et al. Tecnológico Nacional de México Sede Conkal, Yucatán, Mexico

16. MONOPISTHOCOTYLAN PARASITES OF TWO ORNAMENTAL FISH OF CICHLIDAE*, Astonotus ocellatus*, AND *Pterophylum scalare*, RECEIVED FROM INDONESIA, SRI LANKA, AND THAILAND. Přikrylová I. et al. DSI-NRF SARChI Chair, Department of Biodiversity, University of Limpopo, South Africa
17. *Diplostomum* (DIGENEA: DIPLOSTOMIDAE) IN THE MOLECULAR ERA: STILL A LONG ROAD AHEAD. Repullés Albelda A. et al. Marine Zoology Unit, Cavanilles Institute of Biodiversity and Evolutionary Biology, Science Park, University of Valencia, Paterna, Spain
18. DIVERSITY OF MYXOSPOREAN PARASITES (CNIDARIA, MYXOZOA) INFECTING GUINE SOLE STOCKS FROM NORTHEAST ATLANTIC WATERS. Rocha S. et al. ICBAS School of Medicine and Biomedical Sciences, University of Porto, Porto, Portugal
19. EVALUATING THE USEFULNESS OF THE DNA METABARCODING TECHNIQUE FOR ASSESSING MYXOSPOREAN INFECTION IN OLIGOCHAETES. Rocha S. et al. ICBAS School of Medicine and Biomedical Sciences, University of Porto, Porto, Portugal
20. HELMINTH PARASITES OF THE YELLOWFINNED MOJARRA, *Gerres cinereus* (Walbaum, 1792) IN TWO COASTAL LAGOONS “LA CARBONERA” AND CELESTUN OF YUCATAN, MEXICO. Rodríguez M.A.P. et al. Departamento de Biología Marina, Campus de Ciencias Biológicas y Agropecuarias, Universidad Autónoma de Yucatán, Mexico
21. DIVERSITY OF OPECOELID TREMATODES (OPECOELIDAE) FROM THE AREA OF CALIFORNIA: HISTORY, CHALLENGES AND PERSPECTIVES. Santillán-Pérez et al. Laboratorio de Zoología Acuática, Facultad de Ciencias, Universidad Nacional Autónoma de México, Mexico
22. A REVIEW OF THE PARASITE COMMUNITIES IN THE STINGRAY GENUS *Hypanus*. Sargent S. et al. Halmos College of Arts and Sciences, Nova Southeastern University, Dania Beach, FL USA
23. UNRAVELING PARASITE DIVERSITY ALONG A RIVER STREAM IN THE STATE OF SÃO PAULO, BRAZIL. Silva R.J. et al. Section of Parasitology, Institute of Biosciences, São Paulo State University (UNESP), Botucatu, São Paulo state, Brazil
24. PARASITOLOGICAL FINDINGS IN OCEAN SUNFISH STRANDED ALONG THE ITALIAN COASTS. Tedesco P. et al. Department of Veterinary Medical Sciences, Alma Mater Studiorum, University of Bologna, Italy
25. NEMATODE DIVERSITY OF THE ELUSIVE ENDEMIC FISHES OF THE AUSTROGLANIDIDAE IN SOUTH AFRICA. Truter M. et al. Water Research Group, Unit for Environmental Sciences and Management, North-West University, Potchefstroom, South Africa
26. DIGENEANS OF MEDITERRANEAN SPARIDS: A WELL-STUDIED SYSTEM WITH A NEED FOR AN IN-DEPTH REVISION. Villar-Torres M. et al. Marine Zoology Unit, Cavanilles Institute of Biodiversity and Evolutionary Biology, Science Park, University of Valencia, Paterna, Spain
27. MONORCHIIDS OF SOUTH AFRICAN HAEMULID FISHES, WITH CHARACTERISATIONS OF TWO NEW TAXA. Yong R.Q.Y. et al. Water Research Group, Unit of Environmental Sciences & Management, North-West University, Potchefstroom, South Africa
28. PARASITE FAUNA OF THE INVASIVE LIONFISH *Pterois volitans* (PISCES: SCORPAENIDAE) IN TULUM (BAHIA PRINCIPE) MEXICAN CARIBBEAN. Aznar C.E.G. et al. Instituto de Ciencias del Mar y Limnología, Estación “El Carmen”, Universidad Nacional Autónoma de México. Ciudad del Carmen, Campeche, México

ORAL PRESENTATIONS

FIRST SURVEY OF PLATYHELMINTH ECTOPARASITES FROM THE GILLS OF *Diplodus capensis* (SMITH) (TELEOSTEI: SPARIDAE) FROM THE COAST OF SOUTH AFRICA

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South Africa is recognised as a megadiverse country, with approximately 2,000 fish species along its coast, many of which are endemic. However, the true diversity of the parasitic fauna associated with these fishes remains underexplored. *Diplodus capensis* (Smith) (Teleostei: Sparidae), a southern African endemic, dwells near-shore habitats from Angola to Mozambique. In this study on the ectoparasitic platyhelminths of *D. capensis* collected from five localities along the South African coast, six species of the Diplectanidae (Monopisthocotyla: Dactylogyridea) were found parasitising the gill filaments of this host. Based on morphological and molecular analyses, these dactylogyrids were identified as six distinct species of *Lamellodiscus*: *L. donatellae*, *L. elegans*, *L. furcosus*, *L. ignoratus*, *L. mirandus*, and *Lamellodiscus* sp 1. Partial rDNA sequences of the 18S were newly generated for these six *Lamellodiscus* species, with the first 28S for *L. donatellae*, *L. ignoratus*, and *L. mirandus*. Additionally, two microcotylids (Polyopisthocotyla: Microcotylidae) were also found on the gills of *D. capensis*. These were morphologically and molecularly identified as *Atriaster* n. sp. 1 and *Polylabris* n. sp. 1. Sequences of the partial rDNA 28S and mitochondrial COI genes were newly generated for both species. This study represents the first comprehensive survey of polyopisthocotylan and monopisthocotylan ectoparasites of *D. capensis* from the South African coast. Moreover, it is the first record of *Lamellodiscus* spp. in marine fish from South Africa, and the first molecular characterisation of microcotylids from this region, significantly contributing to the knowledge of the platyhelminth diversity in South African waters.

IF YOU BUILD IT, THEY WILL COME: PARASITES AS BIODIVERSITY SURROGATES FOR HABITAT RESTORATION

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Parasites have been identified as key bioindicators for myriad conservation related questions, including serving as surrogate taxa for community biodiversity. Here, we discuss the importance of including parasites in investigations of community biodiversity as well as their utility in demonstrating temporal changes in community assembly, species composition, and taxa diversity following oyster reef restoration. Our study examined restoration efforts along the coast of North Carolina, USA, where we surveyed for free-living and parasite biodiversity in reef-resident snails, crustaceans, and fish hosts. We found restoration had a significant positive effect on biodiversity, with reef design having a strong influence on recruiting hosts and parasites. In addition, using a space-for-time design, we found parasite taxa were better indicators of community succession than free-living species—presumably because parasites better represent the diversity of taxa that must be present in a system for parasites to complete life cycles compared with the taxa we were actually able to sample using standard biodiversity surveying techniques (e.g., passive fish and crustacean samplers). Altogether, our study adds to the growing literature demonstrating the utility of parasites as surrogate taxa for biodiversity assessments across numerous systems and questions, providing another tool in our toolbox for evaluating the success of conservation efforts that aim to enhance biodiversity, such as habitat restoration.

eDNA METABARCODING IN MYXOZOAN RESEARCH: NEW PERSPECTIVES

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Amplicon sequencing and metabarcoding of environmental DNA (eDNA) have become powerful methods for identifying the diversity of eukaryotic organisms, including parasites. Myxozoan diversity can be effectively studied through the release of their infectious spores into the aquatic environment from their hosts. By capturing these spores in water or sediment samples, we can assess parasite diversity in specific localities without the need for host collection and parasitic dissection. In this study, we optimized sampling methods and extrapolated estimates of true myxozoan diversity at a given site using a small stream as a model system. We then applied our eDNA metabarcoding approach to: i) monitor changes in myxozoan diversity along the entire length of a larger river; ii) assess seasonal variability in myxozoan abundance in fish-rearing ponds (via detection of fish-infecting actinospores); iii) compare myxozoan diversity in a watercourse connected to a system of intensively farmed ponds with that in an unaffected watercourse; iv) evaluate the distribution of myxozoans in localities near fish-rearing farms versus more distant locations on the same stream. We successfully detected a large number of myxozoan species, particularly at sites with high fish densities. This has enabled us to assess myxozoan richness at specific locations and address the key questions of our broader ecological research. Our findings demonstrate that eDNA metabarcoding is a powerful tool for investigating various ecological aspects of myxozoan research. Research support: MEYS, Inter-Action-LUAUS24 (project No. LUAUS24281); Interreg (project No. BYCZ01-020).

HAVING IMPACT ON MONITORING PARASITE DIVERSITY – FIRST EXPERIMENTAL RESULTS EVALUATING EDNA AS AN INTEGRATIVE TOOL FOR STUDYING FISH PARASITES

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Global parasite biodiversity is facing an extinction crisis, with up to 30% of species in each major parasite group predicted to be extinct by 2070. Although parasites can serve as integrative biological indicators of ecosystem responses to global change, parasites remain the most neglected components of biodiversity monitoring and have only recently begun to be considered in conservation discussions. Monitoring of parasite biodiversity is hampered by inefficient tools for its detection, with current methods involving the sacrifice of many hosts. Thus, it is necessary to develop less invasive and non-lethal monitoring approaches. Environmental DNA (eDNA) offers a potential solution, particularly for studying aquatic parasites by allowing them to be detected in environmental matrices without sampling the hosts. Given that eDNA is increasingly used in aquatic biodiversity monitoring worldwide, it offers a great opportunity for obtaining parasite diversity data from existing monitoring programs. Recent literature reviews show that eDNA has proven useful in the detection of single parasite species. However, there is no consensus on the optimal sampling conditions (i.e., filter pore size and water volume) for detecting certain parasite groups. Moreover, there are very few studies targeting multiple parasite species within and across defined parasite groups at once. Here, we will present the first results from an indoor experiment conducted within the framework of the newly acquired project IMPACT where multiple filter types were tested for the simultaneous detection of multiple fish parasite groups using eDNA.

HISTORY, ADVANCES, AND PERSPECTIVES ON THE STUDY OF THE PARASITIC TRICHODINIDS ASSOCIATED WITH FISHES IN MEXICO

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Ciliates of the family Trichodinidae are among the most common fish parasites from both natural and cultured environments. This family comprises a high number of species, which were extensively recorded during the 20th century, mainly for some regions in the world where several specialists established lines of research devoted to the knowledge of these organisms. However, some countries, including Mexico, traditionally have lacked researchers focused on describing those species of protozoans associated with cultured and wild fishes; thereby, the diversity and relevance of trichodinid ciliates in Mexico was practically unknown. For this reason, in Mexico, there were only five records for species of *Trichodina* for the whole 20th century, mainly for exotic introduced fish species. In the last decade, we have aimed to establish a robust research program focused on trichodinids, exploring their diversity through Mexico's epicontinental and marine environments and attending native and exotic cultured or wild fish hosts. During this time, we have contributed to extending the taxonomic knowledge of trichodinid species and to creating the basis of studies involving different biological perspectives such as systematics, biogeography, integrative taxonomy, and biodiversity. These approaches have allowed collaboration with diverse research centres, which have generated new information not only for Mexican aquatic environments, but also from other distant places such as Argentina and South Africa.

A REPORT OF FRESHWATER *Kudoa* sp. FROM THE HEART OF ARCTIC CHARR *Salvelinus alpinus* IN ICELAND

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Arctic charr *Salvelinus alpinus* is a common wild salmonid in Iceland, where it is mostly resident in freshwater lakes and rivers, but also anadromous where it spends a part of its life in marine water. Significant farming of this species has been employed in Iceland since the early 1980s and is at present the world's largest producer with annual production around 6000 tn. Arctic charr were sent to Keldur Institute from a fish farm for routine diagnosis. At this farm, the fish are reared in freshwater which originates from nearby springs. Furthermore, resident Arctic charr and brown trout *Salmo trutta*, were collected from three lakes in Iceland. All fish were subjected to histological examination, and some for molecular analysis. Myxozoan parasites were observed in the heart of all the farmed Arctic charr, and 10% of the Arctic charr from one of the three lakes sampled. No infections were observed in the brown trout. The myxozoan was found in the muscular part of the heart, where it was seen in polysporous plasmodia. The spores were tiny, measuring around 3.5-4.5 µm, each with two polar capsules. PCR using primers designed to be more specific for multivalvulid myxosporeans successfully amplified partial SSU rDNA from extracted DNA samples of infected heart muscle. These amplicons were sequenced and compared to those in available databases, which revealed a >98% similarity to other Kudoid parasites of fish musculature. This is the first report of a kudoid myxozoan from Arctic charr. Furthermore, kudoids have almost exclusively been described from marine waters, rendering this previously unidentified species particularly interesting.

GENETIC DIVERSITY OF THE ANISAKID NEMATODE *Contracaecum osculatum* sp. B OVER A TEMPORAL SCALE: A TOOL FOR UNDERSTANDING AND MONITORING A PARASITE SPECIES RESPONSE TO THE GLOBAL CHANGE OF THE ARCTIC MARINE ECOSYSTEM?

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Global changes in the marine Arctic ecosystem affecting the demography of fish and seal populations may also alter anisakid population size, leading to potential genetic erosion in parasites' gene pools. *Contracaecum osculatum* sp. B is a sibling species of the *C. osculatum* (s.l.) complex parasitizing Arctic and sub-Arctic seals and fish. This study aimed to compare the parasite genetic diversity from these areas, over a 35-year time-scale. Historical (years 1985-1986) specimens from seals were compared with contemporary (years 2021-22) ones sampled from fish in the same areas. They were first identified using mtDNA *cox2* and ITS rDNA and then genotyped at 7 newly developed DNA SSRs loci. High values of genetic diversity at both nuclear and mitochondrial level were observed. Rare alleles lost, allele frequencies reduced at certain SSRs loci, as well as rare haplotypes lost, were found in the current samples. In contrast, they showed unique alleles and haplotypes not observed in the historic ones. Demographic inference based on genetic data over the studied period showed an initial parasite population decrease, followed by a period of demographic stability, and finally, a population increase in recent years. Similar fluctuations have been documented in the demography of the parasite's hosts over the same temporal scale. The occurrence of new polymorphisms at the analysed gene loci could be also be the result of adaptive response to selective pressures of environmental variables (i.e sea temperature) in the studied area. Genetic polymorphisms of anisakids over spatio-temporal scales may aid in puzzling out and monitoring global change in this marine ecosystem.

PARASITES AND DIET OF THE INVASIVE FISH *Oncorhynchus mykiss* FROM LAKE CHUNGARÁ, NORTHERN CHILE: SPILLBACK EFFECT?

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The rainbow trout, *Oncorhynchus mykiss*, is one of the most notorious invasive species worldwide. Naturally, *O. mykiss* ranges from the Bering Sea (Alaska) to Baja California. In Chile, *O. mykiss* since its introduction has a distribution from Chungara lake (18S°) to Tierra del Fuego (51S°). Parasitological studies are crucial in invasion ecology. Introducing a new species into an area can either increase (spillback effect and spillover effect) or decrease (dilution effect) the parasite load on native hosts. We examined the species composition of parasites and the diet of *O. mykiss* from Lake Chungará. Forty specimens were collected and dissected during May 2023 for parasitological and diet studies. The parasites were collected, fixed, and identified using conventional parasitological techniques. Our results revealed five parasite taxa: two cestode larvae (Diphyllobothriidea gen. sp. and Cyclophyllidea gen. sp.), an acanthocephalan larva (*Pseudocorynosoma* sp.), a digenean metacercaria (*Tylodelphis* sp.), and an adult nematode (*Hedruris* sp.). High prevalence rates were found for Cyclophyllidea gen. sp. (59%) and Diphyllobothriidea gen. sp. (48%). Regarding stomach content, the amphipods *Hyalella* sp., the beetles Corixidae, and the fish *Orestias chungariensis* were the most preferred prey-items in the diet of *O. mykiss*, with prevalence rates of 86%, 52%, and 52%, respectively. Canonical correspondence analyses linked the endoparasites to their diet, suggesting interactions between Cyclophyllidea gen. sp. with *Hyalella* sp. and Diphyllobothriidea gen. sp. and *Tylodelphis* sp. with *O. chungariensis*. These prey-items likely form part of the life-cycle of these endoparasites. We conclude that *O. mykiss* is acquiring parasites from the native fauna. Funding: "Sistema articulado de investigación en cambio climático y sustentabilidad de zonas costeras de Chile", Código "RED21992" CUECh and ANID Millennium Science Initiative NCN 2021_056: Millennium Nucleus of Austral Invasive Salmonids.

IS THE RICHNESS OF METAZOAN ENDOPARASITES HIGHER IN DEEP SEA FISHES THAN SHALLOW WATERS FISHES: THE CASE OF THE HUMBOLDT CURRENT SYSTEM AND ATACAMA TRENCH

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The coasts of the Southeastern Pacific Ocean are influenced by the Humboldt Current Large Marine Ecosystem and by the presence of strong upwelling that in turn generate a Minimum Oxygen Zone (MOZ) with impact in both, benthic and pelagic communities. Due logistic challenges, the diversity of Atacama Trench remain virtually unknown, including parasites of deep-sea fishes. We analyzed a total of 1495 specimens of deep-sea fishes (> 200 m depth) belonging to nine species (range 61 – 360 specimens per host species), obtained as by-catch of the deep sea fishery of the Patagonian tooth fish, as well as 2947 specimens of shallow waters fishes (15 species, range 38 – 584 specimens per host species) in order to test if metazoan parasites of fishes are affected by the MOZ. Our data indicated that parasite richness is not affected by sample effort. The richness of the whole parasite fauna does not differ (but marginally) between deep sea fishes (15.6 species) and shallow waters fishes (10.9 species) (F = 4,18, p = 0.053) and the richness of ectoparasites (deep sea = 3.7, shallow water = 5.3) does not differ significantly (F = 2,62, p = 0.12) but richness of trophically transmitted parasites is significantly higher in deeps sea fishes (11.8 species) than in shallow water fishes (5,6 species) (F = 12,8, p = 0.002). The higher value for trophically transmitted parasites suggests a high richness of invertebrates (but also vertebrates) that are intermediate host for metazoan parasites of deep-sea fishes.

AN AMERICAN TAPEWORM OF THE BLACK BULLHEAD (*Ameiurus melas*) (SILURIFORMES: ICTALURIDAE) INVADES EUROPE

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The black bullhead *Ameiurus melas* is an invasive fish species that has been introduced into Europe. In this account, proteocephalid tapeworms of the subfamily Essexiellinae, which are specific intestinal parasites of ictalurid catfishes in North America, are reported from *A. melas* in the Danube River in Slovakia. Tapeworms were found in nine out of 11 black bullhead examined in 2023 (prevalence 82%) and in two of 15 in 2024 (prevalence 13%). The overall prevalence was 42% in both years and the mean intensity of infection was 13, ranging from 1 to 44 specimens in infected fish. The highest intensity of infection (44 worms per fish) was found in a 16.5 cm long black bullhead. According to the *in situ* observations, neither pathological changes at the tapeworm site of attachment nor poor physiological conditions were observed in the infected fish. Molecular phylogenetic analysis based on sequences of 28S rRNA and COI genes revealed that the tapeworms from Slovakia are almost identical to *Corallotaenia* sp. 1 from *A. melas* in Oklahoma and Wisconsin, USA, and are morphologically similar. This is the second report on the occurrence of essexielline tapeworms in Europe after 35 years. The relatively frequent occurrence of these tapeworms in black bullheads from one of the largest European rivers connecting Western and Eastern Europe is alarming, and their further spread of these parasites throughout Europe is likely. This study was supported by the Slovak Research and Development Agency (APVV SK-CZ-RD-21-0078), the Ministry of Education, Youth and Sports of the Czech Republic (project LUASK 22045), and Bilateral Mobility Project CAS-SAS-2022-05 and SAV 23-08.

LINKING DIGENEANS IN FRESHWATER FISH TO THEIR SNAIL HOSTS IN PUERTO RICO

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Digeneans are among the most common macroparasites in freshwater fish, generally in Puerto Rico, where this study takes place. For years our lab has been surveying digeneans in fish in several small waterbodies, and in this study, we attempted to find molecular links to the cercaria in sympatric streams and lagoons. Freshwater mollusks, including *Tarebia granifera, Melanoides tuberculata, Marisa cornuarietis,* and ancylinid limpets, were surveyed from 2021-2024 and trematodes were identified through morphological characteristics and molecular analyses (28S and COI sequences), leading to the identification of fish-borne digeneans such as *Stellantchasmus, Renicola, Dulcitransversotrema, Centrocestus, Posthodiplostomum,* and Echinochasmidae gen. sp. The cercariae and intramolluscan stages of digeneans such as *Centrocestus, Posthodiplostomum, Dulcitransversotrema,* and *Stellantchasmus* were found in both snails and fish, but several taxa (*Ascocotyle, Uvulifer, Pseudoparacreptotrema, Cryptogonimidae,* and *Saccocoelioides*) were found exclusively in fish, belonging to families not detected in mollusk surveys. In addition, fish-borne digeneans *Renicola* and Echinochasmidae gen. sp. were found only in snails. These results indicate that surveys of digeneans in mollusks can provide information that is both incomplete (not capturing the full range of trematodes in fish) and complementary (detection of taxa overlooked in fish). Combined surveys are a valuable approach for understanding trematode diversity and transmission within an ecosystem.

TINY HOST, MIGHTY LOAD: THE PARASITE DIVERSITY OF *Chiloglanis pretoriae* AND *Amphilius uranoscopus* FROM THE LIMPOPO RIVER SYSTEM, SOUTH AFRICA

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Chiloglanis pretoriae Van der Horst, 1931 (Mochokidae) and *Amphilius uranoscopus* (Pfeffer, 1889) (Amphilidae) are relatively small, endemic freshwater fish species of Southern Africa with limited information on their parasite diversity. Between September 2021 and May 2022, a total of 171 fishes were collected from four rivers (Mutshundudi, Nwanedi, Lutanandwa, and Politsi) within the Limpopo River System using electrofishing. This included 127 *C. pretoriae* and 44 *A. uranoscopus*. Standard methods were used for collection, fixation and preservation of parasites. Species richness and parasite diversity from fish from the four rivers were calculated using Margalef's richness index and Shannon-Weiner diversity index, respectively. Three parasitic groups (Monopisthocotylea, Digenea and Hirudinea) were found from *C. pretoriae* which comprised of two ectoparasite species (Dactylogyridae gen. sp. and an unidentified leech) and three endoparasite species (*Clinostomum* sp., Diplostomidae gen. sp. larva and Cephalogonimidae gen. sp.). Two endoparasite groups, digeneans (*Clinostomum* sp., *Uvulifer* sp. and Cephalogonimidae gen. sp.) and nematodes (*Labeonema* sp., *Contracaecum* sp., *Rhabdochona* sp., *Gendria* sp. and *Gendria cf. paski*) were recorded from *A. uranoscopus*. Results from this study include new species as well as new host and locality records contributing to global parasite distribution records. This research was supported by the DSI-NRF SARChI Chair in Ecosystem Health (No.101054).

MONOGENEAN DIVERSITY ON NORTH AMERICAN CATOSTOMIDS (CYPRINIFORMES): FIRST INSIGHTS INTO THE PHYLOGENY OF THE PSEUDOMURRAYTREMATIDAE

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Catostomoidei (suckers) are one of four suborders of Cypriniformes with a holarctic distribution, with the greatest diversity occurring in North America (78 spp.) and only two species occurring in Asia. In order to address the considerable lack of information on monogeneans that parasitize these fishes, a thorough research survey was initiated in 2018. So far, nineteen catostomid species from nine US states, the Canadian province of Québec, and northern Mexico have been surveyed. Fourteen of them were positive for monogeneans of the Pseudomurraytrematidae. A total of 25 species across three genera of this family (*Anonchohaptor*, *Icelanonchohaptor*, *Pseudomurraytrema*) were collected from the gills and/or fins of the examined catostomid hosts. *Pseudomurraytrema* was the most diverse genus with fourteen species, followed by *Anonchohaptor* with seven species and *Icelanonchohaptor* with four species. The greatest species richness of monogeneans was recorded on *Hypentelium nigricans* (four species of *Pseudomurraytrema*). Phylogenetic reconstructions based on sequencing of nuclear genes (18S, ITS1 and 28S rDNA) demonstrated the monophyly of the Pseudomurraytrematidae with high support and showed that this family shares a close phylogenetic relationship with the Diplectanidae within the Dactylogyrinea. *Pseudomurraytrema asiaticum* from the Chinese sucker was in a basal position relative to all Nearctic pseudomurraytrematids. The Nearctic pseudomurraytrematids formed two clades, one including species of *Pseudomurraytrema* and the other including species of *Anonchohaptor* and *Icelanonchohaptor*. Terminal position of two species of *Icelanonchohaptor* within the clade containing *Anonchohaptor* spp., together with their morphological similarity to the latter genus, suggests synonymy between the two genera.

YOURS, MINE AND OURS: GYRODACTYLIDS INFECTING THE FISH COMMUNITY IN AN ENCLOSED NEOTROPICAL LAKE

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Catemaco is a Neotropical volcanic lake in the Papaloapan river basin in southern Veracruz, Mexico, and home to several freshwater fishes, including endemic species. Over an action-packed weekend in October 2023, we collected native and introduced fishes in different localities all around Catemaco – the place where the first transfer of exotic monogeneans to native fishes was documented in Mexico at the turn of the XXI century. A quarter century later, we characterized the species of *Gyrodactylus* infecting native and introduced fishes from 7 families (Poeciliidae, Cichlidae, Characidae, Clupeidae, Heptateridae, Eleotridae and Loricariidae); in total, we sampled 1041 fishes and recovered 675 gyrodactylids. Poeciliids and cichlids are the most speciose fish families in Catemaco, with five species each; and both host several species of *Gyrodactylus*. Following our tongue-in-cheek title, host-parasite associations do indeed exhibit this “Yours, mine and ours” pattern: while some gyrodactylid species are strictly associated to certain fish species/genera, others are able to infect fishes from different families. Thus, while *G. unami* is restricted to *Poeciliopsis* spp., some gyrodactylids are able to infect several species within fish families (e.g. *G. xtachuna/pseudobullatarudis* infecting 4 out of 5 poeciliids sampled) and, in the other extreme, some species are able to parasitize members of different fish families – like *G. chiapaneco*, which we recorded from poeciliids and characids in Catemaco, and this species is also known to infect profundulid fishes in Mexico. Cichlid fishes had their own suite of gyrodactylids; none of them invasive species in this survey.

UNSEEN AND UNCOUNTED: THE HIDDEN GAPS IN FISH PARASITE DETECTION

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Postmortem examination of fish for parasites is critical in fields such as species identification, parasite prevalence, population dynamics, seafood safety, fisheries resource management, international trade, and biosecurity. However, the effectiveness of current methods in accurately detecting parasites during postmortem exams remains uncertain. This presentation reviews the common techniques used in postmortem parasitological investigations, assessing their strengths and limitations, and identifies overlooked aspects that can reduce detection accuracy. Furthermore, examples are provided to demonstrate how a deeper understanding of parasite life cycles, host behaviour, and interactions between parasite species can significantly improve the accuracy and efficiency of postmortem examinations. Addressing these gaps is essential not only for improving parasite detection but also for obtaining a more realistic understanding of host-parasite relationships. Ultimately, this knowledge leads to wiser decision-making in the stewardship of the environment, ensuring better management of natural resources and ecosystem health.

POLLUTION'S RIPPLE EFFECT: UNRAVELING PESTICIDE INFLUENCE ON FISH PARASITE DIVERSITY IN SOUTH AFRICA'S COASTAL ECOSYSTEMS

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South Africa's coastal regions are increasingly affected by pollutants from industrial and agricultural runoff, sewage discharge, stormwater drainage, and effluents from informal settlements. Among these stressors, persistent organic pollutants (POPs), such as polychlorinated biphenyls (PCBs) and organochlorine pesticides (OCPs), have significant ecological impacts. While many studies have examined pesticides' effects on aquatic organisms, research on the influence of POPs on marine fish parasite communities is limited. This study investigates the impact of POP contamination on parasite community structure within the Evileye blaasop, *Amblyrhynchote honckenii* (Bloch), along the South African coast. Fifty-five fish were collected from five sites within, adjacent to, and outside marine protected areas (MPAs). Metazoan parasite communities were identified, and OCP and PCB concentrations were measured in the fish liver tissues. Eighteen parasite taxa were recorded across seven taxonomic groups: Acanthocephala (2), Cestoda (3), Copepoda (4), Isopoda (2), Monogenea (1), Nematoda (2) and Trematoda (4). Higher POP concentrations were detected in fish from non-MPA sites, while fish from MPAs and near-MPA sites exhibited lower levels. Nine OCP and 16 PCB congeners were detected, with significant shifts in parasite communities at sites with elevated POP levels. Endoparasites such as acanthocephalans, cestodes, and trematodes declined in non-MPA sites, while resilient species like nematodes and cymothoid isopods thrived. Parasite cysts increased in high-POP areas but were rare in MPAs. This study highlights the persistence of PCBs and OCPs in coastal ecosystems and their complex effects on parasite dynamics, offering insights into pollution's long-term impacts on biodiversity and ecosystem health.

THE ROLE OF MARINE PROTECTED AREAS IN THE CONSERVATION OF PARASITE DIVERSITY: METAZOAN PARASITE COMMUNITY COMPOSITION OF *Diplodus capensis* (SMITH) (TELEOSTEI, SPARIDAE) AS A CASE STUDY

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Whereas the community composition of fishes has been vastly studied, research examining the community position of parasites that live within fishes is limited. Even more sparse are data that can work towards describing what drives parasite community composition and distribution. To collect such baseline data, we examined the metazoan parasite communities of *Diplodus capensis* (Smith) (Teleostei: Sparidae), a fish endemic to the coast of southern Africa, and which is heavily relied on for subsistence and sport angling. We were also curious to know if metazoan parasite communities of *D. capensis* varied between marine protected areas (MPAs) and non-MPAs, to assess whether parasites are also inadvertently being protected by these conservation efforts. Accordingly, we collected sixty specimens of *D. capensis* across two MPAs and three non-MPAs and performed parasitological dissections of the fish. The parasites were identified using morphological and molecular analyses. Using these data, we analysed the alpha and beta diversity of the parasites among fish, among localities, and between protection statuses using Shannon-Wiener and Simpson's diversity metrics, and Bray Curtis dissimilarity metrics, respectively. Thirty parasite taxa were identified, and the proportional abundance of parasite taxa varied greatly across fish. Non-MPAs had a slightly higher richness of parasitic taxa with fewer dominant families than MPAs, albeit a less even richness compared to the MPAs. This is one of the first studies to describe the relationship between protection status and parasite biodiversity in South Africa and provides foundational data for understanding how protected areas might influence the distribution of parasitic taxa.

POSTER PRESENTATIONS

LITTLE-KNOWN MEMBERS OF THE KELP FOREST: HELMINTH PARASITES OF THE GARIBALDI DAMSELFISH *Hypsypops rubicundus* (POMACENTRIDAE) FROM BAHÍA DE TODOS SANTOS, BAJA CALIFORNIA, MEXICO

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The Garibaldi Damselfish *Hypsypops rubicundus* is distributed from Monterey Bay, California (USA), to Magdalena Bay, Baja California Sur (Mexico), including the Guadalupe Island. It is a pomacentrid fish commonly found over rocky bottoms on exposed or semi-protected coasts having clear water, on rocky reefs with crevices and small caves for cover, and on columns of giant kelp for searching for food. In this study, twenty individuals of the Garibaldi Damselfish were examined for parasites. Six helminth taxa were found. Three of these were trematodes of the family Opecoelidae. We also recorded an additional trematode species belonging to the family Hemiuridae. The helminthological fauna of *Hypsipops rubicundus* is complemented by one nematode of Cucullanidae and one acanthocephalan of Transvenidae. All the species were found as adults, and except for one, all the helminth species represent new host records. These findings suggest that the study of hosts from open-sea Mexican waters will allow the recording of a still unrevealed diversity of parasite species.

METAZOAN PARASITE FAUNA OF JUVENILES OF THE WHITE MULLET, *Mugil curema* (MUGILIDAE) IN COASTAL LAGOONS OF NORTHERN YUCATÁN PENINSULA, MEXICO

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The white mullet, *Mugil curema* (Valenciennes) (Mugilidae) is an omnivorous fish that mostly feeds on microscopic or filamentous algae and other planktonic organisms. This euryhaline fish is mostly distributed along the Pacific and Atlantic coasts of the Americas, and the eastern Atlantic coast of Africa. Mullets represent an important economic resource for the artisanal fisheries in Mexico. We analyzed 73 individuals of *M. curema* (TL=7–33 cm) between 2022 and 2023 in four coastal lagoons of the northern Yucatán Peninsula. Metazoan parasites were identified using molecular and morphological data. Twenty-one parasite taxa were found, including monogenean (1), trematodes (15), acanthocephalan (1), nematodes (2), argulid (1), and copepod (1). Of these parasites, 59% were adult forms and 41% were larval stages. The prevalence and mean intensity of infection were calculated for each parasite taxon in each locality. The monogenean *Ligophorus yucatanensis* reached the highest prevalence of infection, whereas the metacercariae of the trematode *Bucephalus* sp. was the most abundant. These two species were the only recorded in the four localities. We report the metacercariae of *Saccularina* sp., *Cardiocephaloides medioconiger* and *Mesostephanus microbursa* for the first time in the white mullet. Finally, we compared the parasite species richness of *M. curema* in Yucatán with regard to that recorded for this host species across the Atlantic coast of the Americas. This study was supported by the program PAPIIT-UNAM IN200824.

MORPHOLOGICAL AND MOLECULAR DESCRIPTION OF *Contracaecum quadripapillatum* LARVAE INFECTING NORTH AFRICAN CATFISH (*Clarias gariepinus*) FROM LAKE HULA, ISRAEL

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Within the family Anisakidae, the genera *Anisakis*, *Pseudoterranova* and *Contracaecum* are considered of zoonotic or potentially zoonotic importance. With over 60 described species, the genus *Contracaecum* is the most speciose of the three; however, the distribution of *Contracaecum* species in fish hosts is underreported. In April 2024, we conducted a parasitological survey on the ichthyofauna of Lake Hula, located in the northeastern part of Israel. Among the different native and non-native fish species considered for the study, 18 specimens of North African catfish (*Clarias gariepinus*) were analyzed. Of these, ten (55.5%) were infected with nematodes referable to *Contracaecum* larvae in their abdominal cavity. The number of larvae collected from infected specimens varied from a single larva up to 100 larvae in a single fish. Morphological and molecular (ITS rDNA and *cox2* mtDNA) analysis of the collected larvae revealed that all the infected fish were parasitized by the species of *Contracaecum quadripapillatum*. Different studies have described the presence of *Contracaecum* larvae in North African catfish; however, none provided their specific identity. Regarding Lake Hula, the only parasitological survey carried out dates back to 1964. Further analyses, including a larger number of specimens of North African catfish, may shed light on the role of this fish host in the life cycle and epidemiology of *C. quadripapillatum*.

METAZOAN PARASITES OF THE OCELLATED KILLIFISH *Floridichtys polyommus* THROUGHOUT ITS DISTRIBUTION RANGE IN THE YUCATÁN PENINSULA, MÉXICO

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The Ocellated killifish, *Floridichtys polyommus* is a cyprinodontiform fish endemic to the Yucatán Peninsula, Mexico. Their parasite fauna has been reported only in two localities, Celestún and La Carbonera lagoons, in Yucatán. Here, we report the results of a survey to inventory the parasite fauna of *F. polyommus* throughout its geographical distribution range. Between 2022 and 2024, 502 individuals were collected in nine localities of Yucatán Peninsula. Fish were examined for ecto and endoparasites; parasite taxonomic identification was accomplished using morphological and molecular data. The prevalence and mean abundance were calculated for each parasite taxa and locality. A total of 25 parasite taxa were found, including 13 digeneans, three cestodes, two copepods and one of the following: acanthocephalan, nematode, isopod, argulid, hirudinean, and pentastomid; eleven of them represent new records, raising the number of parasite taxa of *F. polyommus* to 35. The metacestode of *Glossocercus caribaensis,* the digeneans *Ascocotyle diminuta* and *Rhipidicotyle* sp., and the copepod *Ergasilus* sp. reached the highest prevalence values in two of the nine sampled localities. Species richness was variable among localities; the higher values were found at La Carbonera and Dzilam, with 10 species. The larval forms of *Contracaecum* spp. were found in all localities, whereas *G. caribaensis* and *Ergasilus* sp. were found in six localities. We further discuss the variability in composition of the parasite fauna among localities, suggesting that local biotic and abiotic factors are key determinants of species richness in each locality. This study was supported by the program PAPIIT-UNAM IN200824.

COMMUNITIES OF METAZOAN PARASITES OF *Haemulon aurolineatum* FROM THE NORTH OF THE YUCATAN PENINSULA, MEXICO

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305 specimens of Tomtate grunt, locally known as "Sac-Chacchí" *Haemulon aurolineatum* were captured in the north of the Yucatan Peninsula, Mexico for metazoan parasite searching. Fish were caught between 15 and 40 m depth during oceanographic cruises "Trampas 1" (TI) and "Trampas 2" (TII). All examined fishes were adults. Sixty-five parasite species were morphologically identified from a total of 32,619 parasitic individuals. Four of these species belonged to the Monogenea, 30 to the Digenea (15 adult and 15 metacercariae), seven to the Cestoda (all larvae), nine to the Nematoda (seven adult and two larvae), four to the Acanthocephala (adults), five to the Copepoda (adults), one to the Hirudinea, three to Isopoda (adults) and two species to the Ichthyostraca (an adult and a larvae). Parasite species composition was dominated by digeneans (46% of species), and the number of adult species was larger than those in the larval stage (40 *vs* 25, respectively). The monogenean *Haliotrematoides* sp. was the most dominant species (74% in TI and 86% in TII) and the most prevalent (75% in TI and 100% in TII) and abundant species (42±49 individuals per host in TI and 131±117 in TII). Parasite species composition at the infracommunity level between oceanographic cruises showed significant differences in both the number of parasite species per fish (Wilcoxon rank sum test, $W_{[0.05,303]}=7900$; $p=1.7\text{e-}06$) and the number of parasitic individuals ($W_{[0.05,303]}=5772$; $p=5.5\text{e-}14$). Environmental variables enhancing differences between cruises are examined and discussed.

UPDATED RECORDS OF PARASITIC ISOPODS OF MARINE FISHES OF THE TROPICAL EASTERN PACIFIC

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Members of the superfamily Cymothoidea include obligate or occasional fish parasites that infest the body surface, buccal cavity, and gill chamber of their hosts. Some species are considered of major concern when infesting fish during aquaculture activities. Here, we report seven parasitic isopod taxa in 17 fish host species occurring in the Pacific coast of Mexico, including *Ceratothoa gilberti* (Richardson, 1904), *Nerocila californica* Schioedte & Meinert, 1881, two new species, provisionally identified as *Cymothoa* sp A and *Cymothoa* sp B, *Rocinela signata* Schioedte & Meinert, 1879, *Glossobius auritus* Bovallius, 1885, *Mothocya gilli* Bruce, 1986 and several praniza and zuphea larvae of the family Gnathiidae. Also, we compiled information on previous records of these species in marine fishes along the Mexican Pacific coast and discussed the importance of our findings for understanding the diversity and distribution patterns of these ectoparasites in the Southeastern Gulf of California. Our results show that the Eastern Tropical Pacific should also be considered one of the regions where the knowledge of the presence of parasitic isopods remains minimal. The results of our study also reveal that the inventory of the parasitic isopods of marine fishes of Mexico is far from complete. We suggest that future studies on the metazoan parasite fauna of marine fishes in this geographic region will reveal an increase in the species diversity of parasitic isopods.

METAZOAN PARASITES IN SNAPPERS (PERCIFORMES: LUTJANIDAE) FROM THE SOUTHERN GULF OF MEXICO AND MEXICAN CARIBBEAN

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Knowledge on the parasitic biodiversity in fish from the Neotropical region is essential and scarce. The parasite fauna of snappers from the southern Gulf of Mexico and Mexican Caribbean is little known despite being one of the most important fishing resources in the region. This work aimed to obtain the richness, species composition, and parasitic infection parameters in snappers from these two regions. Snappers were collected in eight localities on the coasts of Quintana Roo, Tabasco, and Campeche, Mexico, between February 2016 and July 2018. A parasitological examination was performed to search for ectoparasites and endoparasites. A total of 533 fish from 10 species of Lutjanidae were collected, where the schoolmaster snapper *Lutjanus apodus* (n= 251) was the most abundant species, and the locality with the higher number of host species was Xcalak (7 spp.). Almost all (95%) snappers harbored at least one individual parasite. A total of 11,544 individuals from 54 taxa of metazoan parasites are reported. These include six monogeneans, 15 digeneans (11 adults and four metacercariae), three cestodes, three acanthocephalans, 14 nematodes (four adults and ten larvae), 11 copepods and two isopods. The larvae of *Terranova* sp. showed higher infection parameters among snappers. The host with the most remarkable species richness was *L. apodus* (38 taxa), followed by the grey snapper *Lutjanus griseus* (30 taxa). This is the first report of parasitic crustaceans in snappers from the region.

NEGLECTED DIVERSITY OF CATSHARK PARASITES: UNVEILING THE PARASITE COMMUNITY OF ICELANDIC PENTANCHIDS

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Pentanchids (Elasmobranchii) are one of the most species-rich groups of chondrichthyans. Among this group, the Icelandic catshark (*Apristurus laurussonii* Saemundsson), the white ghost catshark (*A. aphyodes* Nakaya & Stehmann) and the mouse catshark (*Galeus murinus* Collett) are commonly found in deep-water habitats in the northern Atlantic Ocean. However, information on their parasite communities is virtually absent. The present work aimed to characterise the parasite community of these three pentanchid species. A total of 17 specimens of *A. aphyodes*, 14 *A. laurussonii* and three *G. murinus* were collected in autumn 2023 in south and western Icelandic waters at depths of 540 to 1,280 m and examined following standardised parasitological protocols including morphological and molecular methods. Sharks were infected with at least one parasite and a total of 12 different taxa were detected, resulting in 20 new host records. Among detected parasites, *Anisakis simplex* (Nematoda), a new genus of hexabothriid (Monogenea) and *Yamaguticestus kuchtai* (Cestoda) were frequently encountered (prevalence > 20%) in both species of *Apristurus*. Overall, the parasite communities were characterised by a moderate richness, abundance and high dominance, particularly in *A. aphyodes*. Despite similar habitat preferences, species of *Apristurus* displayed differences in the composition and structure of their parasite communities, as evidenced by the presence of host-specific parasites, higher Bray-Curtis similarity indices within versus between species (0.42–0.78 vs. 0.27–0.57), nMDS and PERMANOVA outcomes. Present results contribute to the knowledge on the biology and ecology of these little-known deep water chondrichthyans and highlight trophic interaction differences between sympatric congeners.

PARASITE BIOBLITZ: TRACKING HELMINTH LIFE CYCLES ACROSS A BROAD TAXONOMIC SCALE AND INTERCONNECTED ECOSYSTEMS

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Trematodes are the most speciose group among the parasitic helminths. However, the magnitude of their diversity remains vastly unknown due to their relatively small size, high morphological homogeneity of closely related species, and the lack of information about the larval stages for the majority of the species described. A parasite BioBlitz in a coastal South Carolina (USA) wetland provided a unique opportunity to assess how much such intensive and short-term projects can contribute to revealing the trematode and cestode diversity across aquatic hosts. We examined a broad range of fish (122 individuals of 16 species) and invertebrate (mollusks, crustaceans, insects) hosts over 12 days along a forested wetland to a tidal creek continuum. Digeneans and cestodes were studied morphologically and molecularly. Our findings revealed a total of 42 digenean and 8 cestode species. All cestodes were larval metacestodes while the digeneans were comprised of 14 adult, 26 metacercarial, and two cercarial stages, several of which represented new host and/or locality records. Sequence data provided convincing evidence of the transmission pathways for four digenean species. This study highlights how BioBlitz initiatives can enhance both our knowledge of the diversity of metazoan parasites and our understanding of the ecology and evolution of these parasites, providing information about their role in ecosystem functionality that is critical to conservation management. This study was supported by a NOAA/South Carolina Sea Grant. SG benefited from the support of the "Brain Pool" programme for outstanding overseas researchers of the National Research Foundation of Korea *(#2021H1D3A2A02081767).*

EXPLORING PARASITE DIVERSITY ACROSS AN ECOLOGICAL GRADIENT USING ENVIRONMENTAL DNA METABARCODING

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DNA metabarcoding of environmental samples provides an effective and efficient method to assess biodiversity but has lagged in parasite biodiversity assessments; one reason being the high taxonomic diversity and genetic divergence of parasites, which precludes the development of universal parasite primers. Our goal was to implement environmental DNA metabarcoding to determine parasite diversity in sediment and water from four physically connected habitats (wetland, freshwater pond, brackish impoundment, and tidal creek) in coastal South Carolina, USA, as part of a parasite BioBlitz in April 2023. Sediment was collected using a syringe corer, and water samples were collected using two methods (active filtration and passive collection *via* the deployment and recovery of water filters). Six amplicon libraries were produced using metabarcoding primers targeting platyhelminths (two COI mtDNA libraries), nematodes, myxozoans, microsporidians, and a final library targeting all eukaryotes to capture parasite taxa with no available metabarcoding primers (four 18S rDNA libraries). There was variable specificity among the primers targeting specific parasite taxa: *e.g.*, the microsporidian primers exhibited high target fidelity, whereas the nematode and myxozoan primers were less specific. Non-targeted parasite taxa detected included apicomplexans, dinoflagellates, ichthyosporeans, and perkinsids. Results reflect the expected differences in parasite community composition across habitats and demonstrate the potential of using metabarcoding to assess parasite diversity. Results also highlight the need for more comprehensive reference databases, as well as the development of more specific and novel primers for those parasite taxa for which there are no available genetic markers.

METAZOAN PARASITES OF THE "LUMPTAIL SEAROBIN" *Prionotus stephanophrys* (LOCKINGTON, 1881) (PERCIFORMES: TRIGLIDAE) FROM THE MARINE COAST FROM PERU

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The objective of the present study was to determine the parasitic community of the "Lumptail searobin" *Prionotus stephanophrys* (Lockington, 1881) (Perciformes: Triglidae) from the Fishing Terminal of Villa María del Triunfo, Lima, Peru. Forty specimens of *P. stephanophrys* were collected, which were captured in the ports of Piura and Tumbes in the summers of 2023 and 2024. After being dissected, 19 species of parasites were identified: *Anisakis simplex* complex (Rudolphi, 1809), *Phocanema* sp. (Myers, 1959), Anisakidae gen. sp. unidentified, *Bolbosoma* sp. (Porta, 1908), Polymorphidae gen. sp. unidentified, *Grillotia* sp. (Guiart, 1927), *Mecoderus oligoplitis* (Manter, 1940), *Orbocotyle elmernoblei* (Payne, 1987), Piscicolidae gen. sp. unidentified, *Pseudempleurosoma carangis* (Yamaguti, 1965), *Brachyphallus* sp. (Odhner, 1905), Fellodistomidae gen. sp. unidentified, *Ectenurus* sp. (Looss, 1907), *Lecithochirium* sp. (Lühe, 1901), *Nybelinia* sp. (Poche, 1926)), Lernaeopodidae gen. sp. 1 unidentified, Lernaeopodidae gen. sp. 2 unidentified, Trematoda gen. sp. unidentified and Plagiorchiida gen. sp. unidentified. The monogenean *O. elmernoblei* was the most prevalent (30%), followed by the nematode *A. simplex* (22.5%). The Poulin discrepancy index was determined in the most prevalent parasites, establishing that *O. elmernoblei* and *A. simplex* presented an aggregated distribution. The correlation between total length and sex of *P. stephanophrys* with parasitological indices was also evaluated. It was observed that the prevalence of *O. elmernoblei* is associated with the total lenght of the host; unlike sex, which showed no relationship with any of the variables. This is the first research work focused on the parasitic fauna of *Prionotus stephanophrys.*

EXPLORING AFRICAN FRESHWATER FISH *Trypanosoma* WITH MOLECULAR AND MORPHOLOGICAL TOOLS

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Trypanosomes are haemoflagellates that infect all vertebrate groups, including marine and freshwater fish, and in aquatic environments are primarily transmitted by blood-feeding leeches or other invertebrates. Since the early 1900s at least 16 species of trypanosomes were identified from freshwater fishes in Africa. This was later reduced to six and by the late 1990s, researchers suggested that most freshwater fish trypanosome records in Africa represented *Trypanosoma mukasai* Hoare, 1932. In Africa, currently only three species are recognised, *Trypanosoma tobeyi* Dias, 1952 and *Trypanosoma toddi* Bouet, 1909, known from clariid and cyprinid hosts, and *T. mukasai* that has been widely reported from a range of hosts (cichlids, clariids, cyprinids, mochokids and schilbeids). Recent molecular data from Botswana indicated the existence of at least two distinct genotypic groups, of which the clariid genotype most likely represents *T. mukasai.* Thus, this study aimed to use an integrated approach to characterise trypanosomes of *Clarias gariepinus* Burchell, 1822 from seven different populations in three southern African countries, to better understand their biodiversity and systematics. Blood samples were collected at various locations in the Zambezi River (Zambia), Okavango Delta (Botswana) and five different rivers in South Africa (Crocodile, Letaba, Phongolo, Vaal, and Orange rivers) from 2019 to 2024. Giemsa-stained thin blood smears were analysed for trypanosomes with these parasites characterised morphologically. Molecular analysis of the 18S rRNA gene region for positive samples supported the identification of a third *T. mukasai*-group, suggesting that *T. mukasai* from southern Africa represents three genetically distinct species that are morphologically indistinguishable.

METAZOAN PARASITE GUILD COMMUNITY IN *Astronotus ocellatus, Cichla monoculus*, *Hoplas malabaricus* AND *Calophysus macropterus* IN SAN LORENZO, DATEM DEL MARAÑÓN (LORETO – PERU): ICHTHYOZOONOTIC RISK IN PERUVIAN AMAZONIA

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Astronotus ocellatus, Cichla monoculus, Hoplas malabaricus and *Calophysus macropterus* represent some of the most consumed fish species of commercial importance in San Lorenzo Market (Loreto, Peru). During the period from 2022 to 2024, 72 individuals were examined among four species of fish (n = 72). This study aimed to determine the prevalence (P), man abundance (A), mean intensity (MI), and parasite localization in the host (L). Four metazoan species were collected, nematodes *Contracaecum* sp, *Anisakis* sp. and *Eustrongylides* sp., and pentastomid *Sebekia* sp. (nymphal stage). In *A. ocellatus* (n = 30): *Contracaecum* sp (P = 83.33%, A = 149, MI = 5.96, MA = 4.97, L = intestine and coelomic cavity), *Eustrongylides* sp. (P =6.66%, A =2, MI =1, MA =0.07, L = muscle) and *Sebekia* sp. (P = 16.66%, A =5, MI =1, MA =0.17, L = muscle). In *C. monoculus* (n = 10): *Anisakis* sp. (P =50%, A =8, MI =1.6, MA =0.8, L = intestine and stomach) and *Eustrongylides* sp. (P =30%, A =3, MI =1, MA =0.3, L = muscle). In *H. malabaricus* (n = 26): *Contracaecum* sp, (P =19.23%, A =9, MI =1.8, MA =0.35, L = coelomic cavity) and *Eustrongylides* sp. (L4) (P =38.46%, A =11, MI =1.1, MA =0.42, L = muscle) and in *C. macropterus* (n = 6): *Contracaecum* sp, (L3) (P =38.46%, A =11, MI =1.1, MA =0.42, L = intestine and liver). Fish species were found to be intermediate and paratenic hosts. Larval sebekid pentastomes reported mature in crocodiles and freshwater turtles and nematodes in freshwater piscivorous mammals and birds, then them presence was a biodiversity and ecosystem health indicator. Metazoan were found in fishes may represent a zoonotic risk to Amazon rainforest population.

TRYPANOSOMATIDS ASSOCIATES TO *Hypanus americanus* (Hildebrand & Schroeder, 1928) IN NORTH VERACRUZ, MEXICO

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Trypanosomatids are obligate parasitic protozoa belonging to the class Mastogophora within the phylum Euglenozoa. These organisms disseminate through blood-feeding vectors such as leeches and blood-sucking invertebrates and can infect a wide number of aquatic and terrestrial organisms. Only two species of tryponosomatids have been registered parasitizing elasmobranch species: *Trypanosoma haploblephari* in Africa and Chile, and *Trypanosoma boissoni,* also in Africa. The signs of trypanosomiasis in fish can vary from mild anemia to deathly infections resulting in important economic losses. The aims of this work are to identify the species richness, parasitic load and species prevalence of the genus *Trypanosoma* associated with *Hypanus americanus* (Hildebrand y Schroeder, 1928). Four organisms of *H. americanus* were collected in fishing cooperatives in Tamiahua, Veracruz, México. Samples of liver, heart, kidney, stomach, spleen, and pancreas were taken and fixed in 70% ethanol. Furthermore, DNA extraction was performed using the chelating resin CHELEX 100. For the *Trypanosoma* detection, DNA from the organ samples was analyzed by conventional PCR. The prevalence of *Trypanosoma* species in *H. americanus* was 3/4 organisms. This study represents the first work in Mexico of a very understudied subject, which is extremely important since elasmobranchs play a crucial, even indispensable, role as top predators in the food chain of marine ecosystems.

PARASITES OF STRANDING MARINE ORGANISMS BY THE HARMFUL ALGAE BLOOM PHENOMENON "RED TIDE" ON THE COASTS OF YUCATAN

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Harmful algal bloom phenomenon (HAB) or "Red Tide" are common on the coasts of Yucatan and cause mortality of marine species of commercial and ecological importance due to the presence of toxins or anoxia. In August 2022, a "red tide" phenomenon occurred on the coasts of Yucatan, allowing us to expand the information on parasitic fauna in marine species that are not commonly collected for study. The collection was carried out on the coasts of Telchac and Progreso ports. Thirty-four elasmobranchs (2 species), 72 Osteichthyes (25 species) and 34 cephalopods (1 species) were collected and identified by the Necton laboratory at Cinvestav, Mérida Unit. From the Osteichthyes, 46 parasite morphotypes and a total of 16,778 individuals were recovered (18 digenean species with 13,036 individuals, two monogeneans with 1,699 individuals, seven nematodes with 1,787 individuals, six cestodes with 28 individuals, four acanthocephalan species with 33 individuals, seven crustacean species with157 individuals and one hirudinean species with 38 individuals). In elasmobranchs, nine parasite morphotypes and 154 individuals were recovered (one digenean species and 54 individuals, one nematode with two individuals, and seven cestodes with 100 individuals). In cephalopods, 10 species and 4,701 individuals were recovered, eight of them were cestodes (4,698 individuals) and two were crustaceans (three individuals). We provide information for each host species examined. The study contributes to new knowledge on parasite taxonomy and biodiversity for different marine hosts which would be important for future research. Financial support came from Cinvestav research funds and CONAHCyT scholarship I1200/051/2023.

MONOPISTHOCOTYLAN PARASITES OF TWO ORNAMENTAL FISH OF CICHLIDAE, *Astonotus ocellatus,* AND *Pterophylum scalare,* RECEIVED FROM INDONESIA, SRI LANKA, AND THAILAND

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Astronotus ocellatus and *Pterophylun scalare*, native to South America, are some of the most popular ornamental fish. Sixty-one and 55 specimens of *A. ocellatus* and *P. scalare*, respectively, were received from Indonesia (IND), Sri Lanka (SL), and Thailand (THAI) using an established import company. Standard procedures were applied when handling, dissection, and examining fish, including the collection and fixation of parasites. The infestation indices were calculated and 18S+ITS1 and 28S r DNA fragments were sequenced. Specimens of *A. ocellatus* were infected with a prevalence (P) of 100% from all three countries sourced. Infection levels of monopisthocotylan from *P. scalare* varied among the studied countries, with P = 73.3% from Indonesia, P = 85% from Sri Lanka, and P = 100% from Thailand. Monopisthocotylans on *A. ocellatus* were present at higher mean intensity levels (IND = 905.35; SRL = 41.92; THAI = 473.5) than *P. scalare* (IND = 13.45; SRL = 7.71; THAI= 44.1). Four species of *Gussevia* and one species of *Sciadicleithrum* were identified from the collected specimens. Species composition differed between the countries from which the hosts were sourced. *Astronotus occelatus* received from Thailand carried *G. asota* while specimens from Indonesia were infected with *G. asota* and *G. astronoti* and the fish specimens received from Sri Lanka were infected with a single species, *S. iphthimum*. *Gussevia spiralocirra* was found on *P. scalare* received from all three countries. Specimens from Thailand were additionally parasitised with *G. obtusa* and *S. iphthimum*. Supported by the DSI-NRF SARChI Chair (No.101054).

Diplostomum (DIGENEA: DIPLOSTOMIDAE) IN THE MOLECULAR ERA: STILL A LONG ROAD AHEAD

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Species of *Diplostomum* are a diverse group of widely distributed parasites with life cycles involving lymnaeid snails and fish as intermediate hosts and fish-eating birds and mammals as definitive hosts. The metacercariae are considered major fish pathogens causing losses in wild and farmed fish. However, species identification is difficult due to the slight morphological differences at all life cycle stages and the presence of morphologically similar species. The first molecular studies of *Diplostomum* spp. started before 2002 but a "barcoding rush" occurred in the past decade. This has led to a substantial increase in both species and isolates from snails, fishes, birds and mammals characterised molecularly using mitochondrial (*cox*1) and nuclear (28S rDNA and ITS1-5.8S-ITS2) loci. A total of 50 genetically distinct lineages of *Diplostomum* were delineated, predominantly based on the *cox*1 gene. These include 18 named species and 32 species-level lineages. However, an overview of the progress in *Diplostomum* taxonomy and nomenclature resulting from this research highlights some key issues hampering their development: (i) 34 lineages (68%) were characterised based on larval isolates alone, and 11 lineages (22%) are still represented by singletons; (ii) the distribution of species richness is uneven due to the uneven sampling effort (24 spp. in North America, 16 spp. in Europe, 12 spp. in Asia, 3 spp. in Africa and 2 spp. in South America); (iii) misidentifications of sequenced adult isolates; and (iv) naming species based on sequenced larval isolates. Further focused sequencing of adult isolates is required to address these issues.

DIVERSITY OF MYXOSPOREAN PARASITES (CNIDARIA, MYXOZOA) INFECTING GUINE SOLE STOCKS FROM NORTHEAST ATLANTIC WATERS

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Myxosporeans are multicellular endoparasites ubiquitous in aquatic habitats. They mainly use fish as intermediate hosts, being frequently associated with increased morbidity and mortality. The impact of intensive industrial fishing on stocks of wild fish has driven studies focusing on exploratory parasitological research. Soles are benthic species of high commercial interest, however, there is practically no information regarding parasitic infections in these fishes. This study aimed to investigate the diversity of myxosporeans parasitizing stocks of Guinean sole *Synaptura cadenati* caught in Northeast Atlantic waters. Fresh specimens were necropsied and a myxosporean survey was performed in internal organs. When present, myxosporean developmental stages were examined under a light microscope, and infected samples were processed for histology and molecular analyses of the 18S rDNA. A *Ceratomyxa* sp. was found in the gallbladder and an *Ortholinea* sp. in the urinary bladder, with a prevalence of infection of 16.7% and 25.0%, respectively. The *Ceratomyxa* sp. sequence displayed highest similarity to *Ceratomyxa arcuata*. Although the genetic distance to this species (1.2-2.4%) falls within the range reported for other *C. arcuata* occurrences, it cannot be disregarded that differences above 1% are generally representative of interspecific variability, and that *C. arcuata* most probably constitutes a species complex requiring elucidation. In turn, the *Ortholinea* sp. sequence retrieved genetic distances over 10% to other myxosporeans. Considering that morphometric comparisons to congeners without molecular data did not recover significant similarities, these two species are recognized as being potentially new. This study constitutes the first myxosporean report from *S. cadenati*.

EVALUATING THE USEFULNESS OF THE DNA METABARCODING TECHNIQUE FOR ASSESSING MYXOSPOREAN INFECTION IN OLIGOCHAETES

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Myxosporeans are fish endoparasites whose life cycle involves the production of actinospores in annelids. More than 2,600 species have been reported; yet, only about 60 have their life cycle clarified. Difficulties in annelid sampling and examination, and low prevalence of infection in these hosts, hinder our knowledge of myxosporean-annelid interactions. DNA metabarcoding represents an alternative approach to parasite detection, allowing faster and more reliable estimates of diversity than conventional methods. This study aimed to evaluate the usefulness of the metabarcoding technique for assessing myxosporean infection in marine oligochaete communities. Estuarine sediments and coastal substrates were collected monthly, during a year, from a northern Portuguese area. Collected oligochaetes were identified based on morphology and molecular data, and individually examined under a light microscope for the detection of myxosporeans. Oligochaetes displaying infection followed for the morphological and molecular analysis of actinospores. Oligochaetes without microscopic evidence of infection were pooled in groups according to their taxa, sampling date and location, and molecularly screened for myxosporean DNA presence using a metabarcoding approach targeting the 18S rDNA. Microscopy-based results disclosed known and novel Sphaeractinomyxon types infecting the marine oligochaetes. Metabarcoding revealed a richer diversity, having retrieved several OTUs belonging to the *Myxobolus* and *Paramyxidium* clades, some of which representing unknown myxosporean diversity. This disclosed the higher sensitivity of the metabarcoding approach for detecting myxosporean presence in oligochaete tissues, and its utility for estimating their seasonal distribution in these hosts. However, our findings also highlighted important limitations that require protocol optimization and critical evaluation of the results.

HELMINTH PARASITES OF THE YELLOWFINNED MOJARRA, *Gerres cinereus* (Walbaum, 1792) IN TWO COASTAL LAGOONS "LA CARBONERA" AND CELESTUN OF YUCATAN, MEXICO

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On the coasts of Yucatan, fishing is the main economic activity and source of income for 12 thousand fishermen, where 60% of their catch comes from coastal or artisanal fishing. The Gerridae family is among the most abundant and widely distributed yearly in coastal fishing. In this family, the yellowfin mojarra, *Gerres cinereus* (Walbaum, 1792), stands out in the incidence of capture in local fishing. Despite this, few records of *G. cinereus* parasites in Yucatan, where the presence of nematodes of the genus *Contracaecum* and monogeneans of the genus *Aristocleidus* have been reported. Therefore, we decided to record the parasites of this fish in two locations on the coast of Yucatan, Mexico. A total of 112 specimens of *G. cinerus* were examined: 49 from La Carbonera and 63 from Celestún. All specimens were measured for total length, standard length, and weight before being examined for parasites externally and internally. The parasites found were counted, and the site of infection was recorded. Twelve parasite taxa were found in the samples from the two locations; seven are nematodes (three *Contracaecum* species; one *Echinocephalus* sp.; one *Gnathostoma* sp., One Cucullanidae and Nematoda gen. sp.), two are digenean (*Dollfustrema* sp. and *Ascocotyle* sp.), one is monogenean (*Aristocleidus* sp.), and two are acanthocephalan (*Dollfusentis* sp. and *Gorgorhynchs* sp.). All species were recorded at La Carbonera, and only five at Celestún. All except the monogenean were larva stages, indicating the role of *G. cinereus* as an intermediate host in coastal lagoons. Nematodes showed the highest prevalence, mean intensity, and abundance values.

PARASITE FAUNA OF THE INVASIVE LIONFISH *Pterois volitans* (PISCES: SCORPAENIDAE) IN TULUM (BAHIA PRINCIPE) MEXICAN CARIBBEAN

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The Mesoamerican Reef System is the second largest barrier reef in the world and has great ecological and economic importance. In this system, fish play a very important ecological role, and have received special attention from the scientific, commercial and tourist areas. In this region of the Atlantic, it has recently been reported the invasive lionfish *Pterois volitans* (Family Scorpaenidae), widely known for its use as ornamental fish. The main impacts reported by the introduction of this species (native from the Indo-Pacific) in wild environments include negative impacts on biodiversity and economic losses (fisheries). However, little is known whether this invasive species could also be carrier of parasites dangerous to native species or even to humans if consumption is promoted as a strategy control. The objectives of the present study were: to identify the parasite fauna in *P. volitans* in different reef localities of the Mexican Caribbean and to determine if these species could be pathogenic for humans. Lionfish specimens were collected by snorkeling and scuba diving in 8 reef locations. In a total of 70 *P. volitans* individuals (total length between 380 and 455 mm) six main groups of parasites were recorded (Digenea: *Stephanostomum* sp*., Siphoderina* sp*., Lecithochirium* sp. *L. musculus*, *L. microstomum*, *L. floridense*, *Brachyphallus parvus*; Nematoda: *Ascarophis mexicana, Spirocamallanus* sp., *Capillaria* sp., *Histerothylacium* sp.; Acanthocephala: *Gorgorhynchus* sp., *Serrasentis* sp.; Cestoda: *Prochristianella* sp.; Isopoda: *Cymothoa excisa*; Copepoda: *Caligus wilsoni* y *Caligus xystercus*). In both copepod species *P. volitans* is a new host record and extend their known geographic range. This species richness of parasites was relatively low when compared to studies conducted on this invasive species in other locations in the Caribbean Sea. The species of parasites recorded here do not represent a risk to human health.

DIVERSITY OF OPECOELID TREMATODES (OPECOELIDAE) FROM THE AREA OF CALIFORNIA: HISTORY, CHALLENGES AND PERSPECTIVES

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Trematodes of the family Opecoelidae are frequent parasites of marine fishes. There are more than 1,000 described species across multiple marine ecoregions. The study of this family in North America (mainly from the Southern California Bight) was widely developed during the second third of the 20th century by prominent helminthologists such as Manter or Bravo-Hollis, among others, describing numerous species parasitizing diverse marine hosts. At the end of the 20th century, this effort declined, and reports for species of this trematode family became sporadic, maybe considering that few new contributions would be provided. Now, we are creating a line of research focused on the reinterpretation of the knowledge for the diversity of this family. Most of the described species during the "golden age" of traditional taxonomy lack valuable information currently used by contemporary taxonomists, and recent collection and examination of specimens of Opecoelidae strongly suggests that the true diversity is very different when tools of integrative taxonomy, such as ultrastructure, geometric morphometry, or molecular analyses, are added. In this contribution, we provide the historical framework of the study of opecoelids in the Southern California Bight, presenting our research's objectives, perspectives, and first results.

A REVIEW OF THE PARASITE COMMUNITIES IN THE STINGRAY GENUS *Hypanus*

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The stingray genus *Hypanus* includes 9 species distributed throughout the East Pacific and Atlantic oceans. Parasite community studies from this genus date back to 1905, including surveys from the North Atlantic, Northern Gulf of Mexico, Caribbean Sea, and Gulf of California. These studies report diverse parasite communities including members of Cestoda (9 families), Digenean (3 families), Aspidogastrean (2 families), Monogenea (4 families), Acanthocephala (2 families), and Hirudinea (1 family). Data is lacking for three species within *Hypanus* (*H. rudis, H. marianae,* and *H. berthalutzae*) and for many areas of its distribution, including several where they are locally abundant. We conducted parasite community surveys on two sympatric stingrays (*Hypanus sabinus* and *H. say*) in the Indian River Lagoon estuary in eastern Florida (USA). We report data from samples collected monthly since July 2023, having recovered several parasite taxa belonging to Cestoda, Monogenea, and Digenea. We evaluate these results in the context of previously published parasite survey information for this host genus.

UNRAVELING PARASITE DIVERSITY ALONG A RIVER STREAM IN THE STATE OF SÃO PAULO, BRAZIL

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The Pardo River watershed belongs to the Paranapanema River basin in the São Paulo state, Brazil, passing in the central and southwestern regions of the state, including 20 municipalities. This river hosts a diverse range of fish species and is known that fishes are the vertebrates with the highest number of host-parasite associations. However, it is estimated that only 6% of Brazilian fishes have been studied for their parasitic fauna and until recently, neither parasite was reported in the Pardo River. Therefore, considering that the biodiversity of fish parasites is still incipient in Brazil, we evaluate the diversity, taxonomy, and systematics of parasites associated with fishes from the Pardo River, based on an integrative approach, using morphological and molecular data. Fishes (n=711) from 27 species were collected along the longitudinal gradient (from source to mouth) of the Pardo River, Middle Paranapanema River, São Paulo state, Brazil, and examined for infection with copepods, myxozoans, and helminths. The survey revealed a rich diversity of parasites, including myxozoans, monopistocotyls, digeneans, cestodes, nematodes, and copepods, with their phylogenetic positions determined. New species of *Myxobolus* and *Henneguya* (Cnidaria); *Aphanoblastella, Cacatuocotyle, Diaphorocleidus, Jainus, Unilatus*, *Urocleidoides,* and *Phanerothecium* (Monopisthocotyla); *Crepotrematina* and *Wallinia* (Digenea); *Mariauxiella* (Cestoda) and *Tidergasillus* (Copepoda) were discovered, some of them formally described. The results showed a great diversity of parasites in the studied hosts, enhancing our understanding of Neotropical fish parasitology and their evolutionary relationships.
Financial support: FAPESP 2020/05412-9, 2019/26831-2, 2019/19060-0, 2021/12593-2, 2022/04715-3, 2023/11307-1, 2023/10835-4, 2024/05688-5; CNPq 161839/2021-5, 311635-2021-0; PROPe-PROPG/UNESP 04/2022; and CAPES 88887.976117/2024-00.

PARASITOLOGICAL FINDINGS IN OCEAN SUNFISH STRANDED ALONG THE ITALIAN COASTS

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The ocean sunfish *Mola mola* is known to host a rich parasitic fauna, with over 40 parasite species reported worldwide; nevertheless, parasitological data available in the literature are scattered, partly due to the limited accessibility of wild specimens. In this work we analyzed the gastrointestinal helminths of 2 *M. mola* specimens stranded along the Italian coasts of northern Adriatic Sea. Both specimens were found fresh dead and were immediately subjected to necropsy and parasitological examination. Collected parasites were processed for morphological analysis in light and scanning electron microscopy and for molecular analysis (amplification and sequencing of the 28S rDNA). High intensities of cestode and trematode parasites were recorded in the gastrointestinal tract of both stranded specimens. Based on morphological and molecular analyses, two Triaenophorid cestodes (Bothriocephalidea, Triaenophoridae) were identified: the species *Anchistrocephalus microcephalus*, already reported in *M. mola* from Mediterranean and extra-Mediterranean areas, and another Triaenophorid species currently under investigation. Collected trematodes all belonged to the family Accacoeliidae. Our work provides updated parasitological data on *M. mola* from the Mediterranean Sea and stress the importance of collecting information from stranded or by-catched individuals of this charismatic yet elusive fish species.

NEMATODE DIVERSITY OF THE ELUSIVE ENDEMIC FISHES OF THE AUSTROGLANIDIDAE IN SOUTH AFRICA

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Nematodes are a diverse component of the parasite community in freshwater fishes, commonly found as adults or larvae in almost all host organs. South Africa’s freshwater fishes harbour a diverse range of nematodes including the Atractidae, Anguillicolidae, Anisakidae, Camallanidae, Capillariidae, Cystidicolidae, Physalopteridae, Quimperiidae and Rhabdochonidae. However, knowledge of nematodes associated with endemic fishes remains limited, with only unidentified larval anisakiids and undescribed species of *Rhabdochona* reported from just two of over 30 endemic fish species. This study aimed to address this gap by investigating the diversity of nematodes parasitising three fish species belonging to the endemic family Austroglanididae: *Austroglanis barnardi, A. gilli* and *A. sclateri*. Individuals of *A. barnardi* (n = 10, Noordhoeks River), *A. gilli* (n = 15, Krom River; n = 2, Matjies River) and *A. sclateri* (n = 36, Vaal River) were subjected to a complete parasitological screening. Larval *Eustrongylides* sp. were found in the intestine of *A. sclateri* (prevalence [P] = 2%) and larval *Paraquimperia* sp. in the intestines and gallbladders of both *A. barnardi* (P = 50%) and *A. gilli* (P = 70%). Two distinct species of *Rhabdochona* were found in the intestine and gallbladder of *A. gilli* (P = 82%) and intestine of *A. sclateri* (P = 38%). Sub-adults of *Spinitectus* sp. parasitised the intestine of *A. gilli* (P = 5%). This study provides novel knowledge on the diversity, morphological characters and molecular data for parasitic nematodes of freshwater fishes and illustrate the diversity yet to be discovered from diverse fish fauna in South Africa.

DIGENEANS OF MEDITERRANEAN SPARIDS: A WELL-STUDIED SYSTEM WITH A NEED FOR AN IN-DEPTH REVISION

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Sparids are one of the most diverse fish families in the Mediterranean and one of the most exhaustively surveyed for parasites. We used an updated database to review the current knowledge on digenean diversity in Mediterranean sparids. Twenty out of 28 sparid species have been reported to host 81 digenean species of 19 families (66% of the digenean families recorded in the area). The most diverse digenean families are Opecoelidae (17 spp.), Hemiuridae (8 spp.), Mesometridae (7 spp.), Derogenidae (7 spp.), and Aporocotylidae (5 spp.); all species of the Aporocotylidae being described in the past 16 years. The 49 digenean genera are represented by 1–3 species (57% of the genera with a single species), except for *Macvicaria* which is the most species-rich genus (8 spp.). In the past decade, three species of *Macvicaria* have been described in two morphological and molecular studies on two complexes of related species. Of the digenean species described or recorded in Mediterranean sparids, 43 are only recorded in sparid fishes (24 in a single host species and 19 in 2–12 host species). However, there is a significant representation of digeneans with low host specificity (38 spp. recorded in hosts of different fish families). We highlight the need for further efforts to reveal the actual digenean diversity in this system using integrated morphological and molecular approaches. This work was supported by the ThinklnAzul programme supported by the MCIN with funding from the EU NextGenerationEU (PRTR-Cl 7.Il), and by Generalitat Valenciana (THINKINAZUL/2021/029).

MONORCHIIDS OF SOUTH AFRICAN HAEMULID FISHES, WITH CHARACTERISATIONS OF TWO NEW TAXA

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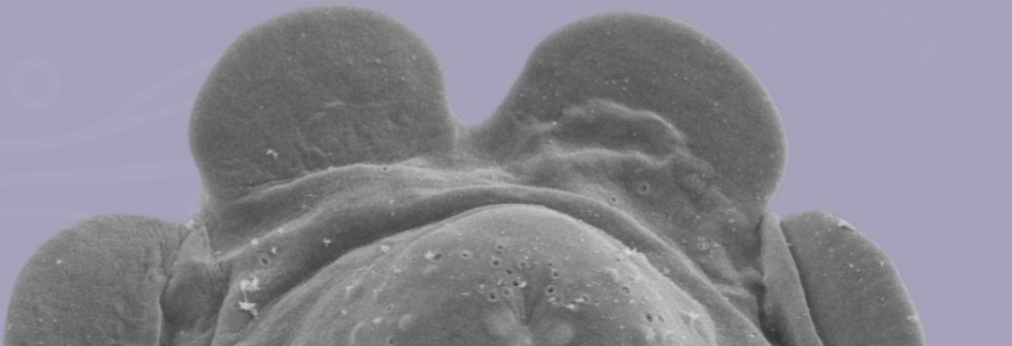
Recent assessments of South African marine fishes uncovered representatives of several trematode families which were under-characterised or unknown from the region. This included the family Monorchiidae, which are otherwise diverse and widely known from other oceanic regions. Two species of monorchiids, the first of this family from South Africa, were found in haemulid fishes of the genus *Pomadasys*. One, from the Banded grunter *P. furcatus*, was morphologically consistent with the obscure genus *Ametrodaptes*; the other, from the Olive grunter *P. olivaceus*, keys to an intermediate position between *Alloinfundiburictus* and *Infundiburictus* on the basis of an ovary that is lobed (a feature of the latter), but not distinctly so. We provide morphological characterisations of both taxa and a refined molecular phylogenetic analysis of the family with novel molecular data.

Thematic areas

3. TAXONOMY, SYSTEMATICS & BIOGEOGRAPHY



ORAL PRESENTATIONS

(Please note the name and institution shown in this list are those of the person presenting the talk, who may not be the first author; the complete author list including all institutional affiliations are shown with the full abstract)

1. CAN MORPHOLOGY AND MOLECULAR DATA TRACE THE SAME EVOLUTIONARY HISTORY? A PHYLOGENETIC ANALYSIS OF THE NON-MONOPHYLETIC *Demidospermus* (MONOPISTHOCOTYLA, DACTYLOGYRIDAE). Aguiar J.C.C. et al. São Paulo State University (UNESP), Botucatu, São Paulo state, Brazil
2. *Pavanelliella pavanellii* (DACTYLOGYRIDAE): A NEWLY PROPOSED SPECIES COMPLEX OF MONOPISTHOCOTYL FLATWORMS. Aguiar J.C.C. et al. São Paulo State University (UNESP), Botucatu, São Paulo state, Brazil
3. RADIATION ACROSS HOST FAMILIES-EVIDENCE FOR MULTIPLE HOST-SWITCHES OUT OF TROPICAL SNAPPERS AMONG THE CRYPTOGONIMIDAE (Trematoda). Armstrong H. et al. School of Environmental and Conservation Sciences, Murdoch University, Western Australia
4. EXPLORING THE LARVAL STAGES OF *Metagonimus romanicus* IN THE INTERMEDIATE HOSTS FROM THE DANUBE RIVER IN EUROPE. Barčák D. et al. Institute of Parasitology, Slovak Academy of Sciences, Košice, Slovakia
5. "DANCING QUEEN: NEW WORMS IN THE MUSEUM SCENE!" Bouguerche C. et al. Department of Zoology, Swedish Museum of Natural History, Box 50007, SE-104 05, Stockholm, Sweden.
6. CHARACTERIZING THE MOST DIFFICULT DIGENEANS–A PARTIAL IDENTIFICATION OF JUVENILE DIDYMOZOIDS IN PUERTO RICO BASED ON MORPHOLOGY, NEXT-GEN AND SANGER SEQUENCING. Colón-Marty Y. et al. Laboratory of Parasitology, University of Puerto Rico at Mayagüez, Puerto Rico
7. *Neohexangitrema* (TREMATODA: MICROSCAPHIDIIDAE) IN INDO-PACIFIC ACANTHURIDAE: HERBIVORES IN HERBIVORES AND PROBLEMS OF SYNONYMY. Cribb T.H. et al. Queensland Museum, Biodiversity and Geosciences Program, South Brisbane, Queensland 4101, Australia
8. PLOTTING DIVERSITY: INSIGHTS INTO THE MORPHOLOGY, GENETIC AND DISTRIBUTION OF FISH PARASITIC GNATHIID ISOPOD SPECIES COMPLEXES IN THE CARIBBEAN. Erasmus A. et al. North-West University, Private Bag X6001, Potchefstroom 2520, South Africa
9. MOLECULAR AND MORPHOLOGICAL INSIGHTS INTO NOVEL FISH-PARASITIC *Trypanosoma* SPECIES FROM SOUTH AFRICA'S SOUTHERN COAST. Le Roux C. et al. North-West University, Potchefstroom, South Africa
10. INVESTIGATING THE TREMATODES IN TROPICAL MARINE FISHES REPORTDEDLY SHARED BETWEEN THE AMERICAS AND THE INDO-WEST PACIFIC. Martin S.B. et al. Centre for Sustainable Aquatic Ecosystems, Harry Butler Institute, Murdoch University, Perth, Australia
11. SEARCHING UDONELLIDS (MONOGENEA) AS EPIBIONTS OF PARASITIC COPEPODS ON CATFISHES FROM THE GULF OF MEXICO. Mendoza-Franco E.F. et al. Universidad Autónoma de Campeche, Campeche, México
12. BACK TO THE PAST: THE IMPORTANCE OF RE-EVALUATING KNOWN SPECIES OF ERGASILIDAE (COPEPODA: CYCLOPOIDA). Narciso R.B. et al. São Paulo State University (UNESP), Botucatu, State of São Paulo, Brazil
13. EVOLUTIONARY INSIGHTS INTO *Dactylogyrus* PARASITES AND THEIR CYPRINOID HOSTS IN THE MIDDLE EAST. Nejat F. et. al. Department of Botany and Zoology, Faculty of Science, Masaryk University, Brno, Czech Republic
14. INTEGRATING MOLECULAR AND MORPHOLOGICAL DATA TO DESCRIBE NEW GENERA AND SPECIES OF CHALCINOTREMATINAE (DIGENEA: HAPLOPORIDAE) FROM SOUTH AMERICA. Pantoja C. et al. Institute of Parasitology, Biology Centre of the Czech Academy of Sciences, České Budějovice, Czech Republic
15. TWENTY YEARS OF *Gyrodactylus* RESEARCH IN MEXICO: EMERGING PATTERNS. Rubio-Godoy M. et al. Instituto de Ecología, A.C., Xalapa, Veracruz, Mexico
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ORAL PRESENTATIONS

CAN MORPHOLOGY AND MOLECULAR DATA TRACE THE SAME EVOLUTIONARY HISTORY? A PHYLOGENETIC ANALYSIS OF THE NON-MONOPHYLETIC *Demidospermus* (MONOPISTHOCOTYLA, DACTYLOGYRIDAE)

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We address the taxonomic instability of the genus *Demidospermus*, which historically served as a catch-all taxon for species parasitizing Neotropical catfishes. To refine species classifications, we conducted two complementary phylogenetic analyses: one based on 60 morphological characters from 46 species, including 4 *Demidospermus sensu stricto* and 42 morphologically similar species, using a combination of sectorial searches, drifting, ratchet, and fusing algorithms, and another using 18S sequences from 1 *Demidospermus s.s.* and 6 *Demidospermus sensu lato*, alongside closely related dactylogyrids, running a Bayesian inference. The morphological phylogeny resulted in the proposal of four new genera and the resurrection of two previously recognized genera, reorganizing 19 species formerly assigned to *Demidospermus*. Additionally, 11 species were classified as *incertae sedis* due to polytomies or insufficient data. The molecular phylogeny recovered *Demidospermus* as sister group to *Demidospermus s.l.* and other *Demidospermus*-like species, emphasizing the need for further sequencing 18S of related genera, such as *Aphanoblastella*, to test the group's monophyly. Morphological phylogeny recovered a clade including *Demidospermus leptosynophallus*, *Demidospermus majusculus*, and *Demidospermus uncusvalidus* (Gen. n. 3), also supported by molecular data for *D. leptosynophallus* and *D. uncusvalidus*. Another clade, composed of Gen. n. 4 sp. n. 1 and *Urocleidoides catus*, was confirmed by molecular inference, with the inclusion of *Urocleidoides amazonensis* despite ambiguous morphological traits. These results highlight the effectiveness of morphological analysis in organizing *Demidospermus*-like taxa, though further molecular sampling is required to fully resolve the phylogenetic relationships within this diverse group. Financial support: FAPESP 2020/05412-9, 2022/04715-3; CNPq 311635-2021-0 and CAPES 88887.976117/2024-00.

Pavanelliella pavanellii (DACTYLOGYRIDAE): A NEWLY PROPOSED SPECIES COMPLEX OF MONOPISTHOCOTYL FLATWORMS

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Pavanelliella species are common ectoparasites of Neotropical catfishes. Specimens resembling *Pavanelliella pavanellii* were discovered in the nares of *Pimelodus maculatus* and *Iheringichthys labrosus* from the Pardo River (Paraná Basin). To investigate if these specimens were conspecific with *P. pavanellii* from *Pseudoplatystoma tigrinum* and *Pseudoplatystoma punctifer* from the Tapajós River (Amazon Basin), Bayesian phylogenetic analyses were conducted using 18S and ITS1 markers, including sequences of *Pavanelliella takemotoi* from *P. maculatus* in the Mogi Guaçu and Pardo rivers, *Pavanelliella jarii* from *Brachyplatystoma rousseauxii* in the Tapajós Basin, *Urocleidoides* sp. from *Hoplias malabaricus* from Mogi Guaçu River, and a capsalid. The phylogenetic trees indicated close relationships between *P. pavanellii* lineages, and were imputed into the species delimitation models (GMYC, PTP, mPTP). These analyses confirmed the presence of distinct lineages, suggesting the need for formal species description for either the Pardo or Tapajós River populations, requiring further samplings. The role of co-speciation was evaluated using PACo and Jane algorithms, and a relaxed molecular clock estimated divergence times. *Pavanelliella* likely originated during the Eocene (~40 Mya) through co-speciation with pimelodid catfishes in the Proto-Amazon Basin. Subsequent isolation of the La Plata and Amazon Basins (~31 Mya) led to further lineage diversification. Host-switching events, such as the movement of *P. pavanellii* between hosts in the Pardo Basin, underscore its low host specificity and adaptability. To advance our understanding of *Pavanelliella*'s host-parasite co-evolution and biogeography, further taxon sampling and node calibration testing are essential. Financial support: FAPESP 2020/05412-9, 2022/04715-3, 22/15973-3; CNPq 311635-2021-0 and CAPES 88887.976117/2024-00.

RADIATION ACROSS HOST FAMILIES-EVIDENCE FOR MULTIPLE HOST-SWITCHES OUT OF TROPICAL SNAPPERS AMONG THE CRYPTOGONIMIDAE (TREMATODA)

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The Cryptogonimidae is a large family of trematodes found worldwide in tropical freshwater and marine ecosystems. Their life cycle apparently always requires trophic transmission of metacercariae in fishes, and definitive hosts are predatory fishes and piscivorous reptiles. In coral reef ecosystems, where the greatest richness and diversity of cryptogonimids occurs, the predominant group of definitive hosts are the tropical snappers (Lutjanidae) and, to a lesser extent, the closely related sweetlips, and grunts (Haemulidae). Therefore, cryptogonimids exploiting definitive hosts other than lutjanids and haemulids are interesting. Novel collection from Australia has included several such examples. In this presentation we will present the phylogenetic positions for these cryptogonimid taxa and consider the evidence in support of a narrative of multiple independent host-switches away from lutjanids and haemulids, against the backdrop of a massive radiation of cryptogonimids in these fishes.

EXPLORING THE LARVAL STAGES OF *Metagonimus romanicus* IN THE INTERMEDIATE HOSTS FROM THE DANUBE RIVER IN EUROPE

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The heterophyid trematode *Metagonimus romanicus* (Ciurea, 1915) (Digenea) is an intestinal parasite with zoonotic potential that is endemic to central and south-eastern Europe. The life cycle of *M. romanicus* is complex, with freshwater snails as first intermediate hosts, fish as second intermediate hosts, and birds and mammals, potentially also humans, as final hosts. In the absence of comprehensive epizootiological and epidemiological studies, snails and fish along the middle reaches of the Danube in Slovakia, Hungary and the Czech Republic were surveyed for the presence of intermediate hosts of *M. romanicus* in 2023 and 2024. The ‘prosobranch’ snail *Esperiana esperi* (Caenogastropoda: Melanopsidae) serves as the first and probably only intermediate host of *M. romanicus*. The prevalence of infection in snails in the Danube in Slovakia was 9%. In contrast, the metacercariae of *M. romanicus* are frequently found in a variety of freshwater fish. A total of 154 specimens of 21 fish species from 9 families were examined for metacercariae. Fish scales were examined under a stereomicroscope and metacercariae were counted in 50 or 100 positive scales to determine the intensity of infection. We found metacercariae of *M. romanicus* in 10 fish species from two different families (Gobiidae, and Leuciscidae) in the Danube River in Slovakia and Hungary, but no fish from the Danube tributaries in the Czech Republic were infected. The most suitable fish intermediate hosts are chub (*Squalius cephalus*) and nase (*Chondrostoma nasus*) with a prevalence of up to 100%. The metacercariae of *M. romanicus* encyst under the scales, with up to 42 metacercariae found in one scale. In this work we also provide the first molecular and SEM data on the developmental stages of *M. romanicus* from the first and second intermediate hosts. This study was supported by the Slovak Research and Development Agency (APVV SK-CZ-RD-21-0078), Scientific Grant Agency of the Ministry of Education, Science and Research of the Slovak Republic and the Slovak Academy of Sciences (VEGA No. 2/0130/24), the Ministry of Education, Youth and Sports of the Czech Republic (project LUASK 22045), and Bilateral Mobility Project CAS-SAS-2022-05 and SAV 23-08.

"DANCING QUEEN: NEW WORMS IN THE MUSEUM SCENE!"

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Several studies have shown that the euryxenic trematode *Derogenes varicus* (Müller, 1784) represents a species complex. Four lineages have been designated (DV1–4) with the DV1 clade corresponding to *D. varicus sensu stricto*. Herein, we investigate newly collected specimens of *D. varicus sensu lato* from Scandinavian and Arctic waters using integrative taxonomy. The trematodes were collected from *Melanogrammus aeglefinus*, *Eutrigla gurnardus*, *Trachinus draco*, *and Merluccius merluccius* off the Atlantic coast of Sweden and from *Hippoglossoides platessoides* from Arctic Svalbard. 28S sequences of derogenids from Sweden were identical to *D. varicus sensu stricto*, confirming its euryxeny. The 28S sequences of *Derogenes* sp. from *H. platessoides* were identical to *Derogenes* DV2 and differed from *D. varicus sensu stricto* by 3% and from *Derogenes* DV3 by 2%. The 28S sequence divergences of *Derogenes* sp. from *H. platessoides* with *D. ruber* and *D. lacustris* were 3 and 10%, respectively. ITS2 and *cox*1 divergences between *Derogenes* sp. from *H. platessoides* and other *Derogenes* species/lineages were at levels of interspecific differences. The species *from H. platessoides* is described here as *D. abba* Bouguerche, Huston, Karlsbakk, Ahmed & Holovachov, 2024. We also examined the type material *of Progonus muelleri* (Levinsen, 1881), the type and only species of the genus *Progonus*, with redescription and designations of paralectotypes. Based on specimens from Theodor Odhner's collections at the Swedish Museum of Natural History, SMNH, Stockholm, we provide novel morphological and anatomical data for *D. varicus sensu lato* species complex. Lastly, we investigated Arthur Looss's "lost collection" of Trematodes at the SMNH and characterised a putative species *Derogenes* sp. "*limula*".

CHARACTERIZING THE MOST DIFFICULT DIGENEANS–A PARTIAL IDENTIFICATION OF JUVENILE DIDYMOZOIDS IN PUERTO RICO BASED ON MORPHOLOGY, NEXT-GEN AND SANGER SEQUENCING.

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The family Didymozoidae comprises a speciose group of tissue flukes parasitizing pelagic fish, notably scombrids. Unusual morphological and life-history characters have led some to call this group the most difficult to identify of all the digeneans. In the Caribbean, juvenile didymozoids are common in benthic fish like snappers, but these developmental stages are known only from morphological descriptions, with no sequence data yet available. This study reports molecular and morphological data from juvenile didymozoids from a snapper from Puerto Real, Cabo Rojo. Both Sanger and next-gen sequencing were conducted, yielding partial 28S, the complete rDNA operon and the first complete mitochondrial genome from the family Didymozoidae. The specimens resembled the Allomonilicaecum morphotype, and phylogenetic analysis suggested they belong to Didymodiclininae, in which the only genus known in the Atlantic region is *Didymoclinus*. However, the morphological and molecular data do not allow a definitive genus-level identification. Mitogenome phylogenies recovered the didymozoids within the Hemiuroidea, but the position of the Hemiurata within the Digenea fluctuated radically in trees with different numbers of taxa and analytic approaches. To our knowledge, this study represents the first report of didymoclinids in the Caribbean. Given the economic importance of the didymozoids, which negatively affect highly valued fishes such as tunas, the present data have regional value for the study of the distribution, life history and diversity of these parasites in the Caribbean.

Neohexangitrema (TREMATODA: MICROSCAPHIDIIDAE) IN INDO-PACIFIC ACANTHURIDAE: HERBIVORES IN HERBIVORES AND PROBLEMS OF SYNONYMY

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The genus *Neohexangitrema* (Microscaphidiidae) comprises one species, *N. zebrasomatis* from the acanthurid *Zebrasoma velifer* from off Japan. We examined 32 species of Acanthuridae from the tropical Indo-west Pacific, finding specimens of *Neohexangitrema* in two species of *Zebrasoma* and three of *Acanthurus*. Specimens from French Polynesia represent a new species and a rare case of parasite endemism in French Polynesia. Two other morphotypes co-occurred in fishes from other localities but not in French Polynesia. The first, from Ningaloo Reef, Okinawa, the Great Barrier Reef (GBR) and New Caledonia, represents a second new species which frequently has large amounts of undigested algae in its guts; it appears to be a herbivore in a herbivore. The second widespread morphotype is consistent with *N. zebrasomatis* as originally described from off southern Japan. Sequence data (*cox*1 mtDNA and ITS2 and 28S rDNA) consistently suggest that the new specimens represent two mutually cryptic species, both infecting both *Zebrasoma scopas* and *Z. velifer*, one from Ningaloo Reef and the other from the GBR and New Caledonia. In the absence of molecular data from the type-locality, neither species can be positively identified as *N. zebrasomatis*. We will propose new names for both taxa, so as to draw attention to our interpretation of their status. This proposal is made with the explicit understanding that one species may well (but will not necessarily) prove a synonym of *N. zebrasomatis*. This approach draws attention to the developing issue of the management of the names of combinations of cryptic trematode species.

PLOTTING DIVERSITY: INSIGHTS INTO THE MORPHOLOGY, GENETIC AND DISTRIBUTION OF FISH PARASITIC GNATHIID ISOPOD SPECIES COMPLEXES IN THE CARIBBEAN

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Gnathiid isopods are temporary parasites in the juvenile stage, while adults are free-living and identifiable by the distinct morphology of adult males. Currently, 138 species of *Gnathia*—the most species-rich genus in Gnathiidae—are known. However, due to limited descriptions and molecular data, relationships among species and genera within Gnathiidae remain poorly understood, which is concerning, as these species play key ecological roles in coral reef ecosystems. Only 12% (16 of 138) of *Gnathia* species have been described from the Caribbean biodiversity hotspot in the Tropical Atlantic Realm (TAR). Moreover, molecular data are scarce, with only *G. marleyi* and *G. jimmybuffetti* molecularly characterised in the past 11 years. This highlights the importance of studying gnathiids in the Caribbean. The present study aims to clarify species complexes in this region by combining morphological and molecular analyses. Recent surveys in the Caribbean yielded 30 molecular sequences (COI and ITS2.2) for 11 potential species. Specimens morphologically identified as *G. marleyi* and *G. virginalis* revealed three genotypes based on COI: for *G. marleyi*—Genotype 1 from St. John (type locality), 2 from St. Kitts, and 3 from Jamaica; for *G. virginalis*—Genotype 1 from the Dominican Republic, 2 from Southeast Florida, and 3 from Jamaica. Additionally, two distinct genotypes were found for *G. calsi* (Barbados and Jamaica) and *G. jimmybuffetti* (Southeast Florida—type locality—and Curaçao). These results further demonstrated that environmental conditions and distribution patterns, for example, the east-west hurricane belt, should be considered when characterising population genetic structures and distinguishing species.

MOLECULAR AND MORPHOLOGICAL INSIGHTS INTO NOVEL FISH-PARASITIC *Trypanosoma* SPECIES FROM SOUTH AFRICA'S SOUTHERN COAST

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The genus *Trypanosoma* includes diverse flagellate and unicellular haemoparasites that infect all vertebrate classes worldwide. While terrestrial mammal infections have been extensively studied, trypanosomes infecting fish are less understood, with limited research on their life cycles and ecological roles. Moreover, the phylogenetic position of several species from aquatic hosts is yet to be confirmed. This is particularly true in South Africa, which has high marine fish diversity but only two known marine trypanosome species—one from teleosts and one from elasmobranchs. This study aims to fill this knowledge gap by investigating marine fish trypanosomes along the southern coast of South Africa. Blood samples were collected from 246 fishes across 23 species at various sites including Chintsa East, Tsitsikamma Storms River Mouth, Boknes, Kariega River Estuary, and Groot River West Estuary from 2020 to 2023. Giemsa-stained blood smears were examined for trypanosomes, these parasites morphologically characterised, with molecular analysis of the 18S rRNA gene conducted on positive samples. Combining morphological and molecular data, four *Trypanosoma* species were identified: *Trypanosoma* (*Haematomonas*) *nudigobii* from Klipfish (*Clinus superciliosus*), and three new species—*Trypanosoma* (*Haematomonas*) sp. A from the Prison goby (*Caffrogobius gilchristi*), *Trypanosoma* (*Haematomonas*) sp. B from White steenbras (*Lithognathus lithognathus*), and *Trypanosoma* (*Haematomonas*) sp. C. from five mullet species (*Chelon dumerili*, *Chelon richardsonii*, *Chelon tricuspidens*, *Mugil cephalus*, and *Pseudomyxus capensis*). This study represents the first molecular characterisation of trypanosomes from mullets and more significantly reports on the first infection of trypanosomes from *Ca. gilchristi* and *L. lithognathus* in southern Africa.

INVESTIGATING THE TREMATODES IN TROPICAL MARINE FISHES REPORTDEDLY SHARED BETWEEN THE AMERICAS AND THE INDO-WEST PACIFIC

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Understanding of distributions for trematode species exploring tropical marine fishes as definitive hosts remains rudimentary. Most of these trematode species are known from single reports. Conversely, many species, across multiple groups, are known from multiple, sometimes numerous reports, which often collectively suggest low host-specificity and/or broad geographic distribution. In particular, early surveys of tropical fish-trematodes in the Indo-West Pacific frequently identified species originally proposed from collections in the West Atlantic. Many tropical marine fishes have broad distributions within each of the West Atlantic, East Pacific and Indo-West Pacific, but few fishes are distributed across these realms. Broadly, it seems unlikely that the genetic connectivity of trematodes in these fishes can be maintained over such geographic range, but few of these reportedly broad distributions have been tested with genetic data. This presentation will summarise, quantify and identify the trematode species of fishes with distributions reportedly ranging from the tropical West Atlantic and/or East Pacific to the tropical Indo-West Pacific, assess the quality of evidence (or lack thereof) supporting these distributions, and recount the few specific cases which have been assessed in the modern, molecular era.

SEARCHING UDONELLIDS (MONOGENEA) AS EPIBIONTS OF PARASITIC COPEPODS ON CATFISHES FROM THE GULF OF MEXICO

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The metazoan ectoparasites on fish, i.e., udonellids-infecting copepods, have received less attention due to field methodological limitations. Udonellids are widely distributed around the world as epibionts on caligid copepods or argulids, which are themselves infesting primarily the skin from numerous fish groups. This component, udonellids-infecting copepods on fish, is still unknown within biodiversity of marine ecosystems in Mexico. In the present study, the catfishes of *Ariopsis felis* and *Bagre marinus* (Ariidae) were collected from June 2023 to March 2024 from the coast of Campeche (southern Gulf of Mexico), and immediately washed them with ethanol 70% for detaching/fixing any ectoparasite on external fish surface. In the laboratory, udonellid-copepods were recovered from the sediment of the skin washings and morphologically and molecularly identified. A total of 153 ariid fishes were examined from which *Udonella* sp. 1 and *Udonella* sp. 2 were found on the copepods of *Lepeophtheirus* spp. (Caligidae) infesting each catfish species, respectively. The udonellid abundances (mean number of parasites per examined fish) revealed to be higher in *A. felis* compared to that in *B. marinus*. There was also a significant association between abundances and host condition factor for *A. felis* and *B. marinus*. Present findings expand the known geographical records of udonellids to the Gulf of Mexico.

BACK TO THE PAST: THE IMPORTANCE OF RE-EVALUATING KNOWN SPECIES OF ERGASILIDAE (COPEPODA: CYCLOPOIDA)

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Ergasilidae is a diverse parasitic family. Recently, several new species have been described globally. While searching for new species is exciting, re-evaluating known species is crucial for improving the taxonomic "health" of taxa. Advancements in microscopy and molecular analyses are key to enhancing older descriptions and resolving longstanding taxonomic issues. Using an integrative approach, this study aimed to redescribe two known South African Ergasilidae species, *Mugilicola smithae* and *Dermoergasilus amplectens*. From July to August 2023, coastal fishes were sampled at Boknes, Eastern Cape (3 3°43'34.0"S; 26°35'06.6"W). Copepods were removed and stored in 70% and 100% molecular-grade ethanol for morphological and molecular studies respectively. Egg sacs of hologenophores were used for DNA extraction (cox1, 18S, and 28S rDNA). Specimens of *M. smithae* were found attached to the gills and mouth of the African longfin eel, *Anguilla mossambica*. Reevaluation of *M. smithae* revealed unprecedented features such as the presence of Leg 4, further strengthening its relationship with the species of *Paeonodes*. Five papers have described the morphology of the globally distributed *D. amplectens*, all reporting variations among specimens. The present specimens also differ from previously described South African specimens in antennule setation and ornamentation of legs and urosome. Our findings raise concerns about the record of *D. amplectens* in South Africa, suggesting that what was previously reported as *D. amplectens* is likely a species new to science. Gene sequences are provided for the first time for both species, and a phylogenetic hypothesis for Ergasilidae is proposed. Funding: FAPESP 2022/16672-7 and 2019/26831-2.

EVOLUTIONARY INSIGHTS INTO *Dactylogyrus* PARASITES AND THEIR CYPRINOID HOSTS IN THE MIDDLE EAST

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Previous studies have focused on the phylogeny and biogeography of *Dactylogyrus* species in the peri-Mediterranean region. Knowledge of the diversity and biogeography of these monogeneans in the Middle East remain largely neglected. Because of reciprocal coevolutionary interactions in host-parasite systems, the biogeography of parasites often reflects that of their hosts. Cyprinoid fish, which host *Dactylogyrus*, are endemic to the Middle East. We aim at invstigating the diversity, phylogeny, and host specificity of *Dactylogyrus* in this region to trace the historical dispersion of cyprinoid fish through the phylogenetic relationships of their associated *Dactylogyrus* parasites. From 2018 to 2023, field expeditions were conducted in Iran, Iraq, and Turkey, the gills of 89 cyprinoid species were examined for *Dactylogyrus* parasites. Seventy-two *Dactylogyrus* species were identified. Among them, *D. vistulae* had the widest host range, infecting 24 cyprinoid species. Fish of the genus *Squalius* were found to harbor the largest number of *Dactylogyrus* species. The study revealed 16 potentially new *Dactylogyrus* species. Phylogenetic analyses were performed using 18S rDNA, 28S rDNA, and complete ITS1 regions. Several *Dactylogyrus* species exhibited high intraspecific genetic variability. Using DNA sequences of *Dactylogyrus* species, eight major clades were revealed. Species from the Middle East were present in five clades, along with species from Europe, North Africa, and East Asia, highlighting the role of the Middle East in *Dactylogyrus* diversification. We also performed the mapping of morphological characters of attachment organ (haptor) onto the parasite phylogeny revealing the evolutionary patterns in haptor adaptation. This study was supported Czech Science Foundation, project no. GA20-13539S.

INTEGRATING MOLECULAR AND MORPHOLOGICAL DATA TO DESCRIBE NEW GENERA AND SPECIES OF CHALCINOTREMATINAE (DIGENEA: HAPLOPORIDAE) FROM SOUTH AMERICA

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The subfamily Chalcinotrematinae (Haploporidae) comprises a relatively understudied group of digenean parasites found in freshwater and brackish water fishes across the Americas and Africa. The systematics of this group have rarely been investigated using molecular data, with only a few species from two genera, *Saccocoelioides* and *Intromugil*, analyzed through ribosomal DNA sequences, leaving a gap in knowledge for other four genera. In this study, chalcinotrematine trematodes were collected from freshwater fishes of the Characiformes and Siluriformes in the Jari River, Amazon Basin, Brazil. These trematodes were characterized using an integrative approach, combining morphological analysis with molecular data (28S and ITS2 sequences), to investigate the taxonomic framework of the Chalcinotrematinae. We tested the monophyly of *Saccocoelioides*, the most species-rich genus within the subfamily, incorporating sequence data from two additional species. Based on molecular evidence, we propose taxonomic changes within the subfamily, including the establishment of a new genus to accommodate three known species from Argentina and the description of two new species from the genera *Chalcinotrema* and *Unicoelium*. Our results also provide the first insights into the phylogenetic relationships of these two genera. These findings contribute to our understanding of the evolutionary history and systematics of Chalcinotrematinae, highlighting the need for further molecular studies across South America.

TWENTY YEARS OF *Gyrodactylus* RESEARCH IN MEXICO: EMERGING PATTERNS

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Two decades ago, only six species of *Gyrodactylus* had been recorded infecting fishes in Mexico, a biodiversity hotspot – plus scores of unidentified parasites all over the country. Today, 47 species have been characterized, the majority from native freshwater fishes: 16 from Poeciliidae, 7 each from Goodeidae and Profundulidae, 6 from Characidae, 5 from Cyprinidae, etc. This eightfold increase of knowledge on gyrodactylids has enabled glimpses of emerging patterns, like the association of parasite lineages to certain fish families – sometimes over time and geography: for instance, some gyrodactylid lineages are associated to poeciliid fishes across their continental distribution range, from Mexico to Argentina; and some parasite lineages of clear Neotropical association, have migrated northwards in the Americas with their fish hosts following the emergence of the Panama Isthmus and are now distributed in Nearctic Mexico! We can now also start analyzing host ranges (host specificity), with some parasite species being recorded on one host species only, while others infect several fish species within the same family; and yet others, are able to infect hosts from different fish families – eventually, we hope the accumulation of fish host-gyrodactylid parasite data will enable to discern the relative weight of capacity and opportunity in the definition of host ranges; as well as the (co-)evolution of both fish hosts and gyrodactylids. Finally, we also hope to be able to assess whether the invasive gyrodactylids that have been translocated with exotic fish and spilled over fish aquaculture farms, have measurable effects on native fishes.

TAPEWORMS OF FRESHWATER FISH IN NORTH AMERICA: WHY SO MUCH NEGLECTED?

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Tapeworms (Cestoda) are an interesting and widespread group of parasites, and represent a suitable model for ecological, evolutionary and co-evolutionary studies due to their close relationship with their hosts. They are also widespread and diverse in North American freshwater fishes. Although the North American freshwater fish fauna is extraordinarily rich, host associations and phylogenetic relationships of their tapeworms remain poorly understood. Most of the current knowledge on fish parasites in North America was accumulated in the 20th century, but this area of research has been largely neglected in recent decades for several reasons, including the continuing focus on parasites of elasmobranchs. To fill the considerable gaps in our knowledge of the diversity and host-parasite relationships of North American fish parasites, the authors collected extensive material of tapeworms at various locations in the United States, Canada, and Mexico. Thanks to the combined efforts of researchers in the U.S. and Europe, several groups of fish tapeworms belonging to the orders Caryophyllidea, Bothriocephalidea and Onchoproteocephalidea were revised and many species redescribed. This presentation will briefly summarise the main results, including the description of new taxa (14 new species, 5 new genera, 1 new subfamily and new family classification) and a more reliable assessment of the host specificity of individual taxa, which is narrower than previously thought. Avenues for future research are outlined, in particular targeted sampling using appropriate methods of collection and integrative taxonomy (heat-fixation, molecular data, vouchers of sequenced specimens, etc.). This study was supported by the Ministry of Education, Youth and Sports of the Czech Republic (projects LTAUSA 18010 and LUAUS 23080) and Fulbright Commission.

NOVEL ULTRASTRUCTURAL FEATURES OF *Clinostomum cutaneum* IN NILE TILAPIA REVEALED BY SCANNING ELECTRON MICROSCOPY

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The parasitic trematode *Clinostomum* presents a huge challenge to freshwater fish species, particularly Nile tilapia (*Oreochromis niloticus*), which plays a vital role in both aquaculture and wild fisheries. In a parasitological survey of 157 Nile tilapia samples from fish farms in the Upper Tana River Region, Kenya, 17.2% of the samples dissected and screened for parasites were found to be infected with *Clinostomum* metacercariae, encysted in the buccal cavity, skin and gills. This study used an integrative identification approach that combined traditional morphological techniques with ultrastructural analysis using scanning electron microscopy (SEM) and molecular methods targeting ribosomal regions (ITS1, 5.8S, ITS2, and 28S). The *Clinostomum* metacercariae were identified both morphologically and molecularly as *C. cutaneum* and *C. phalacrocoracis*. SEM revealed some new ultrastructural features specific to *C. cutaneum*. One of these is an excretory pore surrounded by minute, spiny papillae, a feature which had not been reported in previous studies. Another finding we observed was the presence of an everted cirrus in the metacercariae, a feature seen in the adult stage of *C. cutaneum*. However, in our samples, the cirrus lacked basal papillae, showing that there is morphological variation between the adult and metacercarial stages. Additionally, the tegumental area around the genital pore was surrounded by dome-shaped papillae. Our findings, therefore, provide new taxonomic features for the metacercariae of *C. cutaneum* and demonstrate the value of SEM as a complementary tool for more precise parasite identification and species differentiation.

TWO NEW SPECIES OF *Urocleidoides* (MONOPISTHOCOTYLA: DACTYLOGYRIDAE) PARASITIZING THE GILLS OF *Cyphocharax modestus* (CHARACIFORMES: CURIMATIDAE) SUPPORTED BY MORPHOLOGICAL AND MOLECULAR DATA

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The present study describes two new species of monopisthocotyls parasitizing the gills of *Cyphocharax modestus* (Characiformes: Curimatidae) from the two localities of the Upper Paraná River basin, state of São Paulo, Brazil. *Urocleidoides* n. sp.1 and *Urocleidoides* n. sp.2 closely resemble *Urocleidoides triangulus* (Suriano, 1981) by has a vaginal opening and vaginal sclerite sinistral; an accessory piece comprising 2 subunits and not articulated with the base of MCO; MCO a coiled tube with 2½ counterclockwise; and dorsal bar with a posteromedian projection. However, *Urocleidoides* n. sp.1 and *Urocleidoides* n. sp.2 differ from other congeners by the morphology of the accessory piece (comprising two subunits: one subunit scythe-shaped, adjacent piece with narrow base broadening towards upper end, upper end axe-shaped in *Urocleidoides* n. sp.1 and a straight rod with a bifurcated proximal portion, distal portion ending in a point, two curved handles arise from medial portion uniting close to distal portion in *Urocleidoides* n. sp.2, and the morphology of the ventral and dorsal anchor. The phylogenetic analyses recovered *Urocleidoides* as non-monophyletic, indicating the need for taxonomic review. This study provides the first molecular sequences for *Urocleidoides* spp. parasitizing Curimatidae, including newly described species. These findings revealed distinct clades and suggested possible host specificity, underscoring the importance of additional research to better understand the phylogenetic relationships within the genus. Financial support: Financial support: FAPESP 2020/05412-9, 2021/12779-9; CNPq 140872/2017-5, 151170/2022-3, 161838/2021-9, 311635/2021-0; CAPES 88887.9761172024-00); PROPG/PROPe-UNESP 04/2022); and FUNCAP FPD-0213-00301.01.01/23.

PHYLOGENY OF VIVIPAROUS *Gyrodactylus* (MONOGENEA: GYRODACTYLIDAE) REVEALS INSIGHTS ON HOST EVOLUTION, BIOGEOGRAPHY ACROSS CONTINENTS, AND MORPHOLOGICAL ADAPTATIONS IN THE NEARCTIC REGION

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Gyrodactylid monogeneans offer a unique perspective to study the evolutionary trajectories of their teleost hosts, providing invaluable insights into host-parasite coevolution, biogeography, and ecology. We employed phylogenetic reconstruction to elucidate the relationships among diverse lineages of *Gyrodactylus* spp. using ITS sequences. We aimed to uncover lineage diversification, dispersal patterns, historical biogeography, and morphological evolution based on taxonomically significant haptoral features and DNA sequences. Phylogenetic analysis revealed a paraphyletic origin of Nearctic *Gyrodactylus* indicating the historical connection of fish faunas between North America and Eurasia. These connections, driven by a combination of natural and anthropogenic processes, facilitated the exchange of fish species and contributed to the shared diversity of aquatic biota across continents. The close relationship between *Gyrodactylus* species infecting both freshwater and marine fish underscores the complex evolutionary dynamics and ecological versatility of these parasites. We observed a trend in the evolution of haptoral structures in *Gyrodactylus* spp., from relatively simple to more complex forms, in the Nearctic region. The haptoral sclerites of *Gyrodactylus* spp. displayed a spectrum of morphotypes, ranging from structures similar to those found in globally distributed *Gyrodactylus* species to configurations predominantly found in Nearctic lineages parasitizing Cypriniformes. Characteristic features of "Nearctic" morphotypes included a median knob in the ventral bar and plate-like membranes or additional filaments attached to the handles of the marginal hooks. The unique morphological features in *Gyrodactylus* species parasitizing North American cypriniforms reflects the interplay between host-parasite interactions, ecological factors, and historical contingencies shaping the evolutionary dynamics of these parasites in the region. This study was funded by the Ministry of Education, Youth and Sports of the Czech Republic, project no. LUAUS23080.

CITIZEN SCIENCE IN FISH PARASITOLOGY: RESOLVING THE *Anilocra capensis* (ISOPODA: CYMOTHOIDAE) SPECIES COMPLEX IN SOUTHERN AFRICA

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Cymothoid isopods are large (>3 cm) parasitic crustaceans that attach to the body, fins, gills, and buccal cavity of fish. Their size makes them easily observable, with frequent photographic documentation by anglers and divers. For instance, iNaturalist has over 3,000 observations of fish-associated isopods worldwide. Species from the genus *Anilocra*, which attach to the body and fins, are commonly recorded. In South Africa, *Anilocra capensis* described in 1818 from the Hottentot seabream *Pachymetopon blochii*, caught off Cape Town, was the first marine parasite described from this region. Its large size (up to 7 cm) and wide distribution from Namibia to South Africa make it one of the most observed cymothoid on iNaturalist, with 56 records from more than 10 different fish hosts. However, the question arises: are all of these records truly *A. capensis*? Cymothoids are generally difficult to target in parasitological studies and often collected as bycatch. Using iNaturalist records, we targeted specific host fish at exact locations. We collected *A. capensis* from its type host and *A. capensis*-like specimens from the panga seabream *Pterogymnus laniarius*, super klipfish *Clinus superciliosus* and twotone fingerfin *Chirodactylus brachydactylus* on the south coast of South Africa and from galjoen *Dichistius capensis* and mullet *Chelon richardsonii* in Namibia. Molecular analyses revealed that these specimens represent a species complex, with *A. capensis* comprising at least three distinct species. This study highlights the value of citizen science in fish parasitology, demonstrating how it can focus sampling efforts to help resolve complex taxonomic challenges.

SOUTH AFRICAN PIECES OF THE PUZZLE HELP TO RESOLVE PHYLOGENETIC PROBLEMS WITHIN THE MONOCOTYLIDAE: TWO NEW GENERA AND SPECIES, A NEW SUBFAMILY, AND SOME OTHER NEW DATA

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Two new monocotylids (Monogenea: Monocotylidae) were recovered from the gills of the shovelnose ray *Acroteriobatus annulatus* off South Africa. These monocotylids could not be assigned to any of the known subfamilies but share morphological similarities with members of *Anoplocotyloides*, *Mehracotyle*, *Spinuris*, *Troglocephalus* (*incertae sedis*), and *Neoheterocotyle* and *Nonacotyle*. These latter taxa have historically represented the subfamilies Dasybatotreminae and Heterocotylinae, respectively. The new monocotylids grouped together with *Neoheterocotyle* and *Troglocephalus* in molecular analyses, forming a well-supported monophyletic group. The discovery of the new monocotylids provided the opportunity to address the polyphyly of the Heterocotylinae, evident from the inclusion of *Neoheterocotyle*, which had traditionally grouped with *Troglocephalus* in previous molecular phylogenies. A new subfamily is proposed to accommodate the new monocotylids and all other monocotylids that have numerous single gland duct openings along the anterolateral and lateral margins and four pairs of ventral pits of the anterior head region, a single vagina, and a non-diverticular, non-confluent caecum. Heterocotylinae is subsequently amended in exclusion of *Neoheterocotyle*, *Spinuris* and *Nonacotyle*, and Dasybatotreminae in exclusion of *Anoplocotyloides* and *Mehracotyle*. The previously enigmatic taxon, *Troglocephalus rhinobatidis*, is considered the type-taxon of the new subfamily. Additional new locality records for other monocotylid representatives off South Africa are discussed, including a new host record for *Heterocotyle pastinacae*, from *Dasyatis chrysonota*, which challenge the previously held idea that *Heterocotyle* species are strictly host-specific.

UNIQUE TESTES! A NEW *Trochopus* SPECIES (MONOGENEA: CAPSALIDAE) DISCOVERED FROM THE PECTORAL FINS OF THE CAPE GURNARD, *Chelidonichthys capensis* OFF SOUTH AFRICA

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A detailed account of the first South African *Trochopus* species (Monogenea: Capsalidae) is presented. The new species was collected from the dorsal surface of the pectoral fins of captive Cape gurnard, *Chelidonichthys capensis* (Cuvier), from Two Oceans Aquarium, Cape Town, originally wild-caught in Table Bay, South Africa in 2007. The host microhabitat is uncharacteristic for *Trochopus* species, which are generally known from the gills, and less so from the skin of the body of their hosts. This new species is unique among the known *Trochopus* species, possessing a conspicuous, dark-staining gland on each of the two testes, presumably to produce the contents of the spermatophore plug that is visible in the vagina of two specimens. Two separate individual specimens also presented with unilateral testicular atrophy, which is apparently rare in the Monogenea, or considered a potential artefact of captivity in other capsalids, but is considered a natural occurrence in the current study. Egg hatching and larval haptoral morphology are also discussed. The question of whether the adult haptor is accurately reflective of the total number of sclerite pairs in different *Trochopus* species could be addressed by viewing the oncomiracidia.

PHYLOGENETIC RELATIONSHIPS AMONG CALCEOSTOMATID SPECIES AND HOST-PARASITE ASSOCIATIONS IN MEDITERRANEAN SCIAENIDS

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Calceostomidae (Dactylogyridea) is a relatively small family of parasites inhabiting the gills, the oral cavity and the fins of teleost fish belonging to Eupercaria. This parasitic family currently encompasses six different genera and eleven species, almost half of them exclusively reported from Mediterranean sciaenid hosts. The taxonomic status of the species belonging to this family is mostly based on the morphology of the reproductive system and the haptoral armature. Molecular data is only available for two Calceostomatidae spp., none of them belonging to *Calceostoma*, the type genus of the family, and phylogenetic relationships among calceostomatids remain unexplored. We combine morphological and molecular information to explore the phylogenetic relationships among species of Calceostomatidae and assess the specificity in calceostomatids – sciaenids associations occurring in the Mediterranean. Four sciaenid species, *Argyrosomus regius, Sciaena umbra, Umbrina canariensis* and *U. cirrosa* were collected from Western Mediterranean localities and analysed for calceostomatid parasites. Ten parasites per host species were stained and mounted in permanent slides for morphological identification. Additionally, the DNA of two specimens per morphotype and host species was extracted and the partial 28S rDNA region was amplified. Phylogenetic analysis of Calceostomatidae spp. revealed that the morphotypes found in the sciaenids correspond to different species which cluster together. We discuss the phylogenetic results and the need for combining molecular and morphological data to delve into the taxonomy of Calceostomatidae. This work forms part of the ThinkInAzul programme and was supported by MCIN with funding from European Union NextGenerationEU (PRTR-C17·I1) and by Generalitat Valenciana (GVA-THINKINAZUL/2021/029).

DIVERSITY OF *Proteocephalus* spp. PARASITIZING WHITEFISH *Coregonus lavaretus* IN LAKES OF RUSSIA

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Proteocephalus spp. are widespread parasites of fish. In light of recent systematic rearrangements within the genus *Proteocephalus*, its species diversity remains unclear. Previously, cestodes parasitizing whitefish in Russia were identified as *P. longicollis* and *P. exiguus*. The objective of this study is to identify the species composition of *Proteocephalus* in Russian water bodies using partial sequences of the *cox1* and 28S genes. Cestodes from whitefish residing in four oligotrophic lakes were examined. Teletskoye Lake is part of the Ob River basin and is situated in the Altai Mountains. Baunt Lake and Kapylyushi Lake (the Lena River Basin located within the Baikal Rift Zone). Verkhnee Ondomozero Lake is situated in the Kola Peninsula. Fragments of the 28S and *cox1* genes, measuring 1434 and 1548 bp respectively, were amplified. Phylogenetic reconstructions within the genus *Proteocephalus* were conducted using maximum likelihood (ML) and Bayesian inference (BI) approaches with IQ-TREE 2 and MrBayes v.3.2.1, respectively. The phylogenetic trees reconstructed using ML and BI analyses of the 28S and *cox1* genes exhibited similar topologies. The sequences obtained from the Lena River Basin, Ob River Basin, and Kola Peninsula formed three well-defined clades. The clade formed by samples from Verkhnee Ondomozero Lake included sequences of *P. fallax* from GenBank. For the other two clades, reference sequences are unavailable. Based on our results, we propose that whitefish in Russian lakes host three species of *Proteocephalus* across different regions of their distribution. This work was supported by the Russian Science Foundation, project no. 23-74-10101.

GENETIC ANALYSIS OF MYXOZOANS REVEALS CRYPTIC DIVERSITY OF *Myxobilatus* SPECIES FROM BASSES IN NEW YORK STATE

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A myxozoan parasite, tentatively identified as *Myxobilatus mictospora* based on superficial morphology and known host association, was commonly encountered during a parasitological survey of largemouth and smallmouth bass (*Micropterus dolomieu* and *Micropterus salmoides*) in central NY in 2011-2012. This parasite was found in the urinary bladder of 48% to 90% of largemouth bass (LMB) and 0% to 3% of smallmouth bass (SMB), varying by locality. Recently, we acquired DNA sequences from preserved specimens obtained in this earlier survey to determine if there are genetic differences by locality or by host species. We obtained small and large subunit ribosomal DNA sequences from 123 specimens (122 LMB, 1 SMB), and identified 6 different genotypes. The *Myxobilatus* species sequence from SMB was distinct from all the LMB sequences. Within the LMB samples, there were 5 distinct parasite genotypes, some differed only by a few nucleotides, and others had many sequence differences. Mixed infections were common with 25% of LMB hosts with multiple genotypes. Some *Myxobilatus* genotypes were more common in certain locales than others, but there was no consistent pattern to suggest that these parasites are site specific. Morphologically, the myxospores representing different genotypes could not consistently be distinguished from one another. As such there appears to be a suite of morphologically similar but genetically diverse *Myxobilatus* species that can infect LMB in New York State. This work builds on other studies that have identified multiple genotypes in myxozoans and provides continuing evidence of cryptic species within this broader group.

SYSTEMATIC INSIGHTS INTO THE FISH-INFECTING TREMATODE FAMILY LEPIDAPEDIDAE YAMAGUTI, 1958, GAINED FROM DISCOVERY OF A NEW GENUS FROM OFF NAMIBIA

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The lepocreadioid trematode family Lepidapedidae is characterised by two distinct clades, the primarily deep-sea "*Lepidapedon* clade" and primarily shallow-water "*Doorochen* clade". During recent sampling off Namibia, a new lepidapedid taxon was discovered from the intestine of the galjoen *Dichistius capensis* (Dichistiidae). Second intermediate stages were subsequently found infecting the brown mussel *Perna perna* (Mytilidae) from off South Africa, indicating a temperate southern African distribution for this species is likely. Unique aspects of this species' morphology, most notably the presence of filamented eggs and helical uterus, were sufficient to warrant the proposal of a new genus. Molecular phylogenetic analysis indicated (though with poor support) that this taxon is resolved as basal to both lepidapedid clades. The Lepidapedidae continues to resolve as sister to the monotypic family Gibsonivermidae Bray, Cribb & Cutmore, 2018. Despite its apparently basal position, we consider this taxon to be a representative of the Lepidapedidae due to the morphology of the terminal genitalia, which shows close affinities to some shallow-water lepidapedids, e.g. *Bulbocirrus aulostomi* Yamaguti, 1970 and is greatly dissimilar to that of *Gibsonivermis berryi* (Gibson, 1987), the sole species of Gibsonivermidae. We conclude that the Gibsonivermidae is best maintained as a separate family. Several enigmatic lepocreadioid taxa are currently considered *incertae sedis* due to a lack of molecular sequence data. We consider the discovery of this new taxon indicative of the need to prioritise investigating these taxa, many of which infect endemic fishes of southern Africa and Australia and have morphological affinities with our new taxon.

POSTER PRESENTATIONS

A NEW SPECIES OF *Phanerothecium* (MONOPISTHOCOTYLA, OOGYRODACTYLIDAE), PARASITE OF *Hypostomus strigaticeps* FROM THE PARDO RIVER, BRAZIL

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Phanerothecium is a genus of oviparous helminths characterized by H-shaped vitelline follicles and ducts, a spined (or not), eversible (or not) male copulatory organ (MCO), a thick-walled uterus, and a prominent Melhis’ gland. The type species, *Phanerothecium caballeroi*, was described in *Zungaro zungaro* (Pimelodidae) from Colombia, while six other species have been reported parasitizing various *Hypostomus* species (Loricariidae) in Brazil. During a parasitological survey in the Pardo River, Paranapanema Basin, São Paulo state, we identified specimens of *Phanerothecium* parasitizing *Hypostomus strigaticeps*. Out of 45 fish examined, nine were infected. Morphological analysis revealed that this species closely resembles *Phanerothecium spinatus* but with key differences: a more expanded male copulatory organ (MCO) lumen, with a spear-shaped distal portion and with finer spines, and a more robust anchor with a distinctive elevation between the tip and superficial root. Using the 18S rDNA gene, molecular distance analysis configured with the p-distance algorithm and 1,000 randomizations and Bayesian phylogenetic inference performed with 10^7 generations confirmed that the new species forms a well-supported clade with other *Phanerothecium* species. Our sequences emerged as a sister group to *Phanerothecium sp.* (KX981456), showing a divergence of 0.2–0.9%, compared to 1.6–2% with *P. spinulatum* and *Phanerothecium sp.* (JX840359). These molecular and morphological findings strongly indicate the discovery of a new *Phanerothecium* species, contributing to the understanding of the genus’s diversity. Our study highlights the importance of integrating morphological and molecular data for accurate species identification within this group. Financial support: FAPESP 2020/05412-9, 2022/04715-3; CNPq 311635-2021-0 and CAPES 88887.976117/2024-00.

NEW HOST AND LOCALITY RECORD, AND FIRST PHYLOGENETIC PLACEMENT OF *Cacatuocotyle paranaensis* (MONOPISTHOCOTYLA, DACTYLOGYRIDAE)

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Cacatuocotyle is a Neotropical genus within the family Dactylogyridae, one of the most abundant and diverse groups of fish parasites globally. Of the five known species in this genus, only two have available DNA sequences. In this study, we conducted morphological and molecular analysis to identify the specimens of *Cacatuocotyle* found on the skin of *Characidium zebra*, an ornamental characid fish. Thirteen *C. zebra* individuals were collected from the Indiana stream in Botucatu, São Paulo state, Brazil. The helminths collected were subjected to morphological and molecular analysis extracting the genomic DNA and sequencing the partial 28S rDNA. Molecular distance analysis was performed with the p-distance algorithm, and Bayesian inference was conducted using 10^7 generations. Our findings revealed that five out of thirteen fish were parasitized, with a total of 29 helminths recovered. Morphological characteristics, including a counterclockwise coiled male copulatory organ (MCO) with 3.5 rings, accessory piece articulated with the base of the MCO, left vaginal opening, a sinuous vaginal canal, and a V-shaped bar and one pair of anchors, confirmed the identity of the parasite as *Cacatuocotyle paranaensis*, the type species of the genus. Molecularly, *C. paranaensis* showed 9% divergence from *Cacatuocotyle papilionis* and 10–15% from *Cacatuocotyle cf. chajuli*. Phylogenetic analysis clustered *C. paranaensis* in a well-supported clade exclusive to *Cacatuocotyle*, representing a basal lineage within the genus. This study provides the first molecular data for *C. paranaensis* and reports a new locality and host for this species. Financial support: FAPESP 2020/05412-9, 2022/04715-3; CNPq 311635-2021-0, and CAPES 88887.955939/2024-00.

"FORGOTTEN SPECIMENS, NEW SPECIES": MUSEUM'S HIDDEN POLYOPISTHOCOTYLAN TREASURE!

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Natural history museums worldwide house billions of apposite specimens, offering the potential for cost-free parasitological datasets. Herein, we provide novel morphological and molecular data (28S and *cox*1) for the polyopisthocotylan *Plectanocotyle gurnardi sensu stricto* from *Eutrigla gurnardus* from Sweden based on newly collected specimens (Northeast Atlantic) and specimen from T. Odhner's collections at the Swedish Museum of Natural History. The newly generated 28S sequences of *P. gurnardi* from *E. gurnardus* from Sweden were identical to those from the Mediterranean, suggesting the presence of a single species. A 28S sequences of *P. gurnardi sensu stricto* from Sweden and those from the U.K. (type locality for *P. caudata*) were identical confirming that *P. caudata* and *P. gurnardi* are conspecific. Careful re-examination of *P.* cf. *gurnardi* from *C. lastoviza* from the Mediterranean from the collection of Muséum national d'Histoire naturelle (France) revealed that it differs from all congeners by morphometry (size of clamps, of terminal lappet and its hamuli and uncinuli, and size of atrial spines). The *cox*1 divergences between *P.* cf. *gurnardi* and *P. major*, *P. lastovizae*, and *P. gurnardi sensu stricto* were 10–11 %, 10–11 % and 8 % respectively, falling within the interspecific variations range. *Plectanocotyle* from the Mediterranean is described as a new species, *P. jeanloujustinei* Cappelletti & Bouguerche, 2024. We apprise nomenclature problems in *Plectanocotyle* and consider *P. elliptica* a *species inquirenda*.

Myxobolus n. sp. (CNIDARIA, MYXOZOA) PARASITITIZING THE GILL ARCH OF *Piaractus mesopotamicus* FROM FISH FARM, BRAZIL

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This study increases the know biodiversity of cnidarian parasites in serrasalmid fishes from fresh water. A novel *Myxobolus* species is described based on morphology, ultrastructure, confocal and small subunit ribosomal DNA (SSU rDNA) sequencing. *Myxobolus* n. sp. was found infecting gill arch of *Piaractus mesopotamicus* from the fish farm of São Paulo state, Brazil. Mature myxospores were round-shaped from the frontal view, measuring 9.0 ± 0.3 µm in length, 5.9 ± 0.3 µm in width, and have a thickness of 5.2 ± 0.1 µm in the lateral view. Its polar capsules were elongated and equal size occupying more than half of the myxospore, measuring 4.4 ± 0.2 µm in length, 1.7 ± 0.1 µm in width and polar tubules had 5 – 7 coils. Ultrasctructural analysis revealed that the plasmodial wall was composed of a single membrane and sporogenesis process was asynchronous, with young developmental stages of myxospores in the periphery of the plasmodia and mature myxospores in the central part. Numerous mitochondria and pinocytotic channels were observed in the ectoplasm. Confocal analysis showed the labeling of the nucleus of the sporoplasm, valves and polar capsules and no labeling for mitochondrial activity. Molecular analysis resulted in a partial sequence of SSU rDNA of 1968 bp that according to BLASTn search the closest species was *Myxobolus tambaquiensis* described infecting the operculum of *Colossoma macropomum*. Phylogenetic analysis based on the SSU rDNA sequencing showed that *Myxobolus* n. sp. grouped according to host order, in a subclade together with others species of serrasalmid fishes. This study was financed by Fundação de Amparo à Pesquisa do estado de São Paulo (FAPESP) provided grant 2022/07431-6.

MYXOZOAN DIVERSITY IN FISHES FROM YUCATÁN, MEXICO

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Freshwater fishes in Mexico exhibit a high level of local and regional endemism. In terms of parasitology, an extended host range is followed by increased parasite diversification. Research on fish parasites in Mexico has mainly focused on helminths, while the diversity of other parasitic groups is still poorly understood. The Myxozoa (Cnidaria) are a large and diverse group of microscopic parasites distributed worldwide. Some of them have a detrimental impact on the health fish. To date, only ten valid myxozoan species have been identified in Mexico. As a part of a study conducted between October and December 2023 in the coastal lagoon of Celestún and some sinkholes (cenotes) near the coast of the Yucatán peninsula in Mexico, 78 fish belonging to nine species were collected. All fish were dissected, and each organ was checked for the presence of myxozoan parasites. The descriptions of the myxozoans were executed according to the guidelines of Lom and Arthur (1989). Histopathological analyses were conducted using standard haematoxylin and eosin (H&E) staining, and phylogenetic analyses were performed based on 18S rDNA and 28S rDNA genes. The results indicated a prevalence of infection over >50%and provided morphological and phylogenetic data for the description of four novel species within the genus *Myxobolus* sp., *Kudoa* sp., *Ellipsomyxa* sp., and *Henneguya* sp., which were identified in different organs (gallbladder, gills, kidney, pectoral fins, and spleen). Our study can serve as a basis for future research on myxozoan diversity in fish from Mexico.

A CLOSER LOOK AT *Gnathia tridens* MENZIES & BARNARD 1959 (ISOPODA: GNATHIIDAE): A PRESUMED UBIQUITOUS NEARSHORE TEMPORARY FISH PARASITIC ISOPOD FROM THE TEMPERATE NORTHERN PACIFIC.

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Temporary fish parasitic gnathiid isopods of the genus *Gnathia* Leach, 1814 from the Temperate Northern Pacific (TNP) Realm only constitute 19 of the currently known 138 species. Descriptions of these species span over more than 100 years, yet none of the species reported from the TNP have been molecularly characterised and only a few include detailed descriptions that offer a more accurate understanding of this genus. This study presents a comprehensive integrative redescription of *Gnathia tridens* Menzies & Barnard, 1959, based on material collected from San Diego, California (2018–2019), alongside previously deposited specimens from the Natural History Museum of Los Angeles County and the Santa Barbara Museum of Natural History. The redescription includes both morphological characterisation of the male, using a combination of light and scanning electron microscopy (SEM), as well as molecular characterisation through COI and ITS2.2 genes. A key distinguishing feature identified is the equal trifid frontal margin and ornamentation on the antenna, which sets *G. tridens* apart from other gnathiid species in the TNP. DNA sequencing enhanced the robustness of the identification and offers a foundation for future genetic studies within the genus *Gnathia*. The present study also highlights the importance of integrating available museum samples and multiple methods for characterisation in taxonomic studies.

Sigmomyxa brasiliensis n. sp. INFECTING THE GALLBLADDER OF THE HALF BEAK BALLYHOO *Hemiramphus brasiliensis*

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Myxosporeans are widespread fish parasites with some species causing severe disease outbreaks and others described as potentially suitable for biological tagging. Identifying and classifying parasites, as well as understanding their interactions with hosts, is crucial for comprehending evolutionary processes and effectively managing fisheries and aquaculture systems. During a parasitological survey, a novel species of coelozoic myxosporean was identified in the gallbladder of the halfbeak ballyhoo *Hemiramphus brasiliensis* from the coast of Saint Kitts and Nevis. A total of 30 fish were acquired from local fisherman between late 2016 and early 2017. Mature spores of *Sigmomyxa brasiliensis* n. sp. were observed and photographed in bile aspirates of 14 of the 30 fish, an infection prevalence of 47%. Spores were oval to sigmoid in shape, depending on the plane of view, with two prominent pyriform polar capsules housing 7-9 turns of the polar filament. Spores measured 12.7 (SD 1.3) µm in length and 8.2 (SD 0.9) µm width. DNA extractions and subsequent PCRs, from 5 infected fish, enabled a consensus sequence of 1737bp of SSU rDNA to be reliably constructed. When compared to the databases our consensus sequence was most similar, 98.3%, to that of *Sigmomyxa sphaerica*. *Sigmomyxa brasiliensis* is robustly placed in a phylogenetic context with *S. sphaerica* and members from the genus *Ellipsomyxa*. Only two *Sigmomyxa* species have been reported to date, both of which have been described from beloniform fish. Additional studies will be required to understand whether these parasitic relationships are host specific or if beloniform fish are more broadly infected with myxosporeans from the genus *Sigmomyxa*.

LINKING ADULTS AND METACERCARIAE OF *Posthodiplostomum* DUBOIS, 1936 (DIGENEA: DIPLOSTOMIDAE) IN FISH-EATING BIRDS AND FRESHWATER FISH FROM MEXICO

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The genus *Posthodiplostomum* Dubois, 1936, is globally distributed, parasitizing snails and fish as intermediate hosts, with fish-eating birds as definitive hosts. To date 35 species of *Posthodiplostomum* have been described worldwide, its diversity in Mexico, especially in adult from avian hosts, remains underexplored. In this study, we employed an integrative taxonomic approach combining morphological and molecular data to link adult of *Posthodiplostomum* specimens from fish-eating birds with their metacercariae from fish hosts. Birds of the families Ardeidae (e.g., *Butorides virescens*, *Ardea herodias*, *Nycticorax nycticorax*, *Tigrisoma mexicanum*) and Laridae (*Rynchops niger*, *Leucophaeus atricilla*) were collected in four localities in Mexico, and adult trematodes were obtained. Molecular markers (28S rDNA, ITS1–5.8S–ITS2, and cox1) were sequenced, and phylogenetic analyses were conducted using Bayesian inference and Maximum Likelihood. Our results revealed three species of *Posthodiplostomum*, including one thar represented a new species, which was linked with the metacercariae obtained from freshwater fishes from several localities. Additionally, we documented new records for *Posthodiplostomum macrocotyle* and *Posthodiplostomum pricei*, expanding their known geographic ranges across the Americas.

Neoergasilus africanus: A UNIQUE NEW ADDITION TO THE ERGASILIDAE (COPEPODA: CYCLOPOIDA) FROM AFRICAN FRESHWATER FISH

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Members of the family Ergasilidae are globally distributed parasites of freshwater, brackish, and marine fish. Currently, 30 genera are recognised in this family, of which three—*Ergasilus*, *Neoergasilus*, and *Paraergasilus*—have been reported from African freshwater fish. Twenty-one specimens of an unknown ergasilid were collected from the gills of the North African catfish, *Clarias gariepinus* (Burchell), in the Eastern Cape, South Africa. Morphological examination of the first leg and antennae indicated that these specimens belong to the genus *Neoergasilus*. While the invasive *Neoergasilus japonicus* (Harada, 1930) is the only species of *Neoergasilus* reported from Africa, several distinctive characteristics differentiate the Eastern Cape specimens from *N. japonicus* and the other eight known congeners. Notable features include an inflated cephalothorax, an oval dorsal ornamentation anterior to the cephalosome, a spine on the posterodistal margin of the first antennal segment, and a cone-like process at the proximal margin of the second antennal segment. Additionally, there is a knob-like process on the inner distal margin of the first exopodal segment of leg 1, along with two forked spines on the third exopodal segment. The median caudal rami seta bears an array of spines. Genetic data were obtained using partial ribosomal RNA genes 18S and 28S, along with the mitochondrial DNA gene (COI). Based on morphological and molecular data, the Eastern Cape species was proposed as new to science and described as *Neoergasilus africanus*, marking the first *Neoergasilus* species described from *C. gariepinus* in the southern hemisphere, and the first *Neoergasilus* species in Africa.

BORNEO'S HIDDEN CONNECTIONS: EXPLORING THE LITTLE-KNOWN CORALLANIDAE ISOPODS AND THEIR ELASMOBRANCH HOSTS

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In recent years, the study of global biodiversity has become a central focus in scientific research and conservation efforts. However, much about marine species, particularly microorganisms and parasites, remains unexplored. This knowledge gap is evident for the relatively small group of marine isopods within the family Corallanidae. Majority of these temporary parasites (often referred to as micropredators) feed on host blood before detaching. While primarily found in tropical and subtropical regions, research on Corallanidae biodiversity and biogeography remains limited, particularly regarding their association with elasmobranchs. This project aimed to expand knowledge of corallanid diversity in the biodiverse waters off Borneo. Morphological and molecular analyses were performed on specimens collected from elasmobranch hosts. Of 185 elasmobranchs screened (33 species), three species were infested with corallanids: Hasselt's bamboo shark (*Chiloscyllium hasseltii*), the brown-banded bamboo shark (*Chiloscyllium punctatum*), and the dark-finned numbfish (*Narcine maculata*). In *C. hasseltii*, one out of 10 individuals was infested with two corallanids. In *C. punctatum*, three out of 30 individuals were infested with 1–4 corallanids. The single *N. maculata* harboured one corallanid. Following morphological and molecular studies, three different species of *Argathona* were identified: *Argathona lineata* Bruce, Wong & Merrin, 2022 and two species new to science. This study provides the first record of *Argathona* spp. in Borneo, the first record of corallanids parasitising elasmobranchs, and the first molecular analysis of *Argathona* species. These findings contribute to our understanding of Corallanidae host associations and add to our knowledge on the biodiversity of these understudied isopods.

A NEW MONOGENAN OF THE BLACKCHIN GUITARFISH, *Glaucostegus cemiculus*, IN ANDALUCIA (SPAIN)

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Compared to osteichthyans, chondrichthyans are much less unknown fishes, partly due to the clearly lower number of species and their inferior economic importance. Chondricthyan parasites are even more overlooked species. However, several recent research projects have been focused on the study of these ecologically crucial fishes, including the study of their parasites and epibionts, as they provide valuable indirect information. We present a new monogenean ectoparasite of the blackchin guitarfish (*Glaucostegus cemiculus*) a critically endangered species collected off Cádiz and Huelva (Andalucía, Spain) during the tagging campaign of "Proyecto Glaucostegus". Eighteen *G. cemiculus* were examined for parasites. A total of 48 monogeneans (prevalence = 44,4%) were collected from the posterior region of the base of pelvic fins on the field and preserved in 96% ethanol and absolute ethanol, while some individuals were studied fresh in salt water. These monogeneans belong to the subfamily Dasybatotreminae (Monocotylidae). Previous records report the presence of *Mehracotyle insolita* (Monocotylidae), a strictly specific species; nevertheless, geographic distribution, location within the host, size, and the unique diagnostic traits (presence of several testes and a multilobulate ovary) confirm that it is a different genus and species. Therefore, *G. cemiculus* would at least harbour two specific species and probably two genera. This is a call for action for anyone working with endangered elasmobranchs and might be working unknowingly with endangered parasites too. For parasites, their hosts act naturally as their 'umbrella species' underscoring the need for integrated conservation strategies.

BIOGEOGRAPHIC PATTERNS OF *Anisakis* sp. AND *Adenocephalus pacificus* IN *Trachurus murphyi* ON THE SOUTH AMERICAN PACIFIC COAST ECOSYSTEM: TOP PREDATORS DISTRIBUTION AND ICHTHIOZOONOTIC RISK SENTINEL INDICATORS

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Trachurus murphyi represent one of the most consumed marine resources in Chile, Peru and Ecuador. During the period from July 2020 to March 2021, 142 individuals were examined from 6 different sample points belong to 3 Marine Ecoregions, from north to south: Guayaquil (Ecuador and Paita), Central (Chimbote) and Humboldtiana (Matarani, Ilo y Chile). This study aimed to determine the prevalence, mean intensity and geographic distribution. Two helminth species were collected, *Anisakis* sp. (L3) and *Adenocephalus pacificus* (plerocercoid larval stage). For *Anisakis* sp.: Ecuador (P=4.93%, MI=7.57), Paita (P=3.52%, MI=1.40), Chimbote (P=14.08%, MI=1.75), Matarani (P=2.11%, MI=1), Ilo (P=14.08%, MI =2.70) and Chile (P=7.75%, MI=49.36). For *A. pacificus*: Paita (P=1.41%, MI=4.50), Chimbote (P=5.63%, MI=2.38) and Ilo (P=1.41%, MI=1.50). Different prevalence and mean intensity between sample points was probably correlated with distribution of community trophic structure of marine mammals, fishes and aquatic invertebrates that serve as definitive, paratenic and intermediate hosts along Pacific Coast. Latitudinal gradient of *Anisakis* sp. was observed from fish paratenic host in southern sample points to low ecological indicators in northern sample points. *A. pacificus* distribution was probably

correlation to areas of highest prevalence of human cases. Zoonotic helminths distribution was probably correlated to top predators' distribution that serve as definitive host, for *Anisakis* sp. cetaceans *Physeter macrocephalus* and *Delphinus delphis*, for *A. pacificus* pinnipeds *Arctocephalus australis* and *Otaria byronia*. Raw fish consumption, as "ceviche", in Peru, represent an ichthiozoonotic risk.

COEVOLUTIONARY PATTERNS AND NETWORK DYNAMICS: UNRAVELING HOST-PARASITE INTERACTIONS AT MULTIPLE SCALES

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Understanding how evolutionary histories shape species interactions is key to uncovering current ecosystems dynamics. Cophylogeny, in particular, provides a quantitative framework to evaluate the dependency of two evolutionary histories based on extant relationships. When integrated with ecological network analyses across scales, cophylogeny can shed light on the intricate relationships that define community structure and species interactions. We investigate host-parasite dynamics in postglacial lakes, focusing on three parasite species—two trematodes (*Crepidostomum* spp. and *Phyllodistomum umblae*) and one cestode (*Proteocephalus fallax*)—that infect whitefish (*Coregonus* spp.) in Norway (two lakes) and Switzerland (four lakes). These lakes, with their recent postglacial histories, offer a unique natural experiment to study how hosts and parasites have diversified. Using weighted interaction matrices, we analyze not just the presence but the strength of interactions, adding depth to traditional network approaches. To explore potential cophylogenetic signals, we apply the Procrustean Approach to Cophylogeny (PACo) to quantify the congruence between host and parasite phylogenies. Additionally, we examine the modularity of these interaction networks to test how coevolutionary patterns manifest at both large and fine ecological scales. Statistical significance is assessed through permutation tests, ensuring robust comparisons with randomized null models. We expect to uncover distinct patterns of cophylogenetic signal, with signals potentially varying depending on geographical scale and parasite specificity. This study aims to enhance our understanding of how evolutionary processes and ecological interactions jointly shape host-parasite relationships across different spatial scales.

MOLECULAR AND MORPHOLOGICAL CHARACTERISATION OF THE METACERCARIAE AND ADULTS OF *Cardiocephaloides* SUDARIKOV, 1959 (DIGENEA: STRIGEIDAE) IN BIRDS AND FISH FROM MEXICO

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Cardiocephaloides Sudarikov, 1959 is a cosmopolitan genus of strigeids digeneans parasitic of seabirds distributed worldwide. Life cycle of *Cardiocephaloides* species involves three hosts; nassarid and buccinid molluscs as the first intermediate hosts, fish as the second intermediate hosts, and seabirds as definitive hosts. In their second host, the cercariae migrate to the brain of fish, where they form cysts containing the metacercariae. This genus comprises seven recognized species worldwide. In this study, we employed an integrative taxonomic approach combining morphological and molecular data to characterize adult and metacercariae of *Cardiocephaloides* collected from the intestines of birds (*Leucophaeus atricilla*, *Rynchops niger* and *Hydroprogne caspia*) and brains of fish such as (*Haemulon plumierii*, *Fundulus persimilis, Floridichthys polyommus* and *Mugil curema*) from Mexico. We sequenced molecular markers (28S rDNA, ITS1–5.8S–ITS2, and cox1) and conducted phylogenetic analyses using Bayesian inference and Maximum Likelihood. In addition, detailed morphological measurements, and scanning electron microscopy (SEM) photographs of the specimens were obtained. Our results revealed the presence of five species of the genus *Cardiocephaloides* in Mexico.

MOLECULAR CHARACTERIZATION OF FRESHWATER FISH TREMATODES OF CENOTES (SINKHOLES) OF YUCATÁN: PRELIMINARY RESULTS

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Cenotes (sinkholes) are the dominant freshwater bodies of the Yucatán Peninsula, a unique feature caused by the karstic nature of this peninsula’s platform. According to the Secretariat of Sustainable Development of the Government of Yucatan (SDS), only in the state of Yucatan more than 3000 cenotes have been recorded. The study of the parasitofauna of fishes from cenotes began almost a century ago, in the 1930’s, with the pioneer work of Manter and Pearse, which continued in the 1990’s with the studies of Scholz, Moravec and their colleagues, apart from other sporadic contributions. These studies revealed that trematodes are the dominant group of parasites of cenotes-dwelling fishes; with at least 25 species, considering adults and larval stages. However, trematode species richness in cenotes has probably been severely underestimated, given the low number of studies, the fact that less than 50 cenotes have been sampled, and because species determination was limited to morphological characters. Taking this into consideration, the aim of this study was to determine the diversity of trematodes of sinkholes-dwelling fishes in the Yucatan State, using molecular methods. Fish samples corresponding mainly to species of the families Cichlidae and Heptapteridae were collected from cenotes of Yucatán, and trematodes were isolated for morphological and molecular analysis. Preliminarily, after sequencing ribosomal (28S and ITS) and mitochondrial (COI) DNA, conducting a blast search looking for sequence identity, estimating sequence divergence and phylogenetic interrelationships, we found 15 trematode species, either as adult or metacercaria. This study was supported by the program PAPIIT-UNAM IN200824.

MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION OF *Myxobolus* n. sp. (CNIDARIA, MYXOZOA) INFECTING *Salminus brasiliensis* FROM THE PANTANAL, BRAZIL

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Salminus brasiliensis (Cuvier, 1816), known as dourado, is a carnivorous fish of significant economic importance in Brazil. This species hosts members of the genus *Myxobolus*, the most diverse group of myxozoans, with over 900 species described, some of which are notable fish pathogens. This study aimed to characterize *Myxobolus* n. sp. infecting *S. brasiliensis* in the Pantanal region of Brazil using morphological and molecular analyses. Specimens were collected from the Miranda River, Mato Grosso do Sul, where eleven *S. brasiliensis* were sampled, and seven (67%) were found to be parasitized. *Myxobolus* n. sp. was observed in the gill filaments, forming white, elongated plasmodia measuring 2.1 mm in length. Morphological analysis by light microscopy revealed mature myxospores, pear-shaped in frontal view, measuring 10.1 ± 0.3 μm in length, 6.6 ± 0.2 μm in width, and 5.1 ± 0.2 μm in thickness. In the lateral view, the myxospores were biconvex with symmetrical valves. The polar capsules were elongated, asymmetrical, and occupied more than half of the spore body, measuring 4.9 ± 0.3 μm in length and 1.9 ± 0.2 μm in width. Molecular analysis based on SSU rDNA yielded a 1,954 bp fragment. Phylogenetic analysis revealed clustering by host order with *Myxobolus* n. sp. grouping with *Myxobolus filamentum* and *Myxobolus oliveirai*, previously described in Bryconidae fishes. The results suggest that this is an as-yet undescribed species. This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 001. Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP) provided grant 2023/15107-7 and funding for the thematic project 2018/24980-8. Conselho Nacional de Desenvolvimento Científico e Tecnológico – Brasil (CNPq) provided grant 140004/2023-8.

MORPHOLOGICAL AND MOLECULAR ANALYSIS OF *Myxidium* n. sp. INFECTING *Pimelodus pantaneiro* FROM THE PRATA BASIN, BRAZIL

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Myxozoans are an important group of parasites that mainly affect fish and can lead to great losses, both in natural environments and in fish farming, due to their pathogenic potential. This study aimed to perform a morphological and molecular description based on the sequencing of the small subunit DNA (SSU-rDNA) of myxozoans described in *Pimelodus pantaneiro*. *Myxidium* n. sp. was found free in the bile of *P. pantaneiro* captured in the Prata basin, near the meeting point of the Miranda and Paraguay rivers, in the municipality of Corumbá, state of Mato Grosso do Sul. For morphological analysis, the collected sample was fixed in 10% buffered formalin and for molecular analysis, it was preserved in absolute ethanol. *Myxidium* n. sp. mature myxospores have elongated and fusiform bodies, slightly curved, with pyriform polar capsules of the same size. Morphometric analysis showed a body length of 16.5 ± 0.9 μm, body width of 4.4 ± 0.4 μm, polar capsule length and width of 5.5 ± 0.4 μm and 2.8 ± 0.3 μm, respectively, and thickness of 4.1 ± 0.3 μm. The molecular analysis resulted in a fragment of 2051 base pairs and according to *Basic Local Alignment Search Tool nucleotide* (*BLASTn*) searched the species closest to *Myxidium* n. sp was *Myxidium amazonense* found infecting *Corydoras melini* with 91.4% similarity. Therefore, with the partial results, we suggest that *Myxidium* n. sp. is a new species. This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 001. Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP) provided grant 2023/15107-7 and funding for the thematic project 2018/24980-8.

Lecithaster (TREMATODA: LECITHASTERIDAE) IN INTERTIDAL FISH OF CHILE: ARE THERE NEW SPECIES?

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The genus *Lecithaster* is a small group of digeneans composed of 35 species widely distributed in fish from the tropical to polar zones. In Chile, only one species has been described, *L. pacificum*, in Valdivia (39°S); also, some records of *L. macrocotyle* and unidentified *Lecithaster* species have been found in several coastal fish. In this study, we aim to determine and describe the *Lecithaster* species found in intertidal fish using morphological and genetic methods. Digenean specimens were collected from 6 fish species from the intertidal rocky zone of central (33°S) and central-southern (36°S) Chile. The digeneans were measured, in body and organs, and analyzed genetically using the 18S RNAr V4 region and COI genes. According to molecular analyses, two *Lecithaster* species could be distinguished with the 18S V4 region gene, and 5 species were detected with the COI gene. One *Lecithaster* species, from the clingfish *Sicyases sanguineus*, was genetically clearly distant from other species using both genes; therefore, this digenean is a new species. Another *Lecithaster* species was found in fish from the south (36°–39°S), and Antarctic nototheniid fish. This digeneans' morphology was variable between fish species, although digeneans from nototheniids, was similar to that of *L. macrocotyle* and *L. pacificum*. A third species was found in the clingfish (*Gobiesox marmoratus*) and a labrisomid fish (*Calliclinus geniguttatus*), and two other *Lecithaster* species were found in *Patagonotothen cornucola*. Therefore, there is at least one new species of *Lecithaster* and this genus is diverse in intertidal fish, especially from southern Chile.

FIRST DISCOVERY OF *Stellantchasmus* spp. IN THE AMERICAS: UNVEILING THE LIFE CYCLE WITH MOLECULAR & MORPHOLOGICAL INSIGHTS

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Members of the *Stellantchasmus* genus (Onji & Nishio, 1916) are of zoonotic importance in Southeast Asia. In this report, we present the cercariae of *Stellantchasmus* obtained from naturally infected, introduced *Tarebia granifera* in the Puerto Rican freshwater body, Quebrada de Oro. We also obtained metacercariae of *Stellantchasmus* from naturally infected, native *Dajaus monticola*, with adults recovered from experimentally infected chicks. Morphological and molecular phylogenetic analyses were conducted using partial 28S, internal transcribed spacer 2, cytochrome c oxidase I, and mitochondrial genome sequences. Our results show that the *Stellantchasmus* species discovered in Puerto Rico is closely related to, but distinct from, *S. dermogenysi* from Thailand. Morphological analysis also revealed differences between the species found in Puerto Rico and other known *Stellantchasmus* species. We therefore propose that the specimens represent a novel species of *Stellantchasmus*. Furthermore, a phylogenetic discrepancy between the cercariae from two individual *T. granifera* suggested the presence of another, recently diverged species from the novel *Stellantchasmus* species found in Puerto Rico. However, no complete morphological analysis was possible for this second species, as no metacercarial or adult specimens were recovered. Despite the high infection levels observed in *D. monticola*, the locally occurring novel species of *Stellantchasmus* is unlikely to pose a significant threat to human health in Puerto Rico. This represents the first report of the *Stellantchasmus* genus in the Americas.

Capillaria pterophylli (NEMATODA) FROM THE ORNAMENTAL FISH OF CICHLIDAE: FIRST MOLECULAR DATA AND SEM OBSERVATIONS

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Capillaria pterophyli is one of four species of *Capillaria* known from the neotropical fish of Cichlidae. A total of 248 specimens represented by seven species of neotropical ornamental cichlids were received from Indonesia (IND), Sri Lanka (SL), and Thailand (TH) using an established import company. Internal organs were inspected for the presence of nematodes. Collected nematodes were studied for their morphology using scanning electron microscopy (SEM), and sequencing of 18S rDNA region, was performed. The parasitological examination revealed three fish species were infected with *C. pterophylli*, i.e., *Andinoacara pulcher* (SL)*, Uaru amphiacanthoides* (IND), and *Pterophylum scalare* (IND and SL). The highest infection was found in *P. scalare* from Indonesia with a prevalence (P) of 52.9% and an intensity of infection 1–32. Very low infection levels were observed in *U. amphiacanthoides* (P = 6.67%) and *P. scalare* from Sri Lanka (P = 5%). The newly produced sequence was unique within the database. Phylogenetic analysis placed *C. pterophylli* as a sister taxon to a cluster of avian *Capillaria* spp. The uncorrected *p*-distance between *C. pterophylli* and avian species ranged from 10.9–12.9%. The finding suggests a need for re-evaluation of the taxonomy of *Capillaria* spp. as the genetic distances between different genera included in the analysis were lower than between species of the *Capillaria*. SEM observations allowed us to explore the surface of the parasite’s eggs and confirmed the presence of numerous papillae on the posterior part of the parasite’s body. Supported by the DSI-NRF SARChI Chair (No.101054).

MORPHOLOGICAL AND PHYLOGENETIC DESCRIPTION OF A *Bipteria* sp. (CNIDARIA, MYXOSPOREA) INFECTING THE COMMON TWO-BANDED SEABREAM *Diplodus vulgaris*

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Myxosporeans are economically important fish endoparasites. The common two-banded seabream, *Diplodus vul*garis, is a commercially important sparid fish inhabiting the Mediterranean and eastern Atlantic region. Presently, there is no data concerning the diversity of myxosporean parasites potentially threatening this fish species. Acknowledging this gap in our knowledge, a myxosporean survey was conducted in external and internal tissues of *D. vulgaris* obtained from fishing stocks caught in the eastern Atlantic. Parasitized tissues were examined under a light microscope, and subsequently prepared for molecular and phylogenetic studies targeting the 18S rDNA. Spherical to subspherical disporic plasmodia, and mature myxospores complying with the definition of *Bipteria*, were observed in the urinary bladder. Myxospores were triangular to inverse pyramidal in valvular view and ellipsoidal in sutural view, formed by two symmetric smooth valves united along a sinuous suture line, each bearing a wing-like projection extending from the posterior end. Two spherical polar capsules, symmetric, located at the same level at the anterior end, and opening to opposite sides, each with a polar tubule coiled in 5 turns. Distance estimation revealed the lowest genetic distance (8.1%) to *Bipteria lusitanica*, previously reported from white seabream *Diplodus sargus*, also caught from the eastern Atlantic. No gross morphological similarity was retrieved to other congeners, suggesting the parasite as a potentially new species. Maximum likelihood and Bayesian Inference trees placed the 18S rDNA sequence of the parasite within the highly heterogenous marine urinary bladder clade, reinforcing tissue tropism as a more relevant evolutionary character than myxospore morphology.

FLUCTUATING ASYMMETRY IN THE ATTACHMENT ORGANS OF *Cichlidogyrus* spp. AND *Scutogyrus* sp. (MONOGENEA) ON THE NILE TILAPIA *Oreochromis Niloticus* (L.) FROM A NEOTROPICAL AND NEARCTIC MEXICAN BASINS

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Fluctuating asymmetry (FA) and increased variation in bilateral symmetry in a sample of monogeneans can indicate disturbance in developmental stability caused by environmental and/or genomic stress. This study was conducted to determine the presence of FA in the sclerotized structures of monogeneans from two genera: *Cichlidogyrus* (*C. sclerosus*, *C. halli*) and *Scutogyrus* (*S. longicornis*) collected in the Cuautla River, Morelos (Neotropical basin) and Lake Pátzcuaro, Michoacán, (Nearctic basin) from México. We hypothesize the potential effect of chemical contamination on FA. Geometric morphometrics with Procrustes ANOVA was used to test FA in the ventral and dorsal anchors in these monogeneans from *Oreochromis Niloticus*. Then, Generalized Additive Model for Location, Scale and Shape (GAMLSS) were used to assess the statistical associations of heavy metal concentrations, fish morphometric measurements, physicochemical variables on FA patterns. Principal Component Analysis showed no clear group formation according to shape variability among basins. Evidence of FA for size and shape in ventral anchors of *Cichlidogyrus* spp. and *S. longicornis* was found, in contrast to dorsal anchors, which only displayed shape FA. The GAMLSS models revealed a significant positive relationship between the FA of *C. sclerosus*, *C. halli, S. longicornis* and Pb, Ni, pH and Condition factor (K). These results support our hypothesis that FA in the anchors of monogeneans from *O. niloticus* would be good indicators of aquatic contamination from Neotropical and Nearctic Mexican basins produced by association to environmental variables and host related factors.

A PHYLOGEOGRAPHIC APPROACH OF THREE SPECIES OF *Clinostomum* LEIDY, 1856, FROM THE NEOTROPICAL REGION OF MEXICO, WITH THE DESCRIPTION OF A NEW SPECIES FROM *Ardea herodias*

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Clinostomum Leidy, 1856 is a global group of endoparasites that in adult stage resides attached to mucosa of the mouth cavity and esophagus of fish-eating birds, whereas that the larval form knowns as metacercaria ("yellow grub") produce several damages to their freshwater fish and amphibian that serves as second intermediate hosts. In the Nearctic and Neotropical regions of Mexico species of *Clinostomum* have been intensively studied discovering seven species and appear the inventory of species of *Clinostomum* could be complete in a near future. In the current research, sequences of the ITS from nuclear ribosomal DNA and the *cox 1* from mitochondrial DNA were generated to two species *C. tataxumui*, *C. cichlidorum* and an unidentified species, distributed sympatrically in three biogeographic provinces of Mexico and one in Middle America. The objectives of the current study were to characterise a new species of *Clinostomum*, to compare the population genetic structure of *C. tataxumui*, *C. cichlidorum* and of the new species. The phylogeographic studies inferred with the *cox 1* indicated that the populations of *C. tataxumui* and *C. cichlidorum* lacked a phylogeographic structure and exhibited high haplotype diversity, low nucleotide diversity and low Fst values among the biogeographic provinces; in combination with negative values on the neutrality test, this suggests that the populations are expanding. In contrast, the populations of the new species are less connected and are subdivided into smaller populations, leading to genetic differentiation, suggesting that the populations might experience bottlenecks.

FIRST MOLECULAR CHARACTERIZATION OF *Annulotrematoides* KRITSKY & BOEGER, 1995, PARASITIZING THE GILLS OF *Cyphocharax modestus* (FERNÁNDEZ-YÉPEZ, 1948) IN BRAZIL

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The dactylogyrid genus *Annulotrematoides* includes monopisthocotylids that parasitize the gills of freshwater fishes from the order Characiformes. This taxon currently comprises five species, all of which occur in fishes in Brazil, except for *Annulotrematoides bonaerensis*, which was found in *Cyphocharax voga* in Argentina. Specimens of *A. bonaerensis* were found infecting the gills of *Cyphocharax modestus* from the Pardo River, São Paulo state, Brazil. The morphology of the male copulatory complex (MCO) of *A. bonaerensis* is similar to other species in the genus, featuring a non-coiled tube. *Annulotrematoides amazonicus* is slightly similar but differs with a curved tube, while *A. bonaerensis* has a J-shaped tube with an expanded base and a straight distal end. For the first time, molecular data of *A. bonaerensis* 28S rDNA were obtained and used as a basis for phylogenetic analyses of the genus. The phylogram based on 28S rDNA reveals that *Annulotrematoides* is closely related to sequences belonging to *Urocleidoides*, especially as a sister group of *Urocleidoides parodoni*, *Urocleidoides tenuis*, and *Urocleidoides indianensis*, all found parasitizing fishes from the family Parodontidae (Characiformes), suggesting evolutionary connections, as they are slightly different morphologically. Furthermore, our findings represent the first record of this species in Brazil. Financial support: FAPESP 2020/05412-9; CAPES #88887.955939/2024-00 and 88887.976117/2024-00; PROPG/UNESP 04/2022.

THE UNEXPLORED SPECIES OF SOUTH AMERICA: NEW SPECIES OF *Cacatuocotyle* (MONOPISTHOCOTYLA: DACTYLOGYRIDAE) FROM THE PARDO RIVER BASIN, BRAZIL

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Approximately 8,507 species of freshwater fishes have been recorded in the Neotropical region, with 3,624 of them occurring in Brazilian river systems. The diversity of parasites infecting/infesting these fishes is notably high, yet much of this biodiversity remains poorly understood. Among the parasitic groups, Monopisthocotyla, particularly species of the family Dactylogyridae, is highly diverse and abundant in fishes from South American freshwaters. The genus *Cacatuocotyle* comprises species that parasitize the gills and body surfaces of characids, a prominent fish family in the region. In this study, we report a putative new species of *Cacatuocotyle* collected from the gills and body surfaces of four characid fishes (*Astyanax lacustris*, *Psalidodon bockmanni*, *Psalidodon fasciatus*, and *Psalidodon paranae*) in the Pardo River basin, São Paulo State, Brazil, based on molecular and morphological data, providing a comprehensive understanding of their distinct features. A distinct copulatory complex morphology and bar are observed compared to other described congener species, however, the anchors exhibit a similar morphology to that of *Cacatuocotyle paranaensis*. Phylogenetic analyses placed *Cacatuocotyle* sp. closely related to *Cacatuocotyle papilionis*, suggesting a possible evolutionary link between these taxa. This discovery underscores the largely unexplored diversity of parasitic fauna in Neotropical freshwater systems. The results emphasize the necessity for more detailed studies on parasite-host interactions, which are essential for deepening our understanding of the ecological dynamics and biodiversity within South American freshwater ecosystems. Financial support: FAPESP 2020/05412-9; CNPq 161839/2021-5, 311635-2021-0; PROPe-PROPG/UNESP 04/2022; and CAPES 88887.976117/2024-00.

MONOPISTHOCOTYL GILL PARASITES OF *Astyanax bimaculatus* (CHARACIFORMES, CHARACIDAE) AND ITS LOW PREVALENCE IN THE APODI-MOSSORÓ RIVER BASIN, BRAZIL: A NEW RECORD AND ECOLOGICAL INSIGHTS

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Astyanax bimaculatus is a widespread fish species in Brazil, with a geographic range extending from the Northern to Southern regions of the country. The parasite fauna of *Astyanax* spp. is notably diverse, with monopisthocotyls standing out as the most prevalent fish parasites. This study aimed to investigate the diversity of monopisthocotyls parasitizing *A. bimaculatus* from the Apodi-Mossoró River Basin, municipality of Caraúbas, Rio Grande do Norte state, Brazil, and to compare the findings with previous studies conducted on the same host species in other regions. In August 2020, 35 specimens of *A. bimaculatus* were examined for monopisthocotyl parasites. A putative new species of *Characithecium* was discovered on the gills of 11.43% of the hosts. The mean abundance and intensity of infestation were 0.11 ± 0.06 (0-1) and 1, respectively. Prevalence was significantly lower compared to previous studies. This species exhibits a unique combination of characteristics among congeneric species, with the presence of a median-posterior projection on the ventral bar combined with an accessory piece of the copulatory complex in the shape of a wrench. Considering the ecological factors of the studied sites, we drew inferences regarding the ecology of both fish and parasites, as well as their potential interactions with migratory and non-migratory aquatic birds. Documenting the diversity of monopisthocotyls in *A. bimaculatus* across different locations enhances our understanding of the parasitic fauna of Neotropical fishes. It also provides insights into the geographical distribution patterns of parasites and their relationships with their hosts. Financial support: CNPq 121217-2020-5, 311635-2021-0.

MORPHOLOGICAL AND MOLECULAR INSIGHTS OF AN INTRIGUING DIGENEAN (PLAGIORCHIIDAE) FOUND IN *Corydoras aeneus* (GILL, 1858) FROM BRAZIL

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New digeneans infecting fishes from the Neotropical region have been described continuously over the past years. During a field expedition in March 2024, we recovered 16 digeneans from the intestine of 50 *Corydoras aeneus* (Gill, 1858) (Siluriformes: Callichthyidae) from Capivarinha River, municipality of Botucatu, São Paulo state, Brazil. The digeneans were fixed and prepared for morphological (n = 9), SEM (n = 2), and molecular analyses (28S rDNA sequences, n = 5). The digenean morphologically resembled species of *Choledocystus* Pereira & Cuocolo, 1941 (Plagiorchiidae); however, it differs in the absence of small papillae or a sucker-like structure surrounding the genital atrium, smooth tegument without spines, sinuous intestinal caeca, genital pore located extracaecal at the anterior left margin of the body, follicular vitellaria distributed in the intra and extracaecal region, and ventral sucker larger than the oral sucker. Phylogenetic analyses revealed our digenean as sister species of *Choledocystus hepatica* (Lutz, 1928), parasites of amphibians, with 2.1% of genetic distance, and closely related to species of *Infidum* Travassos, 1916, parasites of reptiles, with 2.5-3.3% of genetic distance. Our results indicated that our digenean might correspond to a new genus and a new species closely related to *C. hepatica* within the Plagiorchiidae. A robust morphological analysis including scanning electron microscopy as well as new molecular data using the COI mtDNA gene should be gathered as part of the characterization and description of the new genus and species in the future. Funding: FAPESP 2022/12376-4 and 2024/05688-5; PROPG/UNESP 04/2022; and CAPES 88887.976117/2024-00).

SOMETHING IS MISSING: ABSENCE OF MUSCULAR LOBES IN *Creptotrema creptotrema* (DIGENEA: ALLOCREADIIDAE) FOUND IN AN UNUSUAL FISH HOST FROM BRAZIL

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The presence of muscular lobes on the oral sucker is one of the main morphological characteristics used to delimit genera among Allocreadiidae. The type-species *Creptotrema creptotrema* exhibits a discrete ventrolateral muscular lobe on either side of the oral sucker, stretching from the ventral to the lateral area. One specimen of *Crenicichla* sp. (Cichlidae) from Tietê River, São Paulo state, Brazil, was found parasitized with 30 digeneans. The worms were fixed and prepared for morphological (n=15), SEM (n=4), and molecular analyses (28S rDNA and COI mtDNA sequences, n=5). The specimens were gravid adults (8-10 eggs per individual) and were consistent with *C. creptotrema*, except for the absence of muscular lobes on the oral sucker. The molecular phylogenetic analyses clustered the newly sequenced individuals together with *C. creptotrema*. Genetic divergence between *C. creptotrema* and our specimens was null for 28S rDNA, and very low (0.7%) for COI mtDNA. This is the first report of an allocreadiid from a cichlid species. *Creptotrema creptotrema* has been only reported parasitizing Characiformes and Siluriformes. We do not consider this as an accidental infection and *C. creptotrema* seems to exhibit phenotypic plasticity; the lack of oral lobes might result from infecting an unusual fish host. Nevertheless, the presence and the number of muscular lobes on the oral sucker of some genera of allocreadiids, including *Creptotrema*, does not appear to be a consistent characteristic for the initial identification of genera and species, and therefore, should be further evaluated with caution. Financial support: 311635-2021-0; PROPe-PROPG/UNESP 04/2022; and CAPES 88887.976117/2024-00.

MORPHOLOGICAL AND MOLECULAR DATA OF A NEW SPECIES OF *Diaphorocleidus* (MONOPISTHOCOTYLA: DACTYLOGYRIDAE), A GILL PARASITE OF THREE NEOTROPICAL CHARACID FISHES FROM BRAZIL

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The Neotropical region harbors the richest freshwater fish fauna in the world. However, the precise estimate of species diversity in this region remains uncertain or even unknown, including the diversity of parasites that infest/infect these fishes. Among the parasites of Neotropical fishes, monopisthocotyls are particularly noteworthy. The genus *Diaphorocleidus* comprises monopisthocotyls that parasitize the gills, nostrils, and body surfaces of freshwater characids. In this study, we describe a putative new species of the genus *Diaphorocleidus*, a parasite from the gills of three characid fish species (*Psalidodon bockmanni*, *Psalidodon fasciatus*, and *Astyanax lacustris*) from the Pardo River basin, a sub-basin of the Paranapanema River, state of São Paulo, Brazil, based on morphological, molecular (based on 28S rDNA sequences), and phylogenetic (Bayesian Inference and Maximum Likelihood) analyses. The new species primarily differs from its congeners by the morphology of the copulatory complex, which presents the smaller subunit of the accessory piece as bifurcated, shaped like a chela or the tip of a fishing hook. The phylogenetic analysis indicated a close relationship of the new species with *Diaphorocleidus neotropicalis*, however, the small subunit of the accessory piece is shaped like a chela (or fishing hook tip) *versus* a leaf-shaped in *D. neotropicalis*. This study contributes to improving the knowledge of Neotropical monopisthocotyls by documenting a putative new species of *Diaphorocleidus* parasitizing the gills of three characid species. Financial Support: FAPESP 2020/05412-9; CNPq 161839/2021-5, 311635-2021-0; and PROPe-PROPG/UNESP 04/2022.

MORPHOLOGICAL AND MOLECULAR DATA OF A NEW SPECIES OF *Henneguya* (CNIDARIA: MYXOZOA) INFECTING *Astyanax bimaculatus* (CHARACIFORMES: CHARACIDAE) IN THE CAATINGA BIOME, BRAZIL

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The Neotropical region has the world's most diverse freshwater fish fauna. However, accurate estimates of species diversity in this region remain unclear, as does the understanding of the parasites that infect these fishes. A large portion of this parasitic diversity remains unstudied to date. Myxozoans are cnidarian parasites of worldwide distribution and they are the most spectacular examples of parasite radiation. Using an integrative taxonomic approach, including spore morphology, molecular data, and host specificity, a new cnidarian myxozoan, *Henneguya* sp., is described. Plasmodia were located in the gills, between the gill lamellar epithelium, without connective tissue surrounding them. Morphometric analysis of mature myxospores, ellipsoidal in frontal view, revealed a unique set of measurements. Histopathological analysis showed large intralamellar polysporic plasmodia associated with displacement, deformation, and fusion of nearby gill lamellae, with adjacent lamellae being pushed laterally. Phylogenetically, the novel species grouped within a clade containing *Henneguya*/*Myxobolus* spp., mostly parasites of South American characins, and appears in a well-supported subclade of *Henneguya* species parasitizing fishes of the genus *Astyanax*. This study highlights the highly endemic diversity still hidden in the Caatinga biome and emphasizes the need to improve protection and conservation strategies for this threatened ecoregion, where biodiversity data remain scarce. Financial support: CNPq #121217-2020-5 and #311635-2021-0; FAPESP #2019/19060-0.

A NEW SPECIES OF *Mariauxiella* (CESTODA: PROTEOCEPHALIDAE) FROM THE DRIFTWOOD CATFISH *Ageneiosus militaris* (SILURIFORMES: AUCHENIPTERIDAE) IN THE PARDO RIVER, SÃO PAULO STATE, BRAZIL

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Siluriforms (catfishes) are highly diverse in the Neotropical region and serve as hosts to an equally diverse fauna of proteocephalid cestodes. These tapeworms are a dominant group of endoparasites in catfishes from South America, primarily found in large pimelodid catfishes (Pimelodidae). However, other catfish groups, such as the auchenipterids (Auchenipteridae) may also host tapeworms in their guts. The species composition of the genus *Mariauxiella* has recently been rearranged based on combined morphological and molecular approaches. *Mariauxiella pimelodi* (type-species) ex *Pimelodus ornatus* (Pimelodidae) and *M. brevifilis* ex *Ageneiosus inermis* (Auchenipteridae) are the only species currently recognized in the genus. In this study, a new species of *Mariauxiella* is described based on two adult specimens found parasitizing the auchenipterid catfish *Ageneiosus militaris* in the Pardo River (Paranapanema River basin), São Paulo state, Brazil. The new taxon is readily distinguished from *M. pimelodi* by having biloculate instead of uniloculate suckers. It differs from *M. brevifilis* by having a larger body (80–92 mm *vs* 22–49 mm), narrower strobila (maximum width of 1.77mm *vs* 5.1mm), and smaller scolex width (0.93–1.02mm *vs* 1.35–1.91mm). Molecular phylogenetic analyses, based on partial 28S rRNA and complete COI, showed the new species exhibiting a sister relationship with *M. brevifilis*, with both forming a sister group to *M. pimelodi*. The integration of morphological and molecular data has once again proven to be useful to accurately delineate closely related species and improve our understanding of the evolutionary history of Neotropical proteocephalid tapeworms. Financial support: FAPESP 2020/05412-9, 2021/12593-2.

NEW SPECIES OF *Rondonia* (NEMATODA, ATRACTIDAE) FROM THE INTESTINE OF *Metynnis lippincottianus* (CHARACIFORMES, SERRASALMIDAE) FROM PARDO RIVER, BRAZIL

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Metynnis lippincottianus is a characid native to the Amazon River in Brazil but can also be found in other regions, such as the Pardo River, municipality of Salto Grande, São Paulo state. The helminth fauna of *M. lippincottianus* is well-known, however, until now, there was no record of species of the genus *Rondonia* parasitizing this host. During a survey of parasites in fishes from the Pardo River, nematodes infecting the intestine of *M. lippincottianus* were observed. Parasites were collected and further processed following parasitological methods. Through morphological (n=10), SEM (n=10), and molecular analyses of the 28S and 18S rDNA gene (n=1), we found that the parasite specimens found parasitizing this host belong to the genus *Rondonia*. However, it differs from the three known species of the genus (*R. lophii, R. batrachogena*, and *R. rondoni*) by the combinations of the number (11 pairs) and organization of caudal papillae (3 pairs pre-cloacal; 2 pairs ad-cloacal, and 6 post- cloacal) and excretory pore located before esophageal bulb, a feature that has never been previously described in *Rondonia* spp. Molecular analyses clustered the new sequence as sister species of *Rondonia rondoni* in both phylogenetic trees with 1% of genetic variation in the 18S rDNA and 2% in the 28S rDNA. Based on the taxonomic analysis, we have evidence that *Rondonia* sp. here studied is a putative new species, that should be properly described in the future. Financial support: FAPESP 2020/05412-9 and 2022/14658-7; PROPG/UNESP 04/2022; and CAPES 88887.976117/2024-00.

OCCURRENCE OF *Hysterothylacium* WARD & MAGATH, 1917 (ASCARIDIDA: RAPHIDASCARIDIDAE) LARVAE INFECTING *Piabina argentea* REINHARDT, 1867 (CHARACIFORMES: CHARACIDAE) FROM PARDO RIVER, SÃO PAULO STATE, BRAZIL

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Piabina argentea is a small characid widely distributed throughout South America, with records from the upper Paraná, São Francisco, Itapicuru, Paraíba, and Itapemirim river basins in Brazil. Despite its wide distribution and ecological importance, no studies about its parasitic helminth fauna have been carried out to date. This study aims to report the occurrence of *Hysterothylacium* sp. larvae in *P. argentea* from the Pardo River, São Paulo state, Brazil. The parasites were analyzed by optical microscopy and SEM, and genomic DNA was extracted and partial 28S rDNA was sequenced. *Hysterothylacium* larvae were isolated from 9 of the 68 examined hosts (prevalence of 13.2%). Mean abundance and mean intensity of infection were 0,34±0,15 and 2,56±085, respectively. These nematodes were usually found as encysted larvae in mesenteries. Recovered larvae were cylindrical and attenuated at both ends. Cuticle with delicate transverse striations. Anterior extremity poorly developed with two labia, one of them provided with prominent boring teeth. Four labial papillae surrounded the triradiate mouth opening. Esophagus with anterior muscular part and a glandular ventriculus. Excretory pore located a small distance (329.3 µm) from anterior extremity. Intestinal caecum shorter than the long ventricular appendix. Rectum short, opening by an anal pore. Tail short and conical, with a nodular protuberance. Phylogenetic analysis grouped *Hysterothylacium* larvae with species of *Raphidascaroides* and *Raphidascaris*, indicating that *Hysterothylacium* is not a monophyletic genus or that the morphological limits that define this genus need to be revised. Financial support: FAPESP 2020/05412-9, 2023/10835-4, 2022/04715-3.

UNRAVELING THE TAXONOMY OF FISH HAEMOGREGARINES, A FEW SPECIES AT A TIME

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Haemogregarines (Apicomplexa: Adeleorina) are obligate parasites of many species of vertebrates, however to date, there is very limited understanding of these parasites in the most diverse group of vertebrates, fishes. While many of these parasites from amphibians, reptiles and mammals have been characterised molecularly using the 18S rRNA gene, identification of haemogregarines infecting fishes has relied solely on morphological identification by microscopy, relying mostly on stages found in the blood of fishes. However, haemogregarines follow a heteroxenous life cycle, which includes stages in both vertebrate and invertebrate hosts, the latter being the definitive host. In fishes, the majority of these parasites belong to the genus *Haemogregarina*, with little knowledge on the definitive host responsible for transmission. Recently, two species of *Haemogregarina*, *Haemogregarina bigemina* and *Haemogregarina daviesensis*, were characterised molecularly using fragments of the 18S rRNA gene and their phylogenetic placement estimated. Whilst the latter species' sequences clustered with other species of *Haemogregarina*, *H. bigemina* clustered with unknown apicomplexan parasites and symbionts of fishes and corals in a clade basal to sequences of members of the coccidia, and as such outside of the *Haemogregarina* clade. While species of *Haemogregarina* are accepted to be leech-transmitted, *H. bigemina* is strongly suggested to be transmitted by gnathiid isopods. This in mind and this species' current phylogenetic placement suggests that not all haemogregarines of fish are leech transmitted and may belong to an entirely new genus. As such this study aimed at identifying further haemogregarines of fishes using a combination of morphology and molecular data.

CHARACTERISING THREE NEW SPECIES OF *Macvicaria* (DIGENEA, OPECOELIDAE) FROM *Diplodus capensis* IN SOUTHERN AFRICA

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Macvicaria Gibson & Bray, 1982 is a genus of one of the most speciose digenean families, the Opecoelidae Ozaki, 1925. Like many representatives of the family, species of *Macvicaria* are notoriously difficult to identify due to their high morphological similarity. Only one species of *Macvicaria* has previously been reported from southern Africa: *Macvicaria obovata* (Molin, 1859). This study aimed to explore the diversity of digeneans from *Diplodus capensis* (Smith) along the coasts of South Africa and Namibia, by employing the use of an integrative approach, including both morphological and molecular (28S rDNA, ITS2 rDNA, *cox*1 mtDNA and *nad*1 mtDNA) data. Based on the combined data, we were able to discern three species of *Macvicaria*, which are all new to science. The most informative genes for species differentiation were the 28S rDNA and the mitochondrial genes, with ITS2 not aiding in species delineation in this case. A haplotype network (based on the *cox*1 mtDNA) revealed a total of seven unique haplotypes for *Macvicaria* sp. 1 (interestingly not grouping according to specific localities), four unique haplotypes for *Macvicaria* sp. 2, and two unique haplotypes for *Macvicaria* sp. 3, thereby highlighting the use of an integrative taxonomic approach, especially when characterising morphoplastic species, such as members of the Opecoelidae. This study provides the first report of *Macvicaria* spp. from *D. capensis*, the first report of this genus from Namibia, as well as the first molecular characterisation of species of *Macvicaria* from this region.

SPATIAL DISTRUBUTION OF DIGENEAN OF THE ACANTHOCOLPIDAE FAMILY IN MARINE FISHES OF GULF OF MEXICO

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Fish parasites are important in ecosystems because they participate in food chains and function as population controllers of their hosts. The digenean parasites are of the most abundant groups, including the Acanthocolphidae family, which includes 144 species, of which little is known in the Gulf of Mexico. This work describes the spatial distribution of Acanthocolphidae family members in the Southern Gulf of Mexico. 1,989 fish (tonguefish, catfish, hemulids, among others) were collected off the coasts of Tamaulipas, Veracruz, Tabasco, Campeche, and Yucatán between 2016 and 2020. 34,683 parasites were recovered and grouped into nine morphs of this family (seven *Stephanostomum* sp., *Acantocolpus* sp. metacercariae and adult of *Stephanostomum minankisi*). Metacercariae morphos *S.*sp. and *S.*sp2 were the most prevalent (26.24 % and 22.62 %) and abundant (10.75 ± 107.43 and 3.33 ±. 24.24). Flounders and haemulids shared eight of the nine recorded morphs. While catfish only shared the adult *S. minankisi* with flounders. On the other hand, fish from other families only shared four morphs with flounders and haemulids. Acanthocolpidae, mostly larval stages morphos were widely distributed in the Gulf of Mexico and the different fish species. This study contributes to the taxonomy and data records of the Acanthocolpidae family in the Gulf of Mexico. However, molecular studies are needed to assign a taxonomic identity to the morphs found.

DIVERSITY OF PARASITIC CRUSTACEANS OF THE GENUS *Salmincola* IN EURASIAN AQUATIC ECOSYSTEMS BASED ON MOLECULAR MARKER ANALYSIS

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Salmincola spp. are commonly reported ectoparasites of salmonid fishes and are significant pathogens warranting surveillance in both wild and cultured salmonid populations. However, there is currently a notable lack of molecular data on this genus. In the present study, we investigate the diversity of Salmincola spp. based on mitochondrial cox1 and nuclear ribosomal 28S gene sequences. Specimens of *Salmincola* spp. were collected from the fins, skin, gills, and nasal fossae of seven fish species across ten localities: *Coregonus lavaretus* (Teletskoye Lake, Altai region; Baikal, Baunt, Dorong, Dood Tsagaan, Khövsgöl lakes, Baikal Rift Zone; Verkhnee Ondomozero Lake, Kola Peninsula), *C. autumnalis* (Baikal Lake), *C. muksun* (Yana, Anabar, and Indigirka rivers, Yakutia), *Thymallus arcticus* (Baikal, Dood Tsagaan; and Khövsgöl lakes), *T. nigrescens* (Khövsgöl Lake), *Oncorhynchus nerka*, and *Salvelinus malma* (Kronotskoye Lake, Kamchatka). Fragments of the 28S and *cox1* genes, measuring 950 bp and 616 bp respectively, were amplified. Phylogenetic reconstructions within the genus *Salmincola* were conducted using maximum likelihood (ML) and Bayesian inference (BI) approaches with IQ-TREE 2 and MrBayes v.3.2.1, respectively. The newly obtained sequences were categorized into nine species-level clades. Seven clades were formed by sequences from *S. extensus*, *S. extumescens*, *S. lavaretus*, *S. thymalli*, *S. svetlanovi*, *S. edvardsii*, and *S. carpionis*, respectively. Distinct phylogenetic lineages were identified from the copepods collected from the fins of *C. lavaretus* and *C. autumnalis* in Baikal Lake, as well as from the nasal fossae of *T. arcticus* from Dood Tsagaan Lake. This work was supported by the Russian Science Foundation, project no. 23-74-10101.

DNA BARCODING OF METACERCARIAE OF *Diplostomum* spp. IN VARIOUS AQUATIC ECOSYSTEMS OF RUSSIA

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Metacercareae of *Diplostomum* spp. parasitize in the eyes and the brain of freshwater fishes and cyclostomata, resulting in impaired spatial orientation, reduced nutritional quality, and decreased growth rates. The identification of *Diplostomum* spp. metacercariae poses significant challenges due to several factors, including weak expression of diagnostic traits, a limited set of morphological characteristics, and the inherent complexities involved in studying metacercarial morphology. Consequently, the taxonomy of this genus remains inadequately resolved, complicating efforts to assess its diversity. The application of molecular markers has proven effective for elucidating species diversity and resolving discrepancies in the interpretation of morphological features. In the present study, we utilized sequences of the mitochondrial *cox1* gene and the nuclear ITS1–5.8S-ITS2 genes to identify *Diplostomum* spp. in fishes from four large lakes in Siberia and the Russian Far East: Chany Lake (West Siberian lowland). Teletskoye Lake (Altay region), Baunt Lake (Baikal region) and Kronotskoye Lake (Kamchatka). As a result, 15 species-level genealogies of *Diplostomum* spp. were recorded. However, the majority of these genealogies remain undetermined at the species level, largely due to the absence of reference data and the frequent challenges associated with reliable species identification based on metacercariae morphological characteristics. In such instances, further investigation of other life cycle stages of *Diplostomum* spp. is necessary for accurate species identification. This work was supported by the Russian Science Foundation, project no. 23-74-10101.

FIRST NOVEL SPECIES OF *Elaphognathia* SPECIES (CRUSTACEA, ISOPODA, GNATHIIDAE) FROM PHILIPPINE CORAL REEFS

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Gnathiids are the most prevalent and ecologically important temporary ectoparasites of coral reef fishes, playing a crucial role in maintaining the functional integrity of coral reefs. Through their role as parasites, gnathiids can influence community dynamics in their ecosystem. The family Gnathiidae constitutes 12 genera, including *Elaphognathia* that can be distinguished from other genera by the deeply excavated frontal border, dramatic lengthening of the mandibles and addition of apical cusps. There are currently 24 known species of *Elaphognathia* described over a period of 130 years, with only two species molecularly characterised. The present study aims to contribute to knowledge on this genus by providing a comprehensive integrative description of the 25th species of *Elaphognathia*. Larval gnathiids were collected in the Central Indo-Pacific (Philippines), using light traps, kept alive to moult into adults and preserved in 95% ethanol for morphological and molecular characterisation. The species description was based on light and scanning electron microscopy of the adult male, and prepared in the DEscriptive Language for Taxonomy program (DELTA) using a general Gnathiidae character set. Key distinguishing features of the new species are two inner lobes on the inferior margin and triangular protrusion on the superior margin of the mandible, as well as the excavated frontal margin with two equal superior frontolateral processes. The novel species can be distinguished from other molecularly characterised *Elaphognathia* (*E. sugashimaensis* and *E. rangifer*) by 28% variation in COI sequences. More molecular data is required in order to elucidate a more accurate phylogenetic analysis of this genus.

Thematic areas

4. ECOLOGY, LIFE CYCLES & EPIDEMIOLOGY

ORAL PRESENTATIONS

(Please note the name and institution shown in this list are those of the person presenting the talk, who may not be the first author; the complete author list including all institutional affiliations are shown with the full abstract)

1. LONG-TERM DYNAMICS OF THE METAZOAN PARASITE SPECIES RICHNESS AND DIVERSITY OF *Mayaheros urophthalmus* FROM CELESTÚN, YUCATÁN, MEXICO. Aguirre-Macedo M.L. et al. Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional Unidad Mérida, Mexico
2. BEHAVIOUR OF *Anisakis simplex* INFLUENCED BY BIOTIC AND ABIOTIC FACTORS. Buchmann K. et al. Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Frederiksberg C., Denmark
3. GASTROINTESTINAL PARASITES OF HARBOUR SEAL (*Phoca vitulina* L.) IN DANISH MARINE WATERS. Buchmann K. et al. Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Frederiksberg C., Denmark
4. TRENDS IN PARASITISM AMONG MARINE FISHES: A COMPREHENSIVE MODEL FROM THE MEDITERRANEAN SEA. Dallarés et al. Departament de Biologia Animal, Biologia Vegetal i Ecologia, Universitat Autònoma de Barcelona, Barcelona, Spain
5. MYXOZOANS UNDER MULTIPLE STRESSORS: HISTORICAL ENVIRONMENTAL IMPACT ON MYXOZOANS OF THE PEARL RIVER, LOUISIANA, USA. Díaz-Morales D.M. et al. University of Washington, Seattle, WA, USA
6. THE ECOLOGY OF BLACK SPOT SYNDROME INDUCED BY *Cryptocotyle* (DIGENEA) INFESTATIONS IN THE ECOSYSTEMS OF THE ENGLISH CHANNEL AND THE NORTH SEA. Duflot. et al. Anses, Laboratory for Food Safety, Boulogne-sur-Mer, France
7. TREMATODE DIVERSITY AND THEIR TEMPORAL PREVALENCE IN LYMNAEID AND PLANORBID SNAILS IN UPPER KLAMATH LAKE, OREGON, USA. Flores S.B. et al. U.S. Geological Survey, Western Fisheries Research Center, Seattle, WA, USA
8. PARASITE WARNING US ON ECOSYSTEM CHANGES. THE CASE STUDY OF FISH-PARASITES IN ANTHROPOGENICALLY IMPACTED LAKE VICTORIA. Gobbin T. et al. Hasselt University, Centre for Environmental Sciences, Belgium
9. SEASONAL GEOGRAPHIC PREVALENCE AND DISTRIBUTION OF *Tetracapsuloides bryosalmonae* IN THE GREAT LAKES BASIN. Gorgoglione B. et al. Fish Pathobiology and Immunology Laboratory, Dept. Pathobiology and Diagnostic Investigation / Dept. Fisheries and Wildlife, Michigan State University, East Lansing, Michigan, USA
10. ROUND AND ROUND WE GO: WHAT WE KNOW AND DON'T KNOW ABOUT THE LIFE CYCLES OF PARASITIC CRUSTACEANS. Hadfield K.A. et al. Water Research Group, Unit for Environmental Sciences and Management, North-West University, 11 Hoffman Street, Potchefstroom 2520, South Africa
11. INFECTION OF *Kudoa* sp. IN ATLANTIC MACKEREL (*Scomber scombrus*) CAUGHT IN IRISH WATERS. Kiralyova V. et al. Marine and Freshwater Research Centre, Atlantic Technological University (ATU), Galway, Ireland
12. RAPID SPECIATION IN HOST LINEAGE MAY LEAD TO ADAPTIVE EVOLUTION OF PARASITES' STRESS RESPONSE GENES IN MONOPISTHOCOTYLAN FLATWORMS. Kmentová N. et al. Centre for Environmental Sciences, Research Group Zoology: Biodiversity and Toxicology, Hasselt University, Diepenbeek, Belgium
13. INTERCELLULAR COMMUNICATORS BETWEEN HELMINTHS AND THEIR FISH HOSTS. Kuchta R. et al. Institute of Parasitology, Biology Centre, Czech Academy of Sciences, České Budějovice, Czech Republic
14. CONTRASTING DEMOGRAPHIC HISTORIES OF A GENERALIST AND SPECIALIST PARASITE INFECTING EUROPEAN WHITEFISH IN POSTGLACIAL LAKES. Llaberia-Robledillo M. et al. Cavanilles Institute of Biodiversity and Evolutionary Biology, University of Valencia, Valencia, Spain
15. FIRST ELUCIDATED LIFE-CYCLE FOR A SOUTHERN AFRICAN MARINE TREMATODE: *Rhipidocotyle* sp. (BUCEPHALOIDEA: BUCEPHALIDAE) IN LEERFISH *Lichia amia* (L.) (CARANGIDAE), VARIOUS FISH INTERMEDIATE HOSTS AND THE BROWN MUSSEL *Perna perna* (L.). Louvard C. et al. Water Research Group, Unit for Environmental Sciences and Management, North-West University, 11 Hoffman St, Potchefstroom 2531, North-West Province, South Africa
16. PATTERNS OF HYBRIDIZATION BETWEEN *Anisakis simplex* (s.s.) AND *A. pegreffii* IN THE SYMPATRIC AREA OF THE NE ATLANTIC WATERS: A POSSIBLE TOOL FOR MONITORING PARASITE DISTRIBUTION SHIFTS IN A CHANGING MARINE ENVIRONMENT? Mattiucci S. et al. Department of Public Health and Infectious Diseases, Sapienza-University of Rome Piazzale Aldo Moro, 5 00185 Rome, Italy
17. "GENDER REVEAL PARTY" IN THE ANISAKID NEMATODE *Anisakis pegreffii*: UNVEILING THE SEX OF LARVAL STAGES BY USING DNA MICROSATELLITE LOCI. Mattiucci S. et al. Department of Public Health and Infectious Diseases, Sapienza-University of Rome Piazzale Aldo Moro, 5 00185 Rome, Italy
18. TROPHIC INTERACTION BETWEEN PARASITIC ISOPODS AND THEIR ASSOCIATED FISH HOSTS. Nachev M. et al. Department of Aquatic Ecology and Centre for Water and Environmental Research (ZWU), University of Duisburg-Essen, Essen, Germany
19. TRANSCRIPTOMIC PLASTICITY OF THE ANTARCTIC PARASITE *Contracaecum osculatum* sp. D (NEMATODA: ANISAKIDAE) IN RESPONSE TO THERMAL STRESS EXPOSURE. Palomba M. et al. Department of Ecological and Biological Sciences, Tuscia University, Viterbo, Italy
20. ASSESSING PARASITE COMMUNITIES IN ANADROMOUS ARCTIC CHARR: IS IT A COST OF MIGRATION? Rochat E.C. et al. Natural History Museum of Geneva, Geneva, Switzerland

21. ESTABLISHMENT OF AN *Ellipsomyxa mugilis* (MYXOZOA) IN VIVO MODEL AND DEVELOPMENT OF A PROTOCOL FOR PURIFICATION OF ACTINOSPORES. Sá M. et al. Institute for Research and Innovation in Health (i3S), University of Porto, Portugal
22. PARASITE INFECTION MAY SERVE AS AN INDICATOR OF HOST POPULATION HISTORY: A CASE OF ACANTHOCEPHALANS *Pomphorhynchus tereticollis* IN A SMALL MOUNTAIN LAKE IN SLOVAKIA. Sarabeev V. et al. Department of Biology, Zaporizhzhia National University, Zhukovskogo 66, 69063 Zaporizhzhia, Ukraine
23. *Gyrodactylus* PARASITES INDUCING DIFFERENTIAL EXPRESSION OF IMMUNITY-ASSOCIATED GENES IN SEXUAL AND GYNOGENETIC FORMS OF FRESHWATER INVASIVE GIBEL CARP (*Carassius gibelio*). Šimková A. et al. Department of Botany and Zoology, Faculty of Science, Masaryk University, Brno, Czech Republic
24. KINETIC CHARACTERISTICS OF DIGESTIVE ENZYMES AS A TOOL IN COMPETITION FOR NUTRIENTS BETWEEN THE HOST AND PARASITES OF THE DIGESTIVE TRACT. Solovyev M.M. et al. Institute of Systematics and Ecology of Animals SB RAS, Novosibirsk, Russia
25. PARASITES OF AQUATIC ANIMALS IN THE ANTHROPOCENE: HOW ENVIRONMENTAL FACTORS SHAPE PARASITE ECOLOGY. Sures B. Department of Aquatic Ecology and Centre for Water and Environmental Research (ZWU), University of Duisburg-Essen, Essen, Germany
26. FROM SNAILS TO SCALES: TREMATODE LIFE CYCLE LINKS IN SOUTHERN AFRICAN FRESH WATERS. Truter M., et al. Water Research Group, Unit for Environmental Sciences and Management, North-West University, Potchefstroom, South Africa
27. BEYOND THE Y-MAZE: OLFACTION IN HOST-FINDING IN A COMMON EXTERNAL PARASITE OF CORAL REEF FISHES. Vondriska C. et al. Department of Marine Biology and Ecology, Rosenstiel School of Marine, Atmospheric, and Earth Science, University of Miami, Miami, Florida, USA
28. HOST RANGE OF MICROSPORIDIAN *Inodosporus fujiokai*. Yanagida T. et al. Laboratory of Parasitology, Joint Faculty of Veterinary Medicine, Yamaguchi University, Yamaguchi, Japan

POSTER PRESENTATIONS

(Please note the name and institution shown in this list are those of the person presenting the poster, who may not be the first author; the complete author list including all institutional affiliations are shown with the full abstract)

1. DO INVASIONS AMPLIFY OR IMPOVERISH NATIVE PARASITE COMMUNITIES? TWO CASE STUDIES IN NORTH AMERICAN FRESHWATER ECOSYSTEMS. Commisso G. et al. University of Washington, School of Aquatic and Fishery Science, USA
2. UNVEILING THE COMPLETE PARASITE COMMUNITY OF *Amblyraja radiata* DONOVAN, 1808 IN THE DEEP SOUTH ICELANDIC SEA: PRELIMINARY RESULTS. Dallarés S. et al. Departament de Biologia Animal, de Biologia Vegetal i d'Ecologia, Universitat Autònoma de Barcelona, Cerdanyola del Vallès, 08193 Barcelona, Spain
3. SNAIL MAIL: DELIVERING PARASITES TO AQUATIC HOSTS. Donough N. et al. Water Research Group, Unit for Environmental Sciences and Management, North-West University, Potchefstroom, South Africa
4. TESTING HOST LONGEVITY AS DETERMINANT OF BETA DIVERSITY COMPONENTS IN METAZOAN PARASITE COMMUNITIES OF MARINE FISH SPECIES. González M.T. et al. Universidad de Antofagasta, Chile
5. THE IMPACT OF THE PROGRESO, YUCATÁN HIGH PIER ON HELMINTH COMMUNITIES OF THE CHAC CHI *Haemulon plumierii* (PISCES: HAEMULIDAE): A PRELIMINARY ANALYSIS. González-Corona B. et al. Universidad de Guanajuato, División de Ciencias Naturales y Exactas, Mexico
6. GENETIC DIVERSITY AND INFECTION PATTERNS OF *Anisakis* spp. IN FISHES AND MARINE MAMMALS FROM PATAGONIA, ARGENTINA. Hernández-Orts J.S. et al. Natural History Museum, London, United Kingdom
7. THE PARVILIFE PROJECT – HOW TO AVOID OR LIVE WITH PARVICAPSULOSIS. Erlingsdóttir Á. et al. University of Bergen, Norway
8. OCCURRENCE OF PARASITIC NEMATODES IN TWO SPECIES OF SMALL PELAGIC FISH FROM NORTHWESTERN MEXICO. López-Moreno D. et al. Facultad de Ciencias del Mar, Universidad Autónoma de Sinaloa, Mazatlán 82000, Mexico
9. INTERACTION NETWORK BETWEEN PARASITES AND CARANGIDAE FISHES IN THE SOUTHEASTERN GULF OF CALIFORNIA. Osuna-Cabanillas J.M. et al. Facultad de Ciencias del Mar, Universidad Autónoma de Sinaloa, Mazatlán, 82000, Mexico
10. PARASITIC ECOLOGY OF *Trachinotus paitensis* (TELEOSTEI: CARANGIDAE) FROM THE MARINE COAST OF PERU. Paiva I.A. et al. Programa de Posgrado en Ciencia Animal, Universidad Estatal de Maranhão, Brazil
11. DISTRIBUTION AND GENETIC DIVERSITY OF *Grillotia adenoplusia* (CESTODA: TRYPANORHYNCHA) IN SMALL DEEP-DWELLING SHARKS FROM DIFFERENT AREAS OF MEDITERRANEAN SEA. Palomba M. et al. Department of Ecological and Biological Sciences, Tuscia University, Viterbo, Italy
12. THE ROLE OF TEMPERATURE AND SALINITY IN HATCHING SUCCESS OF *Contracaecum rudolphii* sp. A AND sp. B (NEMATODA: ANISAKIDAE). Palomba M. et al. Department of Ecological and Biological Sciences, Tuscia University, Viterbo, Italy
13. METAZOAN PARASITE FAUNA OF *Lagodon rhomboides* (SPARIDAE) IN TWO COASTAL LAGOONS OF THE YUCATAN PENINSULA, MEXICO. Pérez-Ortega B. F. et al. Laboratorio de Parasitología y Medicina de la Conservación,

Escuela Nacional de Estudios Superiores Unidad Mérida, Universidad Nacional Autónoma de México (UNAM), Mérida, Yucatán, Mexico

14. SCRUB THE CRAB: PARASITOLOGICAL INVESTIGATION ON THE BLUE CRAB ALONG ITALIAN COASTS. Poggi L. et al. Department of Veterinary Medical Sciences, Alma Mater Studiorum Bologna University, Ozzano Emilia (BO), Italy
15. THE METAZOAN PARASITE COMMUNITIES OF FLOUNDERS AS INDICATORS OF CHEMICAL POLLUTION IN THE SOUTHERN GULF OF MEXICO: FUNCTIONAL TRAIT-BASED. Soler-Jiménez L.C. et al. Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, Unidad Mérida, Laboratory of Aquatic Pathology, Carretera antigua a Progreso Km. 6, 97310 Mérida, Yucatán, Mexico
16. COMMUNITIES OF MULTICELLULAR PARASITES OF A SYMPATRIC PAIR OF WHITEFISH *Coregonus lavaretus* OF TELETSKOYE LAKE. Solovyev M.M. et al. Institute of Systematics and Ecology of Animals SB RAS, Russia
17. LARVAL CESTODES AND POISONOUS INTERMEDIATE HOSTS: RETHINKING TRANSMISSION PATHWAYS AND ECOLOGICAL INTERACTIONS. Van Der Spuy L. et al. Water Research Group, Unit for Environmental Sciences and Management, North-West University, 11 Hoffman Street, Potchefstroom, South Africa
18. BEYOND BIVALVES: THE ROLE OF THE FISH PARASITIC ISOPOD *Cinusa tetrodontis* SCHJÖDTE ET MEINERT, 1884, IN TRACKING MARINE POLLUTION. Van Der Spuy L. et al. Water Research Group, Unit for Environmental Sciences and Management, North-West University, 11 Hoffman Street, Potchefstroom, South Africa
19. THE SUMMER AND WINTER PARASITE FAUNA OF AN APEX PREDATORY FISH, *Esox lucius* (NORTHERN PIKE), FROM TWO LAKES IN WISCONSIN, USA. Wolf M.C. et al. Division of Natural Sciences, St. Norbert College, De Pere, Wisconsin, USA
20. EGG DEVELOPMENT AND ONCOMIRACIDIUM MATURATION OF *Menziesia sebastodis* INFESTING KOREAN ROCKFISH (*Sebastes schlegelii*). Woo W.S. et al. Department of Aqualife Medicine, College of Industrial Science, Kongju National University, Yesan, 32439, Republic of Korea

ORAL PRESENTATIONS

LONG-TERM DYNAMICS OF THE METAZOAN PARASITE SPECIES RICHNESS AND DIVERSITY OF *Mayaheros urophthalmus* FROM CELESTÚN, YUCATÁN, MEXICO

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A monthly database from 2003 to 2023 of the metazoan parasites of *Mayaheros urophthalmus* from the coastal lagoon of Celestún, Yucatán was examined to determine changes in parasite diversity, species richness and species composition over time. A total of 90 metazoan parasites were recovered along this time. Most of them were larval stages of digeneans (37%), nematodes (17), cestodes (5%) and acanthocephalans (Five). Adult worms were represented only by 7% of digeneans, 4% of nematodes and copepods, and 3% of monogeneans and acanthocephalans. Other groups such as branchiurids, leeches and pentastomids had just one species each. Only 22 species have maintained an average of more than 10% prevalence over time. There was an average of 17 ± 4.5 parasite species per month at component community level and 9.3±3.5 species per individual host at infracommunity level. At component community level, an increase in species richness was observed throughout time, with almost twice the number of parasite species recovered after 2007 in comparison with 2003-2005. Time series analysis showed patterns at different temporal scales. There were recurrent peaks of species richness and diversity occurring every 4 years, while parasite abundance increased significantly every 2 and 4.5 years, in all cases a significant correlation with temperature, salinity, and precipitation was observed with a lag of 3 to 13 months. These peaks could be possibly related to pulses of helminth species traveling with their hosts into the lagoon regularly. Research financial support by Cinvestav-Research fund.

BEHAVIOUR OF *Anisakis simplex* INFLUENCED BY BIOTIC AND ABIOTIC FACTORS

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The marine parasitic nematode *Anisakis simplex* has a complex life cycle including marine mammals as definitive hosts, invertebrates (e.g. copepods and euphausiids) as the first paratenic hosts and a wide range of fish species acting as second paratenic hosts. During the life cycle the larva encounters a wide range of biotic (host immune factors and microelectric activity) and abiotic conditions (temperature and pH). We hypothesized that these factors may explain the differential behavior of the nematode, recognized during the different life cycle stages. In this study, third-stage larvae (L3) of *A. simplex* were isolated from freshly caught Atlantic herring (*Clupea harengus*) from FAO zone 27. We exposed nematodes to different pH values (pH 2 to 9) at different temperature levels (4, 14, 21 and 37 °C), electric current (6mA, 12mA, 18mA) and different concentrations of fish immune cells. The nematode larvae exhibited significantly differential behaviour (stretched non-aggregated, spiral non-aggregated and aggregated) and activity levels when exposed to the different physicochemical conditions. We recorded negative correlations between activity and pH (maximum activity at pH 2) and positive correlations between activity and temperature (maximum activity at 37°C). The nematode larvae were affected when exposed to electricity and fish immune cells. Electric currents at 6 mA induced minor changes, but at 12 mA and 18 mA the majority or all nematode larvae aggregated and rolled up into spirals. Exposure to leukocytes, isolated from rainbow trout head kidney and spleen, induced a similar concentration-dependent spiralling process in larvae. We discuss these behavioural patterns of *A. simplex* as adaptations to conditions encountered by the worm larvae during the different stages of its complex life cycle.

GASTROINTESTINAL PARASITES OF HARBOUR SEAL (*Phoca vitulina* L.) IN DANISH MARINE WATERS

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Harbour seals (*Phoca vitulina*) residing in the Danish marine area Limfjorden, which is connecting to the North Sea and the Kattegat Sea, were subjected to a parasitological investigation with focus on the gastro-intestinal tract infections. A range of helminths were recovered from the stomach showing that the seal is serving as the definitive host for the nematodes *Contracaecum osculatum., Phocanema (syn. Pseudoterranova) decipiens* and *Anisakis simplex*. The prevalence of infection for these species were 100 %. Intestinal parasites comprised the acanthocephalan *Corynosoma strumosum* (prevalence 100 %), and the cestode *Dibothriocephalus schistochilus* (7 %). The abundance varied between species with *C. osculatum* as the dominating followed by *P. decipiens*, *A. simplex*, *C. strumosum* and *D. schistocephalus*. We determined the egg content in the female nematode uteri and estimated the potential spread of infection to other trophic levels in the life cycles of these parasites.

TRENDS IN PARASITISM AMONG MARINE FISHES: A COMPREHENSIVE MODEL FROM THE MEDITERRANEAN SEA

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The parasite communities of common fish species of the Balearic Sea (northwestern Mediterranean) from all habitats and depths from surface waters to 2,200 m have been fully characterized during the last 17 years in the framework of different research projects. This unique and complete database based on field data allows a general, in-depth and novel approach to the trends in parasitism for marine fish. Data from 33 fish species and more than 3,000 individuals are presented herein, as well as main parasitological trends in relation to hosts biological and autoecological variables, and environmental gradients. In general, highest parasite prevalence, richness and abundance were recorded in epipelagic and shallow-demersal hosts, whereas the same descriptors were lowest in mesopelagic, bathypelagic and bathydemersal fish. Concordantly, richness and abundance were highest in epi/endobenthophagous and planktonic shallow water species while being generally lowermost in meso- and bathyplanktonic species, and in highly specialized feeders. In general, parasite prevalence, richness and diversity progressively decreased with depth, while a sharp decrease in parasite abundance was only detected at lower depths (i.e. below 1700 m). In deep environments, higher parasite abundance, richness and diversity were observed in the mainland vs. insular slope. Notably, digeneans characterized parasite communities of shallow-dwelling hosts, while larval cestodes were most common in hosts from deep waters. Nematodes were important at all depths, although with compositional changes. Overall, important effects of depth, habitat type, trophic ecology and phylogeny were noted in parasite community composition and descriptors, with a strong emphasis on host autoecological traits.

MYXOZOANS UNDER MULTIPLE STRESSORS: HISTORICAL ENVIRONMENTAL IMPACT ON MYXOZOANS OF THE PEARL RIVER, LOUISIANA, USA

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Anthropogenic change influences host-parasite interactions, but this influence is rarely examined in a multiple stressor context, missing an opportunity to understand how parasite burdens are likely to change in real ecosystems, where stressors rarely occur in isolation. This study aimed to understand how combined stressors such as warming (i.e., temperature), drought (i.e., streamflow), and pollution (i.e., pulp-mill effluent) influence fish parasite abundance in the Pearl River, LA. Seven fish species were seined between 1963-2005 upstream and downstream of a pulp-mill outflow and preserved at the Tulane University Biodiversity Research Institute. In 2024, we dissected 1188 fish individuals representing seven host species and identified myxozoan parasites in six of them. Myxozoans included genera *Chloromyxum* sp., *Henneguya* sp., *Myxidium* spp., *Myxobolus* spp., *Thelohanellus* sp., and *Unicauda* sp. From the six myxozoan-infected fishes, *Hybognathus nuchalis* had the highest myxozoan diversity, while the highest parasite abundance (# of pseudocysts per fish) was observed for *Myxobolus* spp. infecting the gills of *Carpiodes velifer.* This parasite declined significantly over time, from an average of 121 pseudocysts per fish to 18. Preliminary analyses suggest that whether stressors act singularly or in interaction on myxozoan abundance is determined by the myxozoan and host species in question. Results highlight the differential susceptibility of wild fishes to myxozoan infections and provide insights into which stressors may better explain changes in parasite abundance. While investigating multiple stressors simultaneously is difficult, identifying the stressors (e.g., pollutants) to which organisms (i.e., parasites) respond most strongly can inform mitigation efforts.

THE ECOLOGY OF BLACK SPOT SYNDROME INDUCED BY *Cryptocotyle* (DIGENEA) INFESTATIONS IN THE ECOSYSTEMS OF THE ENGLISH CHANNEL AND THE NORTH SEA

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Increasing observations of Black Spot Syndrome in North Sea and English Channel ecosystems have generated questions regarding its cause and concerns over commercially important fish. Some heterophyid cercariae induce cutaneous black spots following penetration and encystation in the intermediate host, the fish. These unaesthetic spots and the presence of parasites may lead to important economic loss in fishery and may have impacts on public health. Several genera such as *Apophallus*, *Cryptocotyle*, *Haplorchis* and *Stellantchasmus* have been associated with this phenomenon. Among them, *Cryptocotyle* seems to be widely distributed in marine fish species. However, so far, its impact on human health is still unknown and few publications exist dealing with its distribution. This study presents a review of the worldwide distribution of *Cryptocotyle* and with a focus on the ecosystems of English Channel and the North Sea. An epidemiological study was performed on seven commercial fish species over 2019, 2020, 2022 and 2023, with more than 3,000 fish sampled. Infestations were estimated for each geographical areas and fish species by counting black spots. Metacercariae were isolated and identified. Variations of the prevalence, intensity and abundancy were observed according to fish species and fishing areas. Encysted metacercariae were found with a global prevalence of 17.6%. Whiting and pout were the most infected species for all sampling areas and years. *C. lingua* and *C. concava* were identified. This survey constitutes the first description of *Cryptocotyle* in these marine ecosystems. It will contribute to a better understanding of the ecology of these trematodes.

TREMATODE DIVERSITY AND THEIR TEMPORAL PREVALENCE IN LYMNAEID AND PLANORBID SNAILS IN UPPER KLAMATH LAKE, OREGON, USA

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Upper Klamath Lake (UKL), Oregon, USA, is a compromised ecosystem affected by hypereutrophication and habitat alteration. Two endangered sucker species, the Lost River sucker (*Deltistes luxatus*) and shortnose sucker (*Chasmistes brevirostris*), are endemic and were once abundant in the Klamath Basin. These fish populations have experienced marginal recruitment to the spawning population over the last 30 years, placing them at high risk for extinction. Recruitment failure is linked to high juvenile fish mortality within the first two years of life, likely due to factors such as habitat loss, water quality, predation, and disease. Prior parasitology surveys in surrogate fish species have shown a high trematode prevalence of eye flukes, *Diplostomum* spp. and *Tylodelphys* spp., which may compromise fish health. Given the complex life cycle of trematodes and the asexual amplification of cercariae by snails, we question if abundant snails in this hypereutrophic environment may favor trematode abundance. To understand the risks posed by pathogenic cercariae to juvenile suckers, we aimed to determine the diversity and temporal prevalence of trematode cercariae in UKL from July and September 2024. Lymnaeid and planorbid snails were collected and immediately screened for cercariae. Species were identified by morphologic and molecular methods, comparing the ITS region of the 18S rRNA and mitochondrial cytochrome oxidase I genes. This study provides the first temporal survey of cercarial species composition in UKL and explores the diversity of fish-infecting trematodes. It offers critical insights into potential fish exposure to pathogenic agents and highlights periods of heightened risk.

PARASITE WARNING US ON ECOSYSTEM CHANGES. THE CASE STUDY OF FISH-PARASITES IN ANTHROPOGENICALLY IMPACTED LAKE VICTORIA

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How parasites are affected by global change is largely unknown, despite their ubiquity and crucial role for ecosystem health in maintaining complexity and contributing to ecosystem robustness. Human-induced environmental changes are expected to alter parasite abundance and host-parasite interactions (e.g. spillovers), but the direction of such changes is unclear, as its consequences for ecosystem health. Lake Victoria, the youngest of the African Great Lakes, is a biodiversity hotspot that experienced simultaneous drastic anthropogenic changes, the main being: Nile perch invasions and eutrophication. We compared gill macroparasite communities of 13 cichlid fish species 20 years before and after the onset of these anthropogenic perturbations, using historical and recent fish collections. We observed a decline in parasite abundance, biodiversity indices, and co-infections. The host-parasite network rearranged, some parasites disappeared from some host species and colonized few new ones, in a way that reduces ecosystem stability. This highlights the need to preserve parasites and their ecosystem services in face of global change. We also disentangled the cause of such changes, by comparing parasite communities between lake ecosystems similar and close to Lake Victoria but differing in perturbation types. This space-for-time approach revealed that the observed changes in parasite communities in Lake Victoria are not due to natural fluctuations, but rather result from the effect of both studied perturbations. Since changes that have occurred in Lake Victoria are also occurring in other ecosystems, we can use parasites as sentinel for ecosystem health, which might contribute to better strategies for linking conservation and ecosystem health.

SEASONAL GEOGRAPHIC PREVALENCE AND DISTRIBUTION OF *Tetracapsuloides bryosalmonae* IN THE GREAT LAKES BASIN

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Migratory Pacific Salmon, including Chinook and Coho fully adapted to freshwater, represent an essential recreational fishery resource for the Great Lakes area. The myxozoan parasite *Tetracapsuloides bryosalmonae* (Malacosporea) may cause Proliferative Kidney Disease (PKD), a severe chronic lymphoid immunopathology, threatening susceptible salmonids in Europe and Northwest America. We are investigating the spatial and seasonal prevalence of *T. bryosalmonae* in Michigan, opportunistically sampling migratory Chinook and Coho Salmon from DNR-operated fish weirs during seasonal spawning migrations. In October 2023 and 2024 up to 60 fish per stock were sampled from fish weirs installed on Lake Michigan and Lake Huron side in Michigan. DNA was extracted from individual posterior kidneys and tested by qPCR specifically targeting *T. bryosalmonae* 18S rDNA. Positive samples were processed by conventional PCR to retrieve larger genomic sequences from the malacosporean SSU rDNA and CO1 for sequence confirmatory analysis. Our examination revealed a variable infection prevalence across sampled stocks and locations, although most of the specimens were asymptomatic (no clinical signs of PKD) and with a low parasite burden (10^^{3}/10^^{5}/g kidney). Sequence analysis confirmed a sensitive detection of *T. bryosalmonae* DNA from these salmonid species and revealed some strain diversity. These findings revealed that *T. bryosalmonae* is widespread in the Great Lakes watershed, where host availability and environmental conditions are becoming more suitable for completing its two-host life cycle. We provide important information for the management of natural population restoking in the Great Lakes area.

ROUND AND ROUND WE GO: WHAT WE KNOW AND DON'T KNOW ABOUT THE LIFE CYCLES OF PARASITIC CRUSTACEANS

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Crustaceans play significant roles in aquatic ecosystems, exhibiting the highest diversity in their parasitic forms and relying on various hosts throughout their life cycles. Parasitic crustaceans occupy a wide range of niches globally and depend on host organisms for key aspects of their life, including nutrition and reproduction. Although several parasitic crustaceans—particularly those associated with economically important fish hosts—have been well studied, many species remain largely unexamined. This is largely due to the inherent difficulties in monitoring these organisms on or within their aquatic hosts, especially those in marine environments. The small size of many parasites, combined with their often inaccessible location on hosts (i.e. gills, buccal cavity etc.), creates significant challenges in tracking and observing morphological changes across different life stages. As a result, it is not surprising that only a limited number of parasitic crustacean species have had their life histories thoroughly documented. This study aimed to summarise the life cycles of some of the more frequently reported parasitic crustaceans (such as Copepoda and Isopoda), highlighting the diversity and complexity of their life histories. Additionally, we identified the groups where information is lacking (such as Tantulocarida and Thecostraca), emphasising the need for further research to fill these gaps. By shedding light on both well-documented and underexplored species, this study aimed to enhance our understanding of the ecological roles of parasitic crustaceans and the factors influencing their interactions with host organisms.

INFECTION OF *Kudoa* sp. IN ATLANTIC MACKEREL (*Scomber scombrus*) CAUGHT IN IRISH WATERS

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Atlantic mackerel (*Scomber scombrus*) is Ireland's most valuable wild-caught fish species. In recent years, Irish pelagic processors have noted an increase in the occurrence of post-mortem myoliquefaction, most commonly known as 'soft flesh' or 'jelly flesh'. Studies from across the Northeast Atlantic on Atlantic mackerel displaying post-mortem myoliquefaction have linked the condition to a myxosporean parasite called *Kudoa thyrsites,* which is known to infect many freshwater and marine fish species. Despite mackerel's economic importance, no previous research has been conducted confirming the causative agent behind the condition and the number of incidents remains largely unknown in Ireland. Here we aimed to examine *Kudoa* in Atlantic mackerel displaying post-mortem myoliquefaction and assess the parasite's prevalence in Irish waters. Through examination of mackerel muscle tissue, we have confirmed the presence of *K. thyrsites* in affected mackerel collected from a major fishing port in the northwest of Ireland (Killybegs). Our *K. thyrsites* isolate matched the identity of previous isolates obtained from Atlantic mackerel in Scotland and Norway. To evaluate the parasites prevalence across multiple fishing areas additional muscle samples of mackerel were collected from scientific surveys and screened for the presence of *K. thyrsites* using qPCR. The findings contribute to the baseline understanding of the parasite's prevalence and highlight the need for long-term monitoring to detect infection trends and elucidate sources of infection and routes of transmission. Ultimately, developing a robust comprehension of *K. thyrsites* infection is essential to assess its impact on the fishing industries in the wider Northeast Atlantic region.

RAPID SPECIATION IN HOST LINEAGE MAY LEAD TO ADAPTIVE EVOLUTION OF PARASITES' STRESS RESPONSE GENES IN MONOPISTHOCOTYLAN FLATWORMS

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Stress responses are key for parasite survival and, thus, also the evolutionary success of these organisms. However, a strong bias in parasite genomic research towards few human pathogens results in a lack of knowledge on evolutionary diversification mechanisms. Comparative studies of closely related and functionally similar lineages are the key for understanding factors driving adaptive evolution of stress responses. To address this knowledge gap, we contrasted evolutionary patterns of several antioxidant, heat shock, osmoregulatory, and behaviour-related genes in two fish parasitic flatworm lineages with varying species and ecological diversity, *Cichlidogyrus* and *Kapentagyrus* (Monopisthocotyla). We assembled the sequences of 48 genes related to stress responses in 11 species through an in-silico exon bait capture approach, applied phylogenetic reconstruction and tested for signatures of selection. The study also reports the first *foraging* (*For*) gene orthologs in flatworms. Additionally, the absence of cytochrome P450 (*Cyp*) and kappa (*Gstk*) and sigma-class glutathione S-transferases (*Gsts*) in monopisthocotylan flatworms is reported, genes typically considered essential for metazoan life. The results reveal copy number differences in heat shock (*Hsp*) and oxidative stress genes between the two parasite lineages potentially linked to the diversity of ecological niches occupied by their respective host taxa. Positive selection is detected in genes related to mitochondrial protein import (*Hsp*) and behaviour (*For*) in species of *Cichlidogyrus* infecting a host lineage under adaptive radiation (East African cichlids), suggesting an adaptive link to a putative co-radiation of parasites and hosts. Therefore, the study identifies the first potential molecular function linked to a flatworm radiation.

INTERCELLULAR COMMUNICATORS BETWEEN HELMINTHS AND THEIR FISH HOSTS

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The coevolution of parasites and their hosts has been linked to a molecular arms race that took place over millions of years. Our persistent inability to suppress helminth infections demonstrates that these pathogens have evolved highly effective strategies to manipulate and evade the human immune system. It is known that parasitic helminths are important pathogens of vertebrates, including humans, and some of them are even able to manipulate their host through excretory-secretory products (ESPs). Furthermore, extracellular vesicles (EVs) have recently been shown to be essential components of ESPs of various cells and organisms, including parasitic helminths. Previously, EVs were considered exclusively as waste products, but more recently they have been found to also contain active proteins, nucleic acids, and lipids that facilitate parasite survival and replication in the host. So far, the production of EVs by helminths has mainly been observed in mammalian helminths (cestodes, trematodes and nematodes). However, the mechanisms of communication between helminths and their evolutionarily older vertebrate hosts, such as bony fish, are still virtually unknown. Only recently have the first studies on fish helminths EVs been published, including the nematodes *Anisakis simplex* and *A. pegreffii*, the cestode *Schistocephalus solidus*, the polyopisthocotylid ("monogenean") *Sparicotyle chrysophrii* and the first unpublished data on the acanthocephalan *Pomphorhynchus laevis*. This study was supported by the Czech Science Foundation (grant No. 19-28399X).

CONTRASTING DEMOGRAPHIC HISTORIES OF A GENERALIST AND SPECIALIST PARASITE INFECTING EUROPEAN WHITEFISH IN POSTGLACIAL LAKES

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Understanding how ecological and environmental changes shape the evolutionary and demographic histories of parasites is essential for uncovering broader patterns of biodiversity and resilience. Glacial cycles have profoundly shaped the evolution of species by driving repeated episodes of range contraction, isolation in refugia, and subsequent expansion during interglacial periods. These processes have left genetic imprints on populations, reflecting how species adapted to environmental changes over time. In this study, we investigate the demographic histories of two parasitic flatworms, *Phyllodistomum umblae*, a generalist trematode, and *Proteocephalus fallax*, a specialist cestode, which parasitize European whitefish (*Coregonus* spp.) in subarctic and perialpine postglacial lakes. Using genomic data and demographic models, our analysis revealed contrasting evolutionary trajectories for these species. *Phyllodistomum umblae* exhibited postglacial expansions following declines during the Last Glacial Period (~115–11 kya). Its generalist nature and broad host range likely facilitated resilience and dispersal across hydrologically connected lakes. In contrast, *Pr. fallax* experienced deeper fluctuations, including Middle Pleistocene (~300 kya) bottlenecks, but maintained stable populations during the Last Glacial Maximum possibly due to its reliance on *Coregonus* hosts and narrower ecological niche. These differences highlight how ecological strategies influence the ability of parasites to adapt to environmental changes. This study underscores the value of parasitic taxa as models for understanding evolutionary resilience and adaptation in freshwater ecosystems, shaped by the dramatic environmental shifts of the Pleistocene glaciations.

FIRST ELUCIDATED LIFE-CYCLE FOR A SOUTHERN AFRICAN MARINE TREMATODE: *Rhipidocotyle* sp. (BUCEPHALOIDEA: BUCEPHALIDAE) IN LEERFISH *Lichia amia* (L.) (CARANGIDAE), VARIOUS FISH INTERMEDIATE HOSTS AND THE BROWN MUSSEL *Perna perna* (L.)

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Little is known about the biodiversity and life histories of marine trematode parasites in southern Africa. We addressed this knowledge gap as part of a broader project on marine parasites from nearshore fishes and invertebrates. Collection of trematode life-stages along the southern African southern and western coasts led to the first elucidated trematode life-cycle for the region, involving intermediate- and definitive hosts across southwestern Indian- and southeastern Atlantic Oceans. Adults of an uncharacterised bucephalid of *Rhipidocotyle* Diesing, 1858 were found in leerfish, *Lichia amia* (L.) (Carangidae), in the Garden Route National Park, South Africa; bucephalid sporocysts were sampled from the brown mussel, *Perna perna* (L.) (Mytilidae), in the same area, while uncharacterised bucephalid metacercariae were discovered in South African mullet, *Chelon richardsonii* (Smith) (Mugilidae), galjoen, *Dichistius capensis* (Cuvier) (Dichistiidae), and Cape white seabream, *Diplodus capensis* (Smith) (Sparidae) along the Namibian coast. Molecular analyses of the 28S rDNA region were conducted using sequences from southern African bucephalids and GenBank. The sequence from adult bucephalids was identical to those of the metacercariae and differed from sporocyst sequences by a single base pair. All the specimens are thus considered to be of the same species, currently being characterised. The Garden Route National Park, influenced by cold Atlantic- and warm Indian Ocean currents, experiences complex hydrological patterns. This novel life-cycle, linking hosts from both oceans, will provide further insights into host- and trematode connectivity in southern Africa. We hypothesise that the life-cycle of *Rhipidocotyle* sp. closes in the Garden Route National Park.

PATTERNS OF HYBRIDIZATION BETWEEN *Anisakis simplex* (s.s.) AND *A. pegreffii* IN THE SYMPATRIC AREA OF THE NE ATLANTIC WATERS: A POSSIBLE TOOL FOR MONITORING PARASITE DISTRIBUTION SHIFTS IN A CHANGING MARINE ENVIRONMENT?

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The distribution of *Anisakis pegreffii* and *A. simplex* (s.s.) in European waters is shaped by both biotic and abiotic factors. In the present study, admixture between the two species was detected by a large-scale multilocus genotyping approach (SNPs from several nDNA genes, 11 SSR loci) and by haplotypes analysis at mtDNA *cox*2 gene, carried out on N= 250 specimens of the two species from their sympatric area of NE Atlantic waters. Differential distribution of hybrid specimens was observed along the northern Iberian Atlantic coast and Alboran Sea waters. F1 hybrids and backcross individuals with the parental *A. simplex* (s.s.) were found in the northern part of Galician waters; this area represents the northern limit of the geographical distribution of the pure parental *A. pegreffii*. Conversely, along the southern Atlantic Iberian coast and Alboran Sea waters, F1 hybrids and several backcrosses with the parental *A. pegreffii* were found; these marine waters represent the southern limit of the geographic distribution of the pure parental *A. simplex* (s.s.). Additionally, mitochondrial inheritance in these hybrids followed a similar trend. Results suggest that hybridization between the two parental species occurs when they greatly differ in abundance, and a tendency of the F1 hybrids to cross with the parental females at the respective limit of geographical distribution of the two species. Monitoring the increase in hybridization events between these two *Anisakis* species in this sympatric area could serve as an indicator of the potential expansion of this contact zone, particularly in the context of climate change scenario.

"GENDER REVEAL PARTY" IN THE ANISAKID NEMATODE *Anisakis pegreffii*: UNVEILING THE SEX OF LARVAL STAGES BY USING DNA MICROSATELLITE LOCI

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In dieciuos parasites, investment in offspring of both sexes is typically equal. However, deviations from this unity can occur as driven by various factors such as mating systems, mating probabilities and parasite populations density. These may lead to adaptive adjustments in the proportions of females *versus* males. Sex determination of larval stages of *Anisakis* spp. is impossible to be determined, as inferred from traditional morphological approach. Instead, it can be possible by using genetic tools. Among the recently developed microsatellite DNA (SSRs) loci in *A. simplex* (s.l.), 5 sex-linked loci were discovered. They were used for gender assignment of N= 998 L3 specimens of *A. pegreffii* collected from Mediterranean Sea *versus* other geographic areas comprised in its range of distribution, to investigate sex distribution in different metapopulations and by infection sites in fish hosts. Female biased sex-ratio was observed in some metapopulations. In addition, a differential gender distribution by site of infection in fish hosts was found. Finally, significant sex distribution was found between L3, L4 and adult worms of the populations of *A. pegreffii* here considered. This study provides a genetic tool for the sex determination at any developmental stage of the parasite life cycle. This will allow to compare the frequency distribution of sex ratio between larval and adult parasite metapopulations also in relation to its population size from different geographic areas. The tool will also permit to investigate the differential gene plasticity between larval males and females in the host environment, in both natural and accidental (human) hosts.

TROPHIC INTERACTION BETWEEN PARASITIC ISOPODS AND THEIR ASSOCIATED FISH HOSTS

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Parasitic isopods of marine fish show various differences in attachment site preference and host specificity, with limited understanding of their feeding strategy (food utilisation), particularly regarding sex and attachment location. To address these aspects, we conducted bulk stable isotope analyses of carbon and nitrogen in two different host-parasite associations - *Cymothoa sodwana* from largespotted dart *Trachinotus botla* (n=11) and *Cinusa tetrodontis* from evileye blaasop (*Amblyrhynchote honckenii*) (n=32). Different fish tissues as well as male and female parasites were collected during different sampling campaigns in June and September 2017 at different localities along the Indian Ocean coast of South Africa. As thorax and legs of the parasites exhibit different turnover rates of stable isotopes, they were considered separately in order to address short- (thorax) and long-term (legs) changes in parasite's diet. Using Bayesian mixing model (MixSIAR) we calculated the dietary proportions of the isopod diets considering the host muscle, scale/skin, gills and heart (representing a proxy for blood) as food sources. The result revealed distinct dietary patterns between males and females of *C. sodwana* as adults (thorax signatures), but similarities in long-term diet (legs). The isopod *C. tetrodontis* from puffer fish showed no differences between males and females in general, however the results pointed on differences between their long- and short-term diets. Thus, our study highlighted flexible nutrition strategy of male and female isopods, which might be attributed to their site of attachment as adults and to the partial free-living mode of life during their development.

TRANSCRIPTOMIC PLASTICITY OF THE ANTARCTIC PARASITE *Contracaecum osculatum* sp. D (NEMATODA: ANISAKIDAE) IN RESPONSE TO THERMAL STRESS EXPOSURE

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Marine parasites, with complex life cycles, involving free-living larval stages, ectothermic intermediate hosts, and homeothermic definitive hosts, offer compelling systems for studying thermal adaptation. Transcriptomic modulation is a key mechanism enabling these parasites to adjust gene expression and physiological processes in response to thermal variations. However, the interplay between molecular responses and environmental thermal stimuli in parasites remains poorly understood. *Contracaecum osculatum* sp. D, is an Antarctic marine parasite, whose life cycle involves free-living larval stages, L3 stages in ectothermic invertebrates and icefish hosts and, finally, adult stages in homeothermic in a pinniped host (*Leptonychotes weddellii*). This study explores the transcriptomic profile of *C. osculatum* sp. D to uncover molecular mechanisms enabling thermal tolerance. It aims to identify genes associated with thermal adaptation and investigate their expression patterns under different thermal conditions. L3 of *C. osculatum* D were obtained from the ice fish in the Ross Sea during the XXXV Italian expedition. L3 were cultured in vitro at −2 °C, 1 °C, 37 °C to simulate temperatures experienced by parasites. RNA was extracted and sequenced by NovaSeq100PE. Bioinformatic analyses were performed. A *de novo* transcriptome was generated. Differential expression analysis revealed genes linked to heat shock proteins, chaperones, and other stress responses, indicating activation of cellular defence pathways under thermal stress. Changes in metabolic gene expression suggested cellular reprogramming to cope with temperature fluctuations. These results provide new insights into the parasite's mechanisms for thermal adaptation and advance our understanding of how they manage temperature shifts during their life cycle.

ASSESSING PARASITE COMMUNITIES IN ANADROMOUS ARCTIC CHARR: IS IT A COST OF MIGRATION?

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This study investigates the potential parasitic infection costs associated with anadromous migration in Arctic charr (*Salvelinus alpinus* L.) by examining their parasite community structure from the freshwater and marine environment across two consecutive years. Our research specifically focuses on how anadromous migration from fresh- to marine-waters and marine feeding behaviour affect the parasite load of the first- and second-year migrants. As hypothesized, marine-migratory Arctic charr exhibited more species-rich and abundant parasite communities compared to pre- and post-migrants caught in freshwater. Additionally, the marine parasite community composition remains consistent over two successive years among the migrants. Our findings confirmed that migratory Arctic charr notably had higher infection rate of trophically transmitted marine parasites, resulting from increased exposure during their short marine feeding migration. Our results show the trade-off between the parasitic burden and the benefits of a forging migration, such as enhanced growth. Importantly, ascendent migration acts as an escape mechanism from many marine parasites, as most are being lost after returning to freshwater. The potential culling effect of parasitism on the migrants, combined with natural selection could be favouring more resistant individuals, potentially improving the population resilience. This research aims to highlights the ecological and evolutionary implications of a potential cost of parasitism in migratory species. This study also emphasizes the importance of ongoing monitoring and further research studies to understand and address the impacts of anthropogenic induced environmental changes on migratory fish populations.

ESTABLISHMENT OF AN *Ellipsomyxa mugilis* (MYXOZOA) *IN VIVO* MODEL AND DEVELOPMENT OF A PROTOCOL FOR PURIFICATION OF ACTINOSPORES

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Myxosporeans are cnidarian endoparasites with a life cycle that alternates between a fish and an annelid host. Several species cause severe fish diseases that threaten the sustainability and economic growth of aquaculture. The lack of commercial treatments or vaccines underscores the urgent need for a better understanding of the Myxosporea infection in both hosts. Yet, advances in this research area are hindered by the scarce number of *in vivo* models available. Moreover, the existing protocols for parasite purification are quite limited, while contamination of isolated parasite populations by host material poses a major challenge for the most needed "omics" studies. Aiming to establish the first marine myxosporean *in vivo* model, we have perpetuated the life cycle of *Ellipsomyxa mugilis* under laboratory conditions by maintaining thinlip grey mullets *Chelon ramada* and polychaetes *Hediste diversicolor* in a shared system. A sustained infection of *H. diversicolor* was obtained, providing enduring access to *E. mugilis* actinospores. Moreover, a protocol for actinospore purification using fluorescence-activated cell sorting is being developed and optimized. By combining the use of a lectin and DAPI, we were able to successfully purify viable actinospores from the remaining host cells present within the polychaete coelom. Sorted actinospores are now being used for genomic and transcriptomic studies to unravel the processes of host recognition and invasion.

PARASITE INFECTION MAY SERVE AS AN INDICATOR OF HOST POPULATION HISTORY: A CASE OF ACANTHOCEPHALANS *Pomphorhynchus tereticollis* IN A SMALL MOUNTAIN LAKE IN SLOVAKIA

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Studies on parasites can provide an important contribution to science in the form of information on host dynamics, particularly in cases where the host population is difficult to measure directly. We analysed seasonal and annual dynamics of infection parameters of the acanthocephalan parasite, *Pomphorhynchus tereticollis*, from definitive (*Phoxinus phoxinus*) and intermediate (*Gammarus balcanicus*) hosts in the small Morske Oko Lake in eastern Slovakia. The parasite and host population data for 4 seasons and two years were used to build two related linear equations: 1) $x_1 \times 5.25 + k \times y \times 0.701 = y \times 0.701$; 2) $x_2 \times 4.5 + k \times y \times 0.066 = y \times 0.066$, where x is the density of fish, y is the density of gammarid hosts (assumed constant), and digits are the mean abundance values of *P. tereticollis*, and k is the proportion of infected gammarids consumed by the definitive host in the ecosystem (assumed constant). The first equation refers to data for May 2001 and the second to May 2023. The solution of equations showed that $x_2 \approx 0.11 \times x_1$, i.e. density of the fish population changed by a factor of approximately 9.12 between the two years. Our efforts to catch fish in May 2024 were unsuccessful, despite using more resources. The survey of gammarids for parasites showed that *P. phoxinus* still plays a role in supporting the acanthocephalan population as the mean abundance in the intermediate host increased from 0.013, 95%CI 0.001-0.022 in October 2023 to 0.026 95%CI 0.008-0.045 in May 2024. Using the same approach but updating the mean abundance of acanthocephalans in gammarids for 2024, the equation results show a 23.14-fold decrease in the fish population between 2001 and 2024. Our findings suggest that the dynamics of parasite infection can be used to infer a host's population history. The work is funded by the EU NextGenerationEU through the Recovery and Resilience Plan for Slovakia under projects #09I03-03-V01-00017, #09I03-03-V01-00016, and was partially supported by the Slovak Research and Development Agency (APVV SK-CZ-RD-21-0078).

Gyrodactylus PARASITES INDUCING DIFFERENTIAL EXPRESSION OF IMMUNITY-ASSOCIATED GENES IN SEXUAL AND GYNOGENETIC FORMS OF FRESHWATER INVASIVE GIBEL CARP (*Carassius gibelio*)

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Parasite-mediated selection is considered one of the potential mechanisms contributing to the coexistence of asexual-sexual complexes in nature. Gibel carp (*Carassius gibelio*), is an invasive cyprinid fish species in Europe. Asexual form (gynogenetic triploid females) and sexual form often coexist in the same populations, multiple mechanisms have been hypothesized to explain this coexistence. The gynogenetic and sexual specimens originated from artificial breeding were used for experimental infection by monogeneans. Among monogenean parasites infecting gibel carp, *Gyrodactylus longoacuminatus* was the dominant species identified on the skin, fin and gills. The transcriptome profile of the spleen was analyzed to reveal the differentially expressed immunity-associated genes related to monogenean infection. The high *G. longoacuminatus* was reported in both gynogenetic and sexual forms. The higher variability in parasite load was reported in sexual specimens when compared to gynogenetic females. Sexual specimens were more infected by gyrodactylids on the body surface, whilst no difference in *Gyrodactylus* load on fins between sexual and gynogenetic gibel carp was found. More than 30 GO terms related to immunity were identified. Similar GO terms related to immunity were significantly enriched in infected fish compared to non-infected ones in both sexual and gynogenetic gibel carp. We identified more than 90 immune genes using interaction model (interaction between fish group and treatment), and we inferred the differences in the differential gene expression between sexual and gynogenetic specimens, suggesting that molecular mechanisms associated with immunity potentially contribute to the coexistence of sexual and gynogenetic gibel carp.

KINETIC CHARACTERISTICS OF DIGESTIVE ENZYMES AS A TOOL IN COMPETITION FOR NUTRIENTS BETWEEN THE HOST AND PARASITES OF THE DIGESTIVE TRACT

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Various aspects of the relationship in the parasite-host system have been intensively studied in the last few decades. Of particular interest are the mechanisms of interaction between the host and helminths of its digestive tract. Cestodes have acquired a number of features in the process of evolution that allow them to successfully implement part of their life cycle in the digestive tract of vertebrates, including fish. One of the key points are various mechanisms that allow them to successfully compete with the host for food substrates. The aim of this work is to determine the kinetic characteristics of some intestinal digestive enzymes of perch (*Perca fluviatilis*) and the tegument of cestodes (*Proteocephalus* sp.). The fish were caught in Chany Lake (Novosibirsk Region, Russia). Cestodes were removed from perch intestines, washed in a sterile solution of 0.9% NaCl, and frozen in liquid nitrogen until subsequent analysis. Then, the perch intestinal mucosa was collected with a scalpel and also frozen in liquid nitrogen. The expression of alkaline phosphatase, aminopeptidase, and amylase was detected in *Protocephalus* sp. based on transcriptome analysis data. We determined the activity of the listed digestive enzymes in perch and cestodes. The kinetic characteristics of cestodes and perch differ significantly for aminopeptidase and alpha-amylase and did not differ for alkaline phosphatase. The Michaelis-Menten constants were significantly lower for aminopeptidase and amylase than the same enzymes in perch, which allows the parasite to hydrolyze these substrates more effectively than the host.

PARASITES OF AQUATIC ANIMALS IN THE ANTHROPOCENE: HOW ENVIRONMENTAL FACTORS SHAPE PARASITE ECOLOGY

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Despite recent progress, our understanding of how environmental conditions influence aquatic parasites is still incomplete. As global ecological changes intensify, an integrative approach is needed to fully grasp the implications of aquatic parasites. Parasites can react to environmental stressors in diverse ways, with their abundance fluctuating based on the nature and intensity of stressors and the complexity of their life cycles. For instance, heteroxenic parasites may decline under increasing stress, while monoxenic parasites might thrive. Research also highlights the interaction between parasitism and pollution, showing both synergistic and antagonistic effects. In some cases, pollution and parasites together worsen the host's condition, while in others, infected hosts may experience reduced pollutant levels compared to uninfected counterparts, which might lessen adverse effects. However, any potential benefit could be outweighed by the parasites' pathological impacts. There are also instances where parasites exacerbate the toxic effects of pollutants by disrupting the host's defense mechanisms, leading to negative impacts on the host's physiological balance. This talk will highlight key aspects of environmental parasitology, focusing on how environmental factors shape parasite-host dynamics in aquatic ecosystems. Selected examples from marine and freshwater ecosystems will illustrate the current understanding of how aquatic parasites fit into food webs and their broader ecological roles.

FROM SNAILS TO SCALES: TREMATODE LIFE CYCLE LINKS IN SOUTHERN AFRICAN FRESH WATERS

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The intermediate life stages of trematodes present in South Africa's freshwater ecosystems remain largely understudied, with these stages often considered elusive. Although some advancement has been made to increase our knowledge on metacercarial diversity utilising freshwater fishes as second intermediate host, less is known about the selection of invertebrate first intermediate hosts and cercarial morphology. Following the discovery of a diverse metacercarial fauna from six freshwater fishes, including the North African catfish *Clarias gariepinus*, sawfin *Cheilobarbus serra*, sawfin suckermouth *Chiloglanis paratus*, shortspine suckermouth *Chiloglanis pretoriae*, chubbyhead barb *Enteromius anoplus* and Clanwilliam yellowfish *Labeobarbus seeberi*, across southern Africa, the present study aimed to identify invertebrate hosts to cercarial life stages and subsequently to metacercarial stages in these vertebrate hosts. Planorbid snails of the genera *Biomphalaria* and *Bulinus* were collected from the Klein Letaba River in March and April 2023. Individual snails were maintained in river water and cercarial shedding was monitored following a three-day screening regime. If no shedding was observed on day three, snails were dissected and screened for the presence of sporocysts or rediae. Both morphological and molecular analyses were conducted on the specimens, with results compared to existing molecular data on metacercariae from fish hosts. Inferences provide evidence for partial life cycle elucidation linking 1st and 2nd intermediate hosts for three trematode genera *Petasiger*, *Tylodelphys* and *Uvulifer*. This study is the first of its kind for southern Africa and provides a significant step forward towards the elucidation of completed life-cycles of African freshwater trematodes.

BEYOND THE Y-MAZE: OLFACTION IN HOST-FINDING IN A COMMON EXTERNAL PARASITE OF CORAL REEF FISHES

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All aquatic organisms rely on chemical signals in at least some aspect of their life cycle. Chemical signals can be used in association with numerous fitness-consequential functions. External parasites experience the unique challenge that they must actively locate at least one host to parasitize. On coral reefs, gnathiid isopods (gnathiids) are among the most common free-living external parasites of fish. Gnathiids are parasitic during each of their three juvenile stages, where they must navigate complex environments to locate multiple hosts. However, the sensory mechanisms used for host-location have remained largely understudied, primarily due to insufficient technology to record these small parasites at their temporal and spatial scales. Here, we implement a novel aquatic olfactometer to investigate gnathiids' use of chemical signals when locating a host. This olfactometer allows us to observe small organisms in a structured chemical landscape while being recorded using a NIR-camera, giving us video data on its behavior. In the olfactometer, we exposed the gnathiid *Gnathia marleyi* to the chemical cues of two common hosts, the French grunt and beaugregory damselfish. *G. marleyi* showed increased activity and frequency of swimming bursts in the presence of host signals. Swimming parameters such as activity time indicate that *G. marleyi* may use chemical signals to initiate searching behaviors before other sensory signals, such as vision or hydrodynamics, assist the gnathiid with making direct contact with their host. They also demonstrate the utility of the olfactometer for similar studies on other free-living aquatic parasites.

HOST RANGE OF MICROSPORIDIAN *Inodosporus fujiokai*

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Inodosporus fujiokai is a microsporidian that infects both fish and crustacean hosts. Previous infection trials demonstrated trophic transmission of *I. fujiokai* from common prawn *Palaemon paucidens* to two trout species, rainbow trout *Oncorhynchus mykiss* and Biwa trout *O. masou* subsp. This microsporidian infects the muscle cells, but showed different modes of development in fish and crustacean hosts. While infections have been confirmed in wild-caught *P. paucidens* in Lake Biwa, Japan, the natural fish hosts have not yet been determined. To assess the host range of *I. fujiokai* and susceptibility of fish species important to aquaculture, infection experiments were conducted utilizing fish species belonging to the family Salmonidae, Cyprinidae, Osmeridae, Siluridae, and Centrarchidae. Salmonids were highly susceptible, with infection rate and mortality up to 100%. *Salvelinus leucomaenis* appeared more vulnerable compared to *Oncorhynchus* spp. Infections were also confirmed in cyprinids (*Gnathopogon caerulescens* and *Cyprinus carpio*) and the osmerid *Plecoglossus altivelis*, but with considerably lower prevalence and mortality compared to salmonids. This study reveals that *I. fujiokai* is capable of infecting an unexpectedly wide range of fish taxa, although the susceptibility varies significantly, even within the same family. The present study also provides an insight into the natural hosts of *I. fujiokai* in the lake. The infection model of *I. fujiokai* is valuable for deepening our understanding of the biology, ecology, and pathology of fish-infecting microsporidians with a complex life cycle.

POSTER PRESENTATIONS

DO INVASIONS AMPLIFY OR IMPOVERISH NATIVE PARASITE COMMUNITIES? TWO CASE STUDIES IN NORTH AMERICAN FRESHWATER ECOSYSTEMS

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Invasive species can have dramatic effects on ecosystem dynamics, but how they influence the parasite community of recipient ecosystems is almost entirely unknown. According to the enemy release hypothesis, species are more heavily parasitized in their native than in their introduced ranges, which may be a factor in invasion success. When ecosystems are flooded with parasite-free invasive hosts, what happens to native parasites and hosts? I am planning two studies to investigate. 1. Dreissenid mussels are prolific invaders of North America. Using 360 specimens from three fish species held at the Cornell Biological Field Station, collected from before and after invasion of Oneida Lake, I will measure how parasite diversity and abundance changes in fishes after the invasion of these low-trophic level filter feeders. I expect to see a reduction in parasites with free-living life stages post-invasion. 2. Western Mosquitofish (*Gambusia affinis*) are native to the southeastern US, but were introduced to the southwest as a malaria control measure with unanticipated collateral impacts. Using >2000 fishes from two long-term collections, I'll compare the rate of change in parasite burden of mosquitofish collected in their native range (Pearl River, LA; Tulane Biodiversity Research Institute) and introduced range (Albuquerque, NM; Museum of Southwest Biology) against the rate of change in parasite burden of other fish species native to both basins. I expect to find that native parasites hosted by invasive mosquitofish are more sensitive to environmental stressors than those living on native fishes.

UNVEILING THE COMPLETE PARASITE COMMUNITY OF *Amblyraja radiata* DONOVAN, 1808 IN THE DEEP SOUTH ICELANDIC SEA: PRELIMINARY RESULTS

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The thorny skate, *Amblyraja radiata* (Donovan) (Rajiformes: Rajidae) is a demersal benthic species distributed on both sides of the northern Atlantic Ocean, where it is commonly found between depths of 25 and 440 m. The present study assesses the entire parasite community structure for the first time and evaluates the potential of obtained parasites to serve as biological indicators of host biology and ecology; both areas remain poorly understood. A total of 28 individuals of varying age groups were captured during an oceanographic survey in winter 2023 on the western continental shelf off Iceland. The complete parasite community was characterized following standardized protocols. The parasite assemblages of *A. radiata* comprised 14 different parasite taxa. Parasite abundance, richness and diversity showed a positive significant correlation with host size ($p < 0.01$). The same trend was observed for some of the most prevalent parasites, namely the larval nematode *Anisakis* type I, the digenean *Otodistomum* sp. and the copepod *Eudactylina similis* ($p < 0.01$). The composition of the parasite community differed between juvenile and adult hosts, as evidenced by the Bray-Curtis dissimilarity index (0.57 and 0.65 within and between these groups, respectively), NMDS and PERMANOVA ($p = 0.01$) analyses. Present preliminary results confirm a diverse parasite assemblage in *A. radiata* and suggest that observed ontogenic changes result from diet shifts undergone by juvenile specimens and an accumulation of parasites in older hosts.

SNAIL MAIL: DELIVERING PARASITES TO AQUATIC HOSTS

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The family Liolopidae Dollfus, 1934 comprises trematodes that parasitise the stomach and intestines of ectothermic tetrapods. Records of species are scarce, with 14 species across five genera being described, including the recently established Paraharmotrema (from terrapins). While adult parasitic forms are well-characterised morphologically, molecular data remain incomplete, and little is known about their life cycles and transmission pathways. This study aimed to identify potential intermediate hosts for Paraharmotrema karinganiense, recently described from the serrated hinged terrapin (Pelosios sinuatus) in Mozambique. African apple snails (Lanistes ovum, n = 10) and turquoise killifish (Nothobranchius furzeri, n = 60) were collected from temporary pans in Karingani Game Reserve, Mozambique. Encapsulated and encysted metacercariae were recovered from killifish, excysted, heat-fixed, and preserved for morphological and molecular analyses. Individuals of L. ovum were maintained in containers with 250mL artificial water. An initial screening regime over three consecutive days was followed by four-day intervals to monitor cercarial shedding. Shed cercariae were examined using light and scanning electron microscopy and preserved for molecular characterisation, targeting the 28S rDNA, ITS and cox1 gene regions. This study provides only the second documented life cycle of a liolopid trematode based on natural infections and the first complete life cycle for freshwater trematodes from southern Africa.

TESTING HOST LONGEVITY AS DETERMINANT OF BETA DIVERSITY COMPONENTS IN METAZOAN PARASITE COMMUNITIES OF MARINE FISH SPECIES

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Beta diversity and nestedness are central concepts of ecology and biogeography. Beta diversity patterns originate from two distinct processes: the replacement (=species turnover) and the loss (or gain) of species. Nestedness patterns in parasite communities have mostly been determined at geographic (local and/or biogeographical) scales as individual hosts represent replicated habitats in time and space. However, there are several intrinsic and extrinsic factors associated to host ontogeny (e.g. fish size, host longevity, changes in diet/feeding habits, differential susceptibility) that shape diversity parasite patterns. Thus, the aim of this study was to determine whether parasite assemblages of marine fish species from the Atlantic and Pacific coast of America show biodiversity patterns associated to species replacement (=turnover) or nested structure, associated to host longevity/age/ontogeny. We analysed the parasite community, ectoparasites and endoparasites separately, using our own data base of 12,306 marine teleost fish belonging to 95 fish species. In addition, we evaluated the effects of selected host biological traits and environmental factors that could explain the observed turnover/nestedness patterns in parasite communities of marine fish species. The Beta-diversity analyses were based on Jaccard index, including only the parasite species with prevalence >5%. All analyses were performed using the Library(adespatial), Libray(ade4) and Betapart implemented in software R-studio. Our results showed that nested component was significantly and positively increased with host age classes for fish endoparasites ($p<0.05$), but this pattern was not clear for fish ectoparasites.

THE IMPACT OF THE PROGRESO, YUCATÁN HIGH PIER ON HELMINTH COMMUNITIES OF THE CHAC CHI *Haemulon plumierii* (PISCES: HAEMULIDAE): A PRELIMINARY ANALYSIS

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Parasites provide valuable insights into ecosystem health, as disturbances are reflected in their prevalence and abundance changes. This study assessed the impact of the Progreso, Yucatan pier on the helminth communities of *Haemulon plumierii* collected in August 2024. Fish samples were collected into high and low wave exposure zones parallel to the fiscal pier. Five fish were collected from each zone using fishing lines with hooks and salted sardines as bait. The specimens were transported to the Aquatic Pathology Laboratory at Cinvestav Mérida for parasitological examination. Twenty-five parasite morphotypes were identified and classified into monogeneans, digeneans, nematodes, acanthocephalans, and crustaceans, totalling 1,533 parasite individuals. Digeneans were the best represented, with 14 morphotypes (10 larvae/four adults), followed by monogeneans (4), nematodes (three), acanthocephalans (one), and crustaceans (four). In the high wave exposure zone, *Haliotrematoides* sp. showed a prevalence and abundance of 60% (12.9 ± 26.70). In the low wave exposure zone, four species prevailed: *Stephanostomum* sp. *Haliotrematoides* sp., *Cardiocephalus* sp., and *Bucephalus* sp., (40%). Furthermore, *Stephanostomum* sp. was the most abundant (21.8 ± 38.93). Twenty-two parasite species (785 individuals) were recorded in the high wave zone, while 17 species (748 individuals) were found in the low wave zone. Despite observed variations, no remarkable differences were noted in total parasite numbers, but differences in species counts were evident. While this provides insight into the ecosystem around the pier, additional analyses are needed to draw definitive conclusions. Financial support came from CONAHCyT-ApoyosLNC-2023-80.

GENETIC DIVERSITY AND INFECTION PATTERNS OF *Anisakis* Spp. IN FISHES AND MARINE MAMMALS FROM PATAGONIA, ARGENTINA

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The genetic diversity of anisakid nematodes of the genus *Anisakis* in fish and marine mammals from the southwestern Atlantic Ocean is still largely unknown. Here we investigate the occurrence and genetic diversity of third-stage larvae (L3) and preadults of *Anisakis* species in fish and pinnipeds from the Patagonian coast of Argentina. We examined 545 fish from 22 species and seven pinnipeds from three species, namely six *Otaria flavescens*, two *Arctocephalus australis* and one *Hydrurga leptonyx*, for the presence of anisakids. In total, 840 *Anisakis* L3 were collected mainly from the body cavity or mesentery, and to a lesser extent, from the musculature of 20 fish species. In addition, 1,763 *Anisakis* L3 and preadults were found in the stomachs of the three pinniped species. Partial fragments of mtDNA *cox*2 were amplified for 40 isolates from 12 fish species. *Anisakis pegreffii* infected ten fish species (i.e., *Acanthistius brasilianus*, *Brama brama*, *Cheilodactylus bergi*, *Cottoperca gobio*, *Genypterus blacodes*, *Gasterochisma melampus*, *Helicolenus dactylopterus*, *Eleginops maclovinus*, *Macruronus magellanicus*, *Merluccius hubbsi*, *Paralichthys isosceles* and *Stromateus brasiliensis*), while a single L3 of *Anisakis berlandi* was detected in *Macruronus magellanicus*. In pinnipeds, six isolates from *O. flavescens* and *A. australis* were identified as *A. pegreffii* based on *cox*2 sequences. The Argentine hake *M. hubbsi* (n=79), one of the most important fishery resources of Argentina, showed a high prevalence (70.9%) but low abundance (2.1) for *Anisakis* L3. No adult worms were found in pinnipeds, suggesting that *Anisakis* may not mature or reproduce in these marine mammals on the Patagonian coast.

THE PARVILIFE PROJECT – HOW TO AVOID OR LIVE WITH PARVICAPSULOSIS

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Parvicapsulosis is a significant disease caused by the myxozoan parasite *Parvicapsula pseudobranchicola* (*P.p*). Initially characterized in 2002 in farmed Atlantic salmon (*Salmo salar*) in Norway, this parasite primarily targets the pseudobranchs. Clinical signs include atypical surface behavior, disorganized swimming patterns, lethargy, and indications of visual impairment. *P.p.* was first documented in Iceland in 2019 and has since persisted as a recurrent issue within the Icelandic salmon farming sector. The parasite has a two-host life cycle, salmonids and an annelid. Recently, the previously unknown final host (polychaete) was identified, which offers novel opportunities to create a basis for mitigating the disease. The ParviLife project, which builds upon prior research conducted in Iceland and Norway, is funded by the Norwegian Seafood Fund (FHF). This initiative aims to provide the aquaculture sector with effective strategies to address parvicapsulosis. This three-year project, that commenced in the summer of 2024, will be introduced.

OCCURRENCE OF PARASITIC NEMATODES IN TWO SPECIES OF SMALL PELAGIC FISH FROM NORTHWESTERN MEXICO

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Parasitic nematodes can infect various host species, including fish intended for human consumption. Their presence can compromise both the quality of the fish and food safety. This issue is particularly relevant in small pelagic fish, which represent one of the most economically important fisheries. The objective of this study was to determine the prevalence, median intensity, and abundance of parasitic nematodes in two small pelagic species: the thread herring (*Opisthonema* spp.) and the Pacific anchovy (*Cetengraulis mysticetus*) from the coasts of Sinaloa, Mexico. A total of 120 specimens of *Opisthonema* spp. and 97 of *C. mysticetus* were examined. Taxonomic identification of the nematodes, carried out through morphological analysis, revealed the presence of three species: *Anisakis* sp., *Contracaecum* sp., and *Pseudoterranova* sp., all in their larval stage. In *Opisthonema* spp., the prevalence, median intensity, and abundance of *Contracaecum* sp. were 26%, 1, and 0.5, respectively, while for *Pseudoterranova* sp. they were 55%, 1, and 0.93, respectively. In *C. mysticetus*, the prevalence, median intensity, and abundance of *Contracaecum* sp. were 69%, 3, and 2.7, respectively, while for *Anisakis* sp. they were 10%, 1, and 0.1. The results of this study provide a deeper understanding of the occurrence of nematodes in these fish species from the Mexican Pacific, which may be important for public health and food safety concerns.

INTERACTION NETWORK BETWEEN PARASITES AND CARANGIDAE FISHES IN THE SOUTHEASTERN GULF OF CALIFORNIA

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Parasites play an important role in nature by regulating free-living populations and providing stability to the ecosystem. Hosts and their parasites interact with each other and form antagonistic networks, which typically have a modular structure. However, nested antagonistic networks have also been documented, often featuring a core of generalist species that provide resilience and stability to the network in the face of potential disturbances. The objective of this study is to describe the interaction patterns between 10 species of Carangidae fish and their parasites in the southeastern Gulf of California using the ecological network approach. Data from 801 fish caught between May 2021 and June 2022 in the coastal waters of Mazatlán, Sinaloa, were analyzed. According to our results, the interaction network showed a significantly nested structure both qualitatively and quantitatively (42.8 and 21.3). The modularity was 0.3 and not significant. Additionally, high robustness (0.8) and low connectance (0.2) were found, as only 20% of the expected 390 connections were recorded. At the core of the network were two fish species: *Caranx caninus* and *Caranx caballus*, and

five parasite species: *Pseudomazocraes selene*, *Anisakis* sp., *Pyragraphorus hollisae*, *Lernanthropus giganteus*, and *Rocinella signata*. This study helps to understand the organizational patterns in the network of some carangid fish species and their parasites, which are potentially susceptible to extinction due to unsustainable fishing in the Gulf of California. Furthermore, it provides a basis for analyzing potential changes in the marine ecosystem, which could positively influence the improvement of conservation strategies for natural resources.

PARASITIC ECOLOGY OF *Trachinotus paitensis* (TELEOSTEI: CARANGIDAE) FROM THE MARINE COAST OF PERU

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The present study aims to analyze the parasitic ecology of *Trachinotus paitensis* from the marine coast of Peru (Teleostei: Carangidae). The study area included the Chorrillos Fishing Terminal, Lima, Peru. 36 specimens of *T. paitensis* were acquired through commercial purchases during June to August 2024. The fresh specimens were transported in isothermal boxes to the laboratory, where after necropsy biometric data were collected: total length (TL) in cm, total weight (WW) in g, and Fulton's condition factor (K). Ecto- and endoparasites were processed following conventional ichthyoparasitological protocols, parasites were identified after dissection, and finally parasitic ecology indices were determined using the Quantitative Parasitology program. The endoparasitic trematode *Lobotostoma pacificum* (prevalence = 94.44 % and mean abundance = 51.08) and two ectoparasitic copepods Bomolochidae gen sp. unidentified (prevalence = 13.88 % and mean abundance = 0.19) and *Caligus quadratus* (prevalence = 5.55 % and mean abundance = 0.05) were found. Three parasite aggregation indices (Variance/mean abundance, Poulin's discrepancy index and negative binomial k exponent) showed an aggregated distribution for *L. pacificum* and Bomolochidae gen sp. unidentified. No association was found between LT, Pt and K with the abundance and prevalence of the two most prevalent parasites, total richness and total mean abundance. Bomolochidae gen sp. unidentified is a new record for Peru.

DISTRIBUTION AND GENETIC DIVERSITY OF *Grillotia adenoplusia* (CESTODA: TRYPANORHYNCHA) IN SMALL DEEP-DWELLING SHARKS FROM DIFFERENT AREAS OF MEDITERRANEAN SEA

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The order Trypanorhyncha (Cestoda) comprises a wide range of heteroxenous parasites, exhibiting a higher degree of host specificity in their adult stages compared to their larval forms. Among these, adults of *Grillotia adenoplusia* exclusively parasitizes the bluntnose sixgill shark *Hexanchus griseus*, while the larval forms infect various teleosts and small to mid-sized benthonic sharks. This study aims to assess the distribution and genetic diversity of *G. adenoplusia* in small deep-dwelling sharks across the Mediterranean Sea, evaluating their potential as indirect indicators of deep-sea trophic web stability, with *H. griseus* as apex predator. A total of 600 *Grillotia* spp. plerocerci were collected from 100 small deep-dwelling sharks (*G. melastomus, E. spinax*), caught as bycatch from commercial trawling in five Mediterranean Sea regions. Parasite species identification was performed by sequence analyses of 18S and 28S rDNA gene loci. In addition, new mitochondrial and microsatellite loci were developed. All specimens were identified as *G. adenoplusia*, with high infection prevalence and abundance in all Italian and Spanish waters. The genetic analysis revealed low genetic diversity within the species. The genetic homogeneity of this parasite, likely associated with the migratory behavior of *H. griseus*, along with its high parasitic burden, suggests efficient life cycle completion of the parasite. This positions *G. adenoplusia* as a potential indicator of deep-sea ecosystem stability, emphasizing its importance for conservation efforts in the face of climate change.

THE ROLE OF TEMPERATURE AND SALINITY IN HATCHING SUCCESS OF *Contracaecum rudolphii* sp. A AND sp. B (NEMATODA: ANISAKIDAE)

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Egg hatching in parasitic nematodes is a complex and poorly understood process. Eggs serve as protective barriers and vehicles for the first larval stage to initiate infection, with abiotic factors, like salinity and temperature, playing crucial roles. Previous studies suggest *Contracaecum rudolphii* sp. A and *C. rudolphii* sp. B have life cycles adapted to brackish and freshwater environments, respectively, with differing proportions in their definitive host, the great cormorant (*Phalacrocorax carbo sinensis*), and intermediate fish hosts. This study investigates how temperature and salinity affect the hatching success of *C. rudolphii* sp. A and B eggs, shedding light on their life cycles in the two different aquatic ecosystems. Eggs from genetically identified female of both species were incubated in water with salinity from 0 to 70 psu and temperatures of 5°C, 13°C, 20°C and 32°C to simulate natural conditions and a heatwave scenario. Both species hatched in freshwater at 13°C, 20°C, 32°C, but not at 5°C. The hatching duration varied, with the shortest at 32°C (three days) and the longest at 13°C (14 days). Significant differences in salinity tolerance were observed: *C. rudolphii* A hatched successfully at salinities from 0 to 70 psu, while *C. rudolphii* B hatched only within 0 to 20 psu. These findings suggest distinct adaptive strategies of *C. rudolphii* sp. A and. B to saline and freshwater environments, respectively. These adaptations likely result from evolutionary pressures shaping their physiological traits, underlying their differential distribution in fish and cormorants from these aquatic ecosystems.

METAZOAN PARASITE FAUNA OF *Lagodon rhomboides* (SPARIDAE) IN TWO COASTAL LAGOONS OF THE YUCATAN PENINSULA, MEXICO

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Coastal lagoons are highly diverse ecosystems because they represent transition sites between the marine and terrestrial environments; they act as nursery sites for many species of fishery importance. Lagodon rhomboides, locally known as "xlavita" or "sargo", is a member of the family Sparidae, and is distributed in coastal lagoons across the Western Atlantic, from Massachusetts USA to Northern Yucatan in the Gulf of Mexico, and also in the West Indies. Lagodon rhomboides feeds mainly upon small animals, including crustaceans, mollusks, worms and occasionally on small fishes. We analyzed 60 individuals of L. rhomboides between 2022 and 2023 sampled using seine nets in La Carbonera (N=29) and Celestún (N=31) lagoons. Fish were euthanized and studied for ecto and endoparasites. Metazoan parasites were identified using molecular and morphological data. Twenty-one taxa were found, including trematodes (eight), monogeneans (two), cestodes (two), acanthocephalan (one), nematodes (four), and copepods (three). Of these parasites 67% were adult forms and 33% were larval stages. Eleven taxa are added to the parasite species list of the host across its distributional range, raising the number to 41. The prevalence and mean intensity of infection were calculated for each parasite taxon per locality, as well as the community attributes such as species richness, abundance and diversity indexes at the infracommunity and component community level. This study was funded by the programs PAPIIT UNAM IN212621 and IN200824.

SCRUB THE CRAB: PARASITOLOGICAL INVESTIGATION ON THE BLUE CRAB ALONG ITALIAN COASTS

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Native to the western Atlantic, the blue crab *Callinectes sapidus* has spread to Europe, likely through ballast water. Its high reproductive rates and adaptability to different salinities and temperatures has favored the invasion of Mediterranean habitats, threatening local biodiversity, disrupting ecosystems, and negatively affecting mussels farming. Due to its feeding habits and benthic lifestyle, the blue crab represents a potential host for a variety of parasitic species. This study investigated the parasitofauna of blue crab populations caught along Italy's northeastern coastline. A total of 126 blue crabs were collected from April to September 2024. *Hematodinium* sp. was investigated by microscopical and molecular analysis of hemolymph. Both the hemolymph and the gills were also tested for the presence of waterborne Apicomplexa. Additionally, portions of the abdomen and claws musculature were observed under a stereoscope to highlight any parasites. *Hematodinium* sp. was detected by specific PCR in 24 crabs out of 73 (32.9%), although developmental stages of the parasite have been observed only in seven individuals; nine crabs (7.1%) showed digenean metacercariae of the genus *Microphallus* encysted in the musculature, seven of which were hyperparasitized by Microsporidia of the genus *Unikaryon* (10.1%) and appeared larger and darker compared to uninfected ones. One specimen showed a single larva of the nematode *Acanthochelius rotondatus* encysted within the inner musculature. The molecular screening for waterborne protozoa is still ongoing and will provide a more complete picture of the health risks and ecological implications related to the spread of the blue crab along the Mediterranean coasts.

THE METAZOAN PARASITE COMMUNITIES OF FLOUNDERS AS INDICATORS OF CHEMICAL POLLUTION IN THE SOUTHERN GULF OF MEXICO: FUNCTIONAL TRAIT-BASED

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Metazoan parasite communities are valuable bioindicators of chemical pollution in marine environments. However, changes in species composition and abundance over increasing geographical distances complicate identifying the processes structuring these communities, as species may respond to local conditions. Fortunately, while species composition changes with distance, functional traits (e.g., transmission, feeding mode, life stage) remain consistent. This suggests that distant sites with similar characteristics (e.g., nutrient levels, pH) may exert comparable selection pressures on parasite communities. This study aimed to assess the effectiveness of functional trait-based approaches as bioindicators of pollution along the South Gulf of Mexico's continental shelf. Data were collected from 152 *Syacium gunteri* and 483 *Syacium papillosum* across 93 sites during 17 oceanographic cruises. Environmental variables, including hydrocarbons, heavy metals, and physicochemical factors, were measured. The study area was divided into three regions: Tamaulipas, Veracruz-Tabasco-Campeche, and the Yucatan shelf. Functional trait variability was analyzed using multivariate methods (PERMANOVA, SIMPER, BIOENV) to determine traits contributing most to regional differences. Five traits were identified as most informative: body tegument, transmission, feeding mode, life stage, and attachment organs. PERMANOVA revealed significant spatial variability in parasite communities across regions and hosts, except in the Yucatan shelf, where no differences between hosts were found. SIMPER analysis showed a higher number of adults in the Yucatan shelf compared to larval stages in Veracruz-Tabasco-Campeche. BIOENV analysis indicated that polyaromatic hydrocarbons explained the greatest variability, making functional trait-based approaches a cost-effective option for environmental monitoring. Financial support came from CONAHCyT-SENER-201441 Hydrocarbons Trust.

COMMUNITIES OF MULTICELLULAR PARASITES OF A SYMPATRIC PAIR OF WHITEFISH *Coregonus lavaretus* OF TELETSKOYE LAKE

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The species composition and structure of parasite communities are closely related to the ecological characteristics of their hosts. In Teletskoye Lake, *pidschian*-like whitefish (*Coregonus lavaretus*) forms a sympatric pair represented by *C. l. pidschian* (benthivorous) and *C. l. pravdinellus* (planktivorous) characterized by significant morphological and ecological differences. The aim of the work is to characterize the effect of feeding habits in a sympatric pair of whitefishes of Teletskoye Lake (Altai Republic, Russia) on the communities of their parasites. The species of parasites were determined based on morphological and molecular data. A total of 455 fish were examined, including 275 and 180 individuals of *C. l. pidschian* and *C. l. pravdinellus*, respectively. In total, 14 species of parasites were found. The community of parasites of studied whitefishes were differed in both the species composition of parasites and the invasion indices (extensiveness and intensity of invasion, abundance index). 14 species of parasites from 8 classes were found in *C. l. pidschian*, and seven species of parasites from five classes were found in *C. l. pravdinellus*. Both whitefish were found to have seven common parasite species: *Henneguya zschokkei*, *Discocotyle sagittata*, *Triaenophorus crassus*, *Dibothriocephalus dendriticum*, *Proteocephalus* sp., *Piscicola geometra*, *Salmincola lavaretus*. Apparently, the species composition of parasites and the invasion rates depended to a greater extent on the diet (food items) and spatial distribution of fish in the lake. This work was supported by the Russian Science Foundation, project no. 23-74-10101.

LARVAL CESTODES AND POISONOUS INTERMEDIATE HOSTS: RETHINKING TRANSMISSION PATHWAYS AND ECOLOGICAL INTERACTIONS

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Cestodes play a crucial role in shaping complex marine food webs, with their larval stages identified in various intermediate hosts, including bivalves, crustaceans, and teleost fish. Studying these larval forms is vital for deciphering transmission pathways and host specificity linked to adult cestodes. This study focuses on the larval cestodes parasitising the poisonous Evileye blaasop, *Amblyrhynchote honckenii* (Tetraodontidae). Fifty-five *A. honckenii* were collected and screened for cestodes from five locations along the South African coast. Our findings revealed high abundances of three distinct larval forms associated with the elasmobranch-infecting genera *Acanthobothrium*; *Nybelinia*; and *Kotorella*. Notably, species of these genera are exclusively documented as adults in elasmobranchs. This suggests that despite being poisonous and generally avoiding predation by other fish or elasmobranchs, *A. honckenii* still functions as an intermediate host. An intriguing possibility is that certain elasmobranchs have developed physiological adaptations allowing them to consume poisonous prey without being negatively affected by the toxins, thereby facilitating a direct transmission pathway for larval cestodes to their definitive hosts. Alternatively, *A. honckenii* may act as a reservoir for these larval forms, promoting their development and persistence within the ecosystem, without predation. This adaptability suggests that some larval stages can survive in non-predated hosts, highlighting a complex ecological strategy that enables cestodes to switch hosts. These findings highlight the need for further research into parasite interactions within marine food webs and their adaptability to environmental changes, enhancing our understanding of the complex relationships among marine fish and their parasites.

BEYOND BIVALVES: THE ROLE OF THE FISH PARASITIC ISOPOD *Cinusa tetrodontis* SCHJÖDTE ET MEINERT, 1884, IN TRACKING MARINE POLLUTION

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Traditionally, pollution monitoring programs in marine environments have relied on free-living bivalves as bioindicator species to assess pollution exposure. However, recent research highlights the effectiveness of using endoparasite species as sentinels for chemical pollution. In contrast, ectoparasites have received comparatively little attention in this context. Therefore, the present study explores the potential use of the parasitic isopod, *Cinusa tetrodontis* Schjödte et Meinert, 1884, together with its fish host, *Amblyrhynchote honckenii* (Bloch) for marine bioaccumulation monitoring. The concentrations of As, Cd, Cu, Mn, Ni, Pb, Se, and Zn were determined in muscle and liver tissues of infested and uninfested fish, and male and female parasites on the South African temperate south coast. The concentrations of Cu and Ni in *C. tetrodontis* differed significantly between two sampling sites, a near-pristine (Breede River Estuary, Witsand) and a more polluted site (harbour area in Mossel Bay). Mossel Bay isopods had higher concentrations of Ni, while Witsand isopods had higher concentrations of Cu. In contrast to fish hosts, parasitic isopods accumulated significantly higher levels of all elements except Cd. Most significant relationships between elements accumulated by *C. tetrodontis* and an increase of elements in fish tissues were seen in liver, rather than muscle tissue samples. Specimens of *C. tetrodontis* can be defined as good bioindicators for elements such as As, Cu, Mn, Ni, Pb, Se, and Zn, as they possess high bioaccumulation capabilities. This study addresses several future directions needed within environmental parasitology and highlights the importance of studying and utilizing this host-ectoparasite model system.

THE SUMMER AND WINTER PARASITE FAUNA OF AN APEX PREDATORY FISH, *Esox lucius* (NORTHERN PIKE), FROM TWO LAKES IN WISCONSIN, USA

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This on-going study on the winter and summer parasite fauna of an apex predatory fish, the Northern Pike, *Esox lucius*, from two limnologically different lakes, Decorah, and Castle Rock, of the Wisconsin River drainage, helps us understand how lake characteristics influence parasite diversity, seasonal parasite circulation, and trophic web dynamics of Northern Pike. To date, 15 and 20 species of parasites have been recorded from winter and summer pike, respectively, comprising 1 Monogenea (*Tetraonchus monenteron*), 1 Cestoda (*Proteocephalus pinguis*), 8 Digenea (3 adults: *Azygia longa*, *Crepidostomum* sp. and *Macroderoides* sp. and 5 spp. as metacercariae), 5 Nematoda (immature *Camallanus oxycephalus*, larval *Spiroxys*, *Spinitectus* sp., *Rhabdochona* sp., and *Raphidascaris acus*), 3 Acanthocephala (*Neoechinorhynchus* sp., *Leptorhynchoides* sp., both immature, and *Acanthocephalus* sp.), 1 leech (Piscicolidae) and 1 Mollusca (glochidia). Four species, *T. monenteron*, *A. longa, P. pinguis* and *R. acus* are pike specialists. Component community richness was higher in the summer. Gravid individuals of *P. pinguis* and *A. longa* were found in both summer and winter samples. Infections with *Leptorhynchoides* sp. and *Neoechinorhynchus* sp. are possibly due to post-cyclic transmission, which is confirmed by data on the diet of these pike. There was no significant correlation between total length of fish and the abundance of the four most common parasites: 'Black spot', gill metacercariae, *T. moneneteron*, and *A. longa*. These parasites were significantly more abundant in the smaller and more heavily vegetated Decorah Lake, suggesting that an interplay of limnological characteristics and habitat use by pike determine their parasite fauna.

EGG DEVELOPMENT AND ONCOMIRACIDIUM MATURATION OF *Menziesia sebastodis* INFESTING KOREAN ROCKFISH (*Sebastes schlegelii*)

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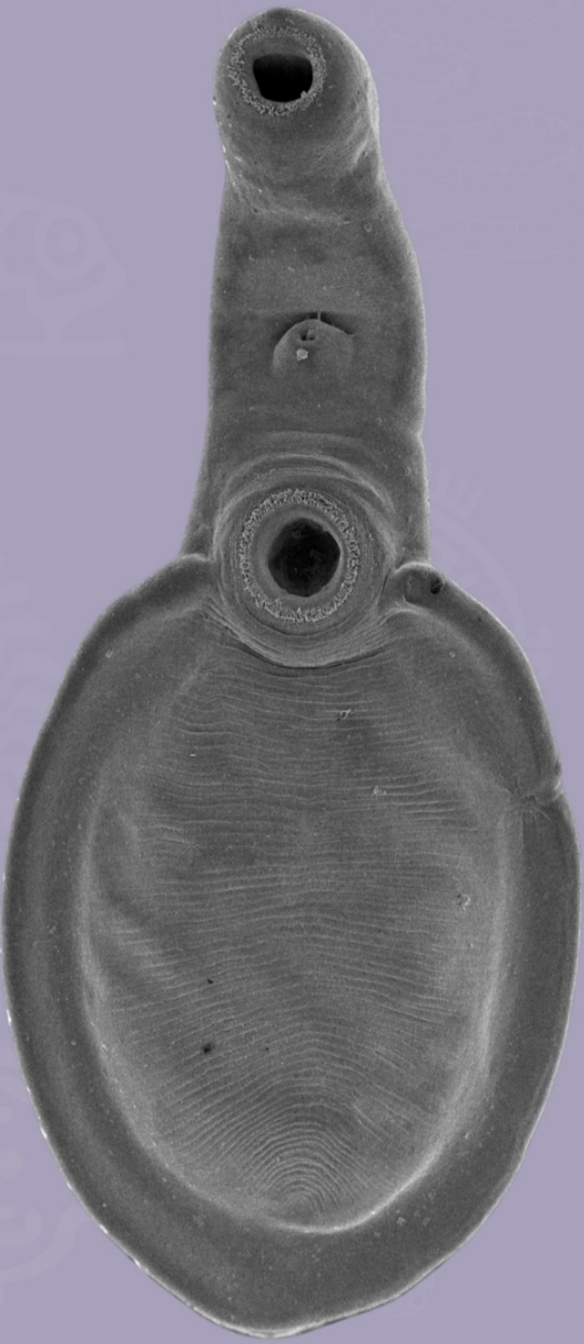
Fish parasites are a common occurrence in aquaculture and are regarded as potential threats. While several methods exist to assess the risks posed by these parasites, studying their life cycles is crucial for identifying key risk indicators. This research examined the egg hatching, maturation, and oncomiracidium developmental stages of *Menziesia sebastodis*, which infests Korean rockfish (*Sebastes schlegelii*). Specimens of *M. sebastodis* collected from Korean rockfish were placed in a 6-well plate containing sterile seawater at 20°C. Microscopic observations revealed that the parasites first produced hollow tubular filaments, which were then filled with material, forming triangular-shaped eggs. The egg-laying process took 10 minutes, and after 11 days of maturation, the oncomiracidium stage hatched. On the first day post-hatch, the cilia on the oncomiracidium disappeared, and by the fifth day, the previously contracted haptor had fully unfolded. Given the limited research on the life cycle of *M. sebastodis*, this study provides new insights into the egg development and post-hatch stages of this parasite and offers a foundation for further investigation into managing *M. sebastodis* infestations in aquaculture systems.

Thematic areas

5. AQUACULTURE & MARICULTURE



ORAL PRESENTATIONS

(Please note the name and institution shown in this list are those of the person presenting the talk, who may not be the first author; the complete author list including all institutional affiliations are shown with the full abstract)

1. APPLIED OUTCOMES LEAD TO FUNDAMENTAL INSIGHTS: OBSERVATIONS FROM A STUDY ON *Cardicola* spp. (APOROCOTYLIDAE) INFECTING RANCHED SOUTHERN BLUEFIN TUNA OFF PORT LINCOLN, SOUTH AUSTRALIA FROM 2019-2022. Bott N.J. et al. School of Science, RMIT University, Victoria, Australia
2. PARASITE PREVALENCE IN *Cyprinus carpio* KOI AND IN VITRO ANTHELMINTIC ACTIVITY OF COPPER NANOPARTICLES AGAINST MONOGENEAN PARASITES. Gomes Santos G.G. et al. Aquaculture Department, Universidade Federal de Santa Catarina, Florianópolis, Brazil
3. TEMPORAL, GEOGRAPHICAL AND ENVIRONMENTAL FACTORS INFLUENCING SEA LICE INFESTATIONS ON MARINE ATLANTIC SALMON FARMS IN IRELAND. Klimešová B. et al. Marine and Freshwater Research Centre, Atlantic Technological University, Ireland
4. REPORTING PARASITIC DISEASES IN AQUACULTURE – COMMON ISSUES. Nowak B.F. Institute for Marine and Antarctic Science, University of Tasmania, Hobart, Australia
5. GOING ALL NATURAL: IN VITRO EVALUATION OF PHYTOGENICS AND ESSENTIAL OILS FOR POLYOPHISTOCOTYLEAN CONTROL IN GILTHEAD SEA BREAM AQUACULTURE. Pirollo T. et al. Instituto de Acuicultura Torre de la Sal (IATS, CSIC), Castellón, Spain
6. PARASITES ASSOCIATED WITH ORNAMENTAL FISH IMPORTED INTO SOUTH AFRICA: COMPLEX, CONCERNING AND INTERESTING ALL IN ONE. Přikrylová I. et al. Department of Biodiversity, University of Limpopo, South Africa
7. METAZOAN PARASITE FAUNA OF WILD SCIEANIDS FROM THE WESTERN MEDITERRANEAN. Repullés-Albelda A. et al. Cavanilles Institute of Biodiversity and Evolutionary Biology, University of Valencia, Valencia, Spain
8. FISH PARASITES IN AQUACULTURE: PROPHYLACTIC MEASURES USING ECOLOGICAL INSIGHTS. Shirakashi S. Aquaculture Research Institute, Kindai University, Japan
9. *Enteromyxum vs Ceratonova*: A COMPARATIVE VIEW OF TWO MYXOZOAN ENTERITIS AFFECTING FISH HOSTS. Sitjà-Bobadilla A. et al. Fish Pathology Group, Instituto de Acuicultura Torre de la Sal (IATS, CSIC), Castellón, Spain
10. A NEW MYXOZOAN PARASITE (*Parvicapsula* sp.) INFECTING FARMED GREATER AMBERJACK (*Seriola dumeri*li). Sitjà-Bobadilla A. et al. Fish Pathology Group, Instituto de Acuicultura Torre de la Sal (IATS, CSIC), Castellón, Spain
11. REDUCING SKIN FLUKE INFECTION USING FISH THAT CONSUME PARASITE EGGS. Tomita Y. et al. Aquaculture Research Institute, Kindai University, Wakayama, Japan

POSTER PRESENTATIONS

(Please note the name and institution shown in this list are those of the person presenting the poster, who may not be the first author; the complete author list including all institutional affiliations are shown with the full abstract)

1. *Microcotyle whittingtoni* (MONOGENEA) INFECTIONS OF CULTURED COMMON DENTEX (*Dentex dentex* L.) FROM THE MIDDLE EASTERN ADRIATIC SEA. Čolak S. et al. University of Zadar, Department of Ecology, Agronomy and Aquaculture, Zadar, Croatia
2. CO-INFECTION OUTBREAK OF TILAPIA FISH FARM ASSOCIATED WITH SEVERE MORTALITY DURING SUMMER IN SINALOA, EASTERN PACIFIC. Grano-Maldonado M. et al. Facultad de Ciencias del Mar, Universidad Autónoma de Sinaloa, Mazatlán, Mexico
3. EXPLORING THE ANTIPARASITIC POTENTIAL OF *Schinus terebinthifolius* Raddi ESSENTIAL OIL AGAINST PROTOZOAN *Epistylis* sp. IN JUVENILE *Oreochromis niloticus*. Jerônimo G.T. et al. Aquaculture Department, Universidade Federal de Santa Catarina, Florianópolis, Brazil
4. *IN VITRO* EFFICACY OF COPPER NANOPARTICLES (CuNPS) AGAINST CESTODES OF *Cyprinus carpio* KOI. Jerônimo G.T. et al. Aquaculture Department, Universidade Federal de Santa Catarina, Florianópolis, Brazil
5. SELECTING CANDIDATE PHARMACOLOGICAL AND PHYTOGENIC ACTIVE INGREDIENTS FOR THE CONTROL OF POLYOPHISTOCOTYLEAN INFECTIONS IN MARINE AQUACULTURE. Palenzuela O. et al. Fish Pathology Group, Instituto de Acuicultura Torre de la Sal (IATS, CSIC), Castellón, Spain
6. AN EXPERIMENTAL STUDY OF HOST-PARASITE INTERACTIONS: A CASE STUDY OF *Glossolepis incisa*. Přikrylová I. et al. Department of Biodiversity, University of Limpopo, South Africa

ORAL PRESENTATIONS

APPLIED OUTCOMES LEAD TO FUNDAMENTAL INSIGHTS: OBSERVATIONS FROM A STUDY ON *Cardicola* spp. (APOROCOTYLIDAE) INFECTING RANCHED SOUTHERN BLUEFIN TUNA OFF PORT LINCOLN, SOUTH AUSTRALIA FROM 2019-2022

Bott N.J.[1]; Power C.[1]; Widdicombe M.[1]; Carabott M.[1]; Hudson J.[1]; Coff L.[1,2]; Rough K.[3]; van Gelderen R.[1]; Ramsland P.A.[1]; Young N.D.[4]; Shirakashi S.[5] & Nowak B.F.[6]

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Aporocotylid blood flukes, *Cardicola forsteri* and *Cardicola orientalis,* are economically significant parasites of Southern bluefin tuna (SBT), *Thunnus maccoyii.* SBT are ranched off the coast of Port Lincoln, South Australia. A multi-year collaboration between the Australian Southern Bluefin Tuna industry and researchers has developed important applied outcomes for the industry. This has been achieved by providing insights into husbandry methods and the use of the anthelminthic praziquantel for the ongoing management of aporocotylids. A novel, rapid, in-field diagnostic molecular test (Recombinase Polymerase Amplification), targeting the 2nd internal transcribed spacer of ribosomal DNA (ITS-2 rDNA) was developed for both *C. forsteri* and *C. orientalis* in-field detection. Importantly this industry-researcher collaboration has allowed important studies on the biology of aporocotylids to be undertaken. Developments in aporocotylid glycomics, genomics and transcriptomics will be discussed, as well as important insights into host-parasite immune interactions. This research not only has importance for aporocotylid management in bluefin tuna, but also provided important information about the Aporocotylidae and the Trematoda.

PARASITE PREVALENCE IN *Cyprinus carpio* KOI AND *IN VITRO* ANTHELMINTIC ACTIVITY OF COPPER NANOPARTICLES AGAINST MONOGENEAN PARASITES

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Thinking about treatment and prevention alternatives to mitigate pathogen-related diseases in Koi carp farming, this study investigated the *in vitro* anthelmintic effect of copper nanoparticles (CuNPs) on the monogeneans *Dactylogyrus minutus*, *Dactylogyrus extensus*, and *Gyrodactylus cyprini*, as well as evaluated the fish for prevalence, mean intensity, and mean abundance of infection. Before the *in vitro* tests, 30 fish were euthanized for parasitological analysis, during which prevalence (P%), mean intensity of infection (MII), and mean abundance (MA) were calculated. To determine the time and efficacy in the mortality of monogenean parasites, the parasites were exposed to CuNPs concentrations of 20, 50, 100, 150, 200, and 300 mg L^{-1}, with a control group in tank water and another with copper sulfate pentahydrate (CuSO4.5H2O) at a concentration of 0.3 mg L^{-1}. All tests were performed in triplicate. The parasites were observed every 10 minutes for 300 minutes, and mortality was recorded. The results showed that *Dactylogyrus* spp. had a P% of 96.67, MII of 18.59 ± 15.68, and MA of 17.97 ± 15.78, while *Gyrodactylus cyprini* had a P% of 13.33, MII of 3.25 ± 3.34, and MA of 0.43 ± 1.65. The results of anthelmintic activity demonstrated a dose-dependent effect, with the most effective concentration being 300 mg L^{-1} at 120 minutes. The study indicated that CuNPs were effective against the parasites studied; however, further investigation is needed to evaluate their potential use in aquaculture.

TEMPORAL, GEOGRAPHICAL AND ENVIRONMENTAL FACTORS INFLUENCING SEA LICE INFESTATIONS ON MARINE ATLANTIC SALMON FARMS IN IRELAND

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The salmon louse, *Lepeophtheirus salmonis*, is a limiting factor for Atlantic salmon aquaculture in the Northern hemisphere. Salmon lice are ectoparasites of Atlantic salmon, feeding on the host's blood, tissue, and mucus. Feeding by lice can damage dermal tissue and lead to secondary infections, and high infestation levels can even increase fish mortality. Salmon lice infestations have a high economic impact on salmon aquaculture, mainly connected with the cost of management strategies and treatment. Meanwhile, effective treatment and management strategies are dependent on the understanding of the dynamics of lice infestations. To better understand these dynamics, a 30-year dataset of lice abundance from Atlantic salmon farms in Ireland was analyzed. Data was collected by the Marine Institute as part of the National Sea Lice Monitoring program and analyzed using generalized linear mixed-effect models. Temporal fluctuations were detected with an overall decrease in sea lice abundance over the last 30 years. Infestation levels varied depending on the characteristics of individual bays where the salmon farms are located (e.g., length of bay, openness of bay). Environmental variables, including salinity and dissolved oxygen, were identified as having a negative effect on sea lice abundance. Understanding the factors influencing lice infection dynamics can aid in predicting periods of higher risk of infestation and implementing successful management strategies to reduce parasite burdens and maintain fish health. The results of this study will be used to inform the national strategy on the management of salmon lice and fish welfare in aquaculture in Ireland.

REPORTING PARASITIC DISEASES IN AQUACULTURE – COMMON ISSUES

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Farmed fish are affected by parasitic diseases which affect the health of the fish and increase the costs of fish production. Reporting parasitic diseases in farmed fish is essential, it increases our knowledge and contributes to assessing the risks and developing management strategies. However, to be helpful the reports need to be accurate. There are cases when the parasites are misidentified or identified only to subphylum or class. In other cases, presence of DNA is assumed to be the same as the presence of the parasite. Furthermore, parasite presence is considered a disease without evaluation of disease signs. When reporting a parasitic infection, it is helpful to determine its severity. Some reports fully rely on prevalence without considering infection intensity. In this presentation all these issues and other issues will be discussed and solutions suggested to improve reporting of parasitic diseases in aquaculture.

GOING ALL NATURAL: IN VITRO EVALUATION OF PHYTOGENICS AND ESSENTIAL OILS FOR POLYOPHISTOCOTYLEAN CONTROL IN GILTHEAD SEA BREAM AQUACULTURE

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The hematophagous polyophistocotylean *Sparicotyle chrysophrii* is a major concern for gilthead seabream (*Sparus aurata*) net cage aquaculture. It is responsible for gill pathologies, severe anemia, and mortality in younger fish. Global warming may exacerbate its impact due to the parasite's rapid development, direct transmission, and lack of registered treatments. Antiparasitic options for open aquaculture systems are currently very limited. FAO, WOAH, and WHO recommend reducing pharmaceutical use in aquaculture to mitigate environmental and public health impacts. This has driven the search for alternative disease control strategies. The goal of this study is to explore active ingredients (AI) alternative or complementary to current pharmacological treatments, aiming to develop functional feeds that are safe, practical, economically viable, environmentally friendly, and effective against *S. chrysophrii*. This work focuses on the effect of a panel of 18 commercial phytogenics and essential oils on the vitality of adult *S. chrysophrii* specimens. Batches of live parasites were harvested from experimentally infected fish, and were exposed *in vitro* to a wide range of doses of each AI. Vitality/mortality at various post-exposure time points within 24h was assessed and data was analyzed to determine the AI concentration causing 50% mortality (LD_{50}). Several compounds have shown to have short-term lethal effects on *S. chrysophrii* at concentrations as low or lower than formalin, which is the only therapy currently registered in the EU for control of sparicotylosis. The results have guided formulation of new diets including phytogenic AIs which are currently being tested *in vivo*.

PARASITES ASSOCIATED WITH ORNAMENTAL FISH IMPORTED INTO SOUTH AFRICA: COMPLEX, CONCERNING AND INTERESTING ALL IN ONE

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Millions of ornamental fish are exported from over 100 countries worldwide. However, there is currently no legislation in South Africa requiring that ornamental fish imported be quarantined. Between October 2020 and July 2024, 748 ornamental fish comprising 38 species from 14 families were received either from Indonesia, Sri Lanka, and Thailand using an established trading company. Standard procedures were applied when transporting, handling, and dissecting fish including the examination, fixation, and preservation of parasites. Molecular data of some parasitic groups were generated to confirm species identification. Of the fish examined, 16 species (42%) were infected by five parasitic groups *i.e.* Ciliate, Monopisthocotyla, Cestoda, Nematoda, and Crustacea, and were represented by 31 species and 21 genera. The monopistocotylans were the most prevalent and were reported from 14 fish species. *Carassius auratus* was the fish species infected with the highest number of parasite species, while an invasive parasite species, *Schyzocotyle acheilognathi*, was found in the fish *Cichlasoma* sp. and a new genus of monopisthocotylan parasite in *Glossolepis incisa*. Species compositions differed when fish were sourced from two or more countries, *i.e. Barbonymus schwanenfeldii*, *Pangasianodon hypophthalmus*, *Pterophylum scalare* and *Astronotus ocellatus*. New molecular data were obtained for *Cichlidogyrus furu* (18S+ITS1 and 28S rDNA) and *Capillaria pterophylli* (18S rDNA). The present study revealed that taxonomic revisions of some taxa would be necessary and that the systematic screening for parasites from ornamental fish and the implementation of quarantine are essential to avoid the introduction of non-native parasites. Supported by DSI-NRF SARChI Chair (No.101054).

METAZOAN PARASITE FAUNA OF WILD SCIEANIDS FROM THE WESTERN MEDITERRANEAN

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Sciaenid fish are among the most promising candidates for species diversification in Mediterranean aquaculture. Despite meeting the main production requirements, there is scarce data on the pathogens affecting these fish species. We analyzed metazoan parasites from three Mediterranean sciaenids, *Sciaena umbra*, *Umbrina canariensis* and *U. cirrosa*. Seasonal samplings of 20 specimens per fish species were obtained from the Western Mediterranean and the parasite fauna was characterized. A total of 14,813 parasites belonging to 34 taxa were collected. Twenty parasites were identified for each sciaenid; i) *S. umbra*: 13 platyhelminths, three nematodes and four arthropods; ii) *U. canariensis*: 13 platyhelminths, three nematodes and four arthropods; iii) *U. cirrosa:* 13 platyhelminths, one acanthocephalan, two nematodes and four arthropods. The parasitological analysis allowed the identification of nine new host records among parasites of *S. umbra* and 13 among parasites of *U. canariensis* and *U. cirrosa*. Most parasites were generalist and only three species were host-family-specific, one genus-specific and four species-specific. Five species were shared by the three Mediterranean sciaenids. The cross-infection risks are discussed, and the potential effects are assessed based on reported damages, parasite life cycle and transmission. This work forms part of the ThinkInAzul programme and was supported by MCIN with funding from European Union NextGenerationEU (PRTR-C17·I1) and by Generalitat Valenciana (GVA-THINKINAZUL/2021/029).

FISH PARASITES IN AQUACULTURE: PROPHYLACTIC MEASURES USING ECOLOGICAL INSIGHTS

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Parasites from diverse taxa threaten sustainable aquaculture, with current control strategies often being reactive, relying on post-infection removal through antiparasitic chemicals. However, these methods may have limited long-term effectiveness and negative environmental consequences. Given the difficulties in developing vaccines for many parasite species, alternative prophylactic approaches are essential. These measures require a deep understanding of the parasites' ecological and biological traits. A crucial step is to elucidate parasite life cycle, focusing on stages that do not involve fish as host. For example, identifying and eradicating the polychaete intermediate host for the aporocotylid blood fluke *Cardicola orientalis* has successfully reduced infections in farmed juvenile Pacific bluefin tuna. Similarly, discovering the invertebrate host for the pathogenic microsporidian *Inodosporus fujiokai* has enabled effective disease prevention in trout farms. For parasites with direct life cycles, such as monogeneans, understating behavioral traits of oncomiracidia and the physical properties of eggs offer new avenues for reducing infections. This approach can lower the labor and costs associated with deworming treatment in aquaculture. These examples highlight the value of ecological insights in developing proactive strategies for managing parasitic threats, shifting the focus from reactive treatment to long-term prevention in sustainable aquaculture.

Enteromyxum VS Ceratonova: A COMPARATIVE VIEW OF TWO MYXOZOAN ENTERITIS AFFECTING FISH HOSTS

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Myxozoa, a diverse group of microscopic parasites within the phylum Cnidaria, are recognized for their significant impact on aquaculture and fisheries. While many Myxozoa species show low tropism for a specific tissue, some specifically target the gastrointestinal tract, leading to severe enteric diseases in farmed fish. *Ceratonova shasta* is one such myxozoan species that has garnered attention due to its impact on salmonid fish in North America. This parasite infects the intestines, causing ceratomyxosis, which is characterized by inflammation, haemorrhaging, and necrosis of the intestinal tissue. The disease can result in high mortality rates, particularly in juvenile fish, posing a significant threat to both wild and cultured salmonid populations. Another group of concern is the genus *Enteromyxum*, particularly *E. leei* and *E. scophthalmi*, which cause severe enteric myxosporidiosis in various marine fish species, including gilthead sea bream, olive flounder and turbot. These parasites invade the intestinal epithelium, leading to chronic enteritis, malabsorption, weight loss, and, in severe cases, death. The enteric infections caused by these myxozoan species represent a significant challenge for aquaculture, as infections can lead to reduced fish growth, increased mortality, and substantial economic losses. Alongside advancements in diagnostic tools, effective management, prevention and treatment strategies require a deep understanding of the biology, transmission, and environmental conditions that favor these parasites. In this work, we compare the infectious strategies of both genera, in terms of transmission, migration and proliferation in fish tissues, parasite release, host response and pathological outcomes such as inflammation and antibody production.

A NEW MYXOZOAN PARASITE (*Parvicapsula* sp.) INFECTING FARMED GREATER AMBERJACK (*Seriola dumerili*)

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The greater amberjack (GA) is highly valued due to its fast growth, market demand, and adaptability to farming conditions. Rearing GA faces several challenges including disease management, particularly against bacterial and parasitic infections. We depict a new renal pathology in juvenile GA reared in Greek sea cages, associated to increased mortality and to the presence of a myxozoan parasite, that we ascribe to the genus *Parvicapsula* on the basis of morphometrical observations and SSU rDNA genotyping. Trophozoites, disporic plasmodia and spores were mainly located in the lumen of renal tubules. Immature spores were most often orientated in opposite directions within the plasmodium; early trophozoites were quite irregular, mainly subspherical to oval, sometimes with filopodial projections intermingled with villi of renal epithelial cells. Most stages floated in the lumen or slightly attached to the epithelia, but some trophozoites (primary cells with secondary cells) were observed in the paracellular space of renal tubule epithelia. Myxospores roughly pyriform; valves smooth; two subspherical polar capsules of equal size, closely apposed, discharging in the same apical direction; a single distinct sporoplasm occupying more than three quarters of the spore, with two prominent nuclei. Renal tubules appeared vacuolized, with increased numbers of rodlet cells. While the morphology and ultrastructure of this new parasite do not allow yet firm ascription, SSU rDNA-based genotyping clearly assigns it to a new *Parvicapsula* sp. with *P. spinachiae* as the closest known relative. This is a clear case of new pathological agents emerging under intensification of production of new fish species.

REDUCING SKIN FLUKE INFECTION USING FISH THAT CONSUME PARASITE EGGS

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Skin flukes (Monogenea: Capsalidae) are major parasites in marine fish aquaculture, causing significant issues worldwide. Current control strategies, primarily focus on deworming treatments, are often labor-intensive, time-consuming, and lack effective preventive measures. The primary source of skin fluke infestations in cage farms is parasite eggs accumulating on netting. Therefore, reducing egg density on netting could lower infection. This study aimed to develop a simple, easy-to-apply, environmentally friendly, and sustainable method for egg removal by co-culturing fish species that consume skin fluke eggs ("egg-remover" species). We first evaluated the feeding preferences of various fish species for skin fluke eggs, identifying five omnivorous species as potential egg-removers. Of those, *Oplegnathus fasciatus*, *Girella leonina*, and *Siganus fuscescens* were selected for co-culturing experiment with juvenile *Seriola* spp. Co-culturing *O. fasciatus* with *Seriola dumerili* was problematic due to aggressive behavior of *O. fasciatus*. In contrast, *G. punctata* and *S. fuscescens* were tame and suitable for co-culturing. In trials, *Neobenedenia girellae* infestations in *Seriola quinqueradiata* co-cultured with *G. punctata* were reduced by more than half compared to mono-cultured controls, with significantly fewer mortalities and improved growth. Similar results were observed in *Seriola aureovittata* co-cultured with *S. fuscescens*. No skin fluke infections were found in the egg-remover species, and significantly fewer biofouling occurrences were observed in co-culturing cages. These findings suggest that using egg-remover fish can effectively reduce skin fluke eggs on cage netting and prevent infections, providing a promising biological control method for managing monogenean infestations in aquaculture.

POSTER PRESENTATIONS

Microcotyle whittingtoni (MONOGENEA) INFECTIONS OF CULTURED COMMON DENTEX (*Dentex dentex* L.) FROM THE MIDDLE EASTERN ADRIATIC SEA

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The common dentex *Dentex dentex* (Linnaeus, 1758) is a widespread fish in the Mediterranean and East Atlantic. The species is interesting for aquaculture due to its high commercial value. Microcotylid infections cause significant problems in fish farming and represent a main threat to the diversification of sparid aquaculture. Within this family, the genus *Microcotyle* is the most speciose, including more than 70 species from a wide diversity of fish hosts. Microcotylid infection with high mortalities of common dentex reared in floating sea cages was observed in June 2024 in a fish farm in the Middle Eastern Adriatic Sea affecting 1+ age class fish (150-200 g). Daily losses ranged from 0.10 to 0.50 % resulting in a final mortality of 5% by the end of June. Affected fish showed lethargy, loss of appetite, anemia, and asphyxia. During parasitological examinations of gill, parasites were counted and preserved in 10% buffered formalin and 70% ethanol for subsequent analyses. Monogenean parasites found on gill arches of common dentex (prevalence 100%, abundance 102) were identified as *Microcotyle whittingtoni*, based on morphological (light and scanning electron microscopy) and molecular analysis (amplification and sequencing of the 28S rRNA gene). Although *M. whittingtoni* has already been described in wild *D. dentex* from different areas of the Mediterranean Sea, we report it for the first time in cage-farmed fish showing clinical signs and mortality, indicating this parasite as a possible health threat for common dentex aquaculture.

CO-INFECTION OUTBREAK OF TILAPIA FISH FARM ASSOCIATED WITH SEVERE MORTALITY DURING SUMMER IN SINALOA, EASTERN PACIFIC

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The present study aimed at describing the massive mortality of farmed Nile tilapia *Oreochromis niloticus* caused by a co-infection during the summer in a fish farm of Sinaloa, Northwestern Mexico. Approximately 55,000 tilapias (250-300 g) were lost over 20 days representing 80-90% of the original fish stocked due to the presence of this co-infection. Fish mortality was exacerbated with the temperature increase during the summer. Fish displayed emaciation, lethargy, and some skin abrasions. The most abundant ectoparasites were peritrichous ciliates on the gills and epithelium of their hosts; four species were identified: *Trichodina heterodentata* Duncan, 1977, *T. magna* Van As and Bassson, 1989*, T. nigra* Lom, 1960*, Trichodina* sp., *Ambiphrya* sp. Raabe, 1952. Monogeneans *Gyrodactylus cichlidarum* and *Cichlidogyrus* sp. were identified using measurements of the hard parts and compared with previous literature. An histopathological examination of the fish gills showed that the protozoans attached to the filaments caused severe hyperplasia and gill epitheliocystis. *Pseudomonas* sp. was identified, probably as a secondary infection agent. Parasite infections have major consequences for fish species under aquacultural fish practice and must consequently be considered as a fundamental factor within any aquaculture system.

EXPLORING THE ANTIPARASITIC POTENTIAL OF *Schinus terebinthifolius* Raddi ESSENTIAL OIL AGAINST PROTOZOAN *Epistylis* sp. IN JUVENILE *Oreochromis niloticus*

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The intensification of Nile tilapia (*Oreochromis niloticus*) production has raised health concerns due to the emergence of parasitic diseases and the indiscriminate and inappropriate use of antibiotics and other chemotherapeutic agents. In this context, phytotherapeutic alternatives, such as the essential oil (EO) of *Schinus terebinthifolius*, may be promising for treating parasites in ornamental fish. This study aimed to perform in vitro antiparasitic tests with the EO of *S. terebinthifolius* against the protozoan *Epistylis* sp. in juvenile *O. niloticus*. The chemical composition of *S. terebinthifolius* EO was determined by gas chromatography. For the antiparasitic test, the protozoan *Epistylis* sp., obtained from naturally parasitized *O. niloticus*, was exposed to different EO concentrations (2%, 1%, 0.5%, 0.25%), with tank water and 1% grain alcohol (EO diluent) serving as controls. Chemical analysis revealed that the main components of *S. terebinthifolius* EO were δ-3-Carene (56.00%) and α-Pinene (16.89%), while the remaining 23 compounds were present in amounts less than 5%. In the antiparasitic test, the 2% EO concentration showed 100% efficacy against *Epistylis* sp. within five minutes, while the 1% concentration achieved the same performance within 10 minutes. Lower concentrations showed less than 100% efficacy within 20 minutes but reached full efficacy (100%) after 40 minutes of exposure. The tank water control did not show any mortality, and the grain alcohol control demonstrated a maximum efficacy of 20% after more than five hours of testing. *Schinus terebinthifolius* EO demonstrated antiparasitic activity at a 2% concentration, standing out as an alternative to conventional treatments.

IN VITRO EFFICACY OF COPPER NANOPARTICLES (CuNPS) AGAINST CESTODES OF *Cyprinus carpio* KOI

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Nanotechnology emerges as an innovative tool in aquaculture due to its continuous advancement. In this context, metal nanoparticles, including copper (Cu), have emerged as potentially effective antimicrobial agents against a variety of microorganisms. Currently, parasitic diseases in fish represent a significant challenge in aquaculture. Cestodes adhere to the intestines of their hosts, feed, and absorb nutrients, which can affect the fish's performance, leading to mortality. Therefore, alternative treatments are being sought to mitigate pathogen-related diseases in the breeding of Koi carp (*Cyprinus carpio*). This study investigated the *in vitro* antihelminthic effect of copper nanoparticles (CuNPs) against the cestode *Schyzocotyle acheilognathi*. To determine the time and efficacy in parasite mortality, the parasites (3-5) were exposed to CuNPs concentrations of 50, 100, 150, and 300 mg L^{-1}, as well as a control group with tank water, with each treatment conducted in triplicate. The parasites were observed every 10 minutes for 300 minutes, and mortality was recorded. At the end of the *in vitro* tests, the parasites were collected for species confirmation and prepared for Scanning Electron Microscopy (SEM) analysis to assess the damage caused when exposed to CuNPs. Subsequently, the antihelminthic efficacy of each treatment was calculated. The antihelminthic activity results demonstrated a dose-dependent effect, with the most effective concentration being 300 mg L^{-1} after 120 minutes. SEM showed wrinkles in the integrity of the parasites' tegument when exposed to CuNPs at the concentration of 300 mg L^{-1} compared to the control group (no exposure). The study indicated that CuNPs were effective against the studied cestodes. Future research is recommended to evaluate the product *in vivo*, as well as its toxicity to fish and the environment.

SELECTING CANDIDATE PHARMACOLOGICAL AND PHYTOGENIC ACTIVE INGREDIENTS FOR THE CONTROL OF POLYOPHISTOCOTYLEAN INFECTIONS IN MARINE AQUACULTURE

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The hematophagous polyophistocotylean parasite *Sparicotyle chrysophrii* is currently the main infectious problem for netpen-based aquaculture of gilthead sea bream throughout the Mediterranean. In Western Europe, the only registered therapy is based on formalin baths which are cumbersome to apply in sea cages and generate major running expenses. In addition, formalin has a narrow therapeutic index for fish and its use in open aquaculture systems poses environmental and workplace safety concerns. There is an extensive demand for in-feed antiparasitic active ingredients (AIs) against polyophistocotyleans, but these should be chosen on the basis of effectivity, safety, and knowledge on their specific mechanisms of action. Although some antiparasitic drugs have shown effectivity against polyophistocotyleans, *in vivo* trials are logistically challenging and often not reproducible. In the framework of a new research project focusing on polyophistocotylean management, a system that allows the maintenance of *S. chrysophrii* infections in RAS circuits was set up. It ensures a continuous supply of parasites which allows us detailed testing of antiparasitic compounds *in vitro* under controlled and reproducible conditions. This has allowed us to evaluate a wide selection of phytogenics, vegetable essential oils, anthelminthic drugs, and related pharmacological compounds shortlisted from computational virtual screening of chemical libraries. On a second phase to this strategy, the focus is currently placed on the *in vitro* maintenance of the worms for longer periods and under conditions closer to the physiological ones, for more precise studies on the mechanisms of action of selected AIs at structural and metabolical levels.

AN EXPERIMENTAL STUDY OF HOST-PARASITE INTERACTIONS: A CASE STUDY OF *Glossolepis incisa*

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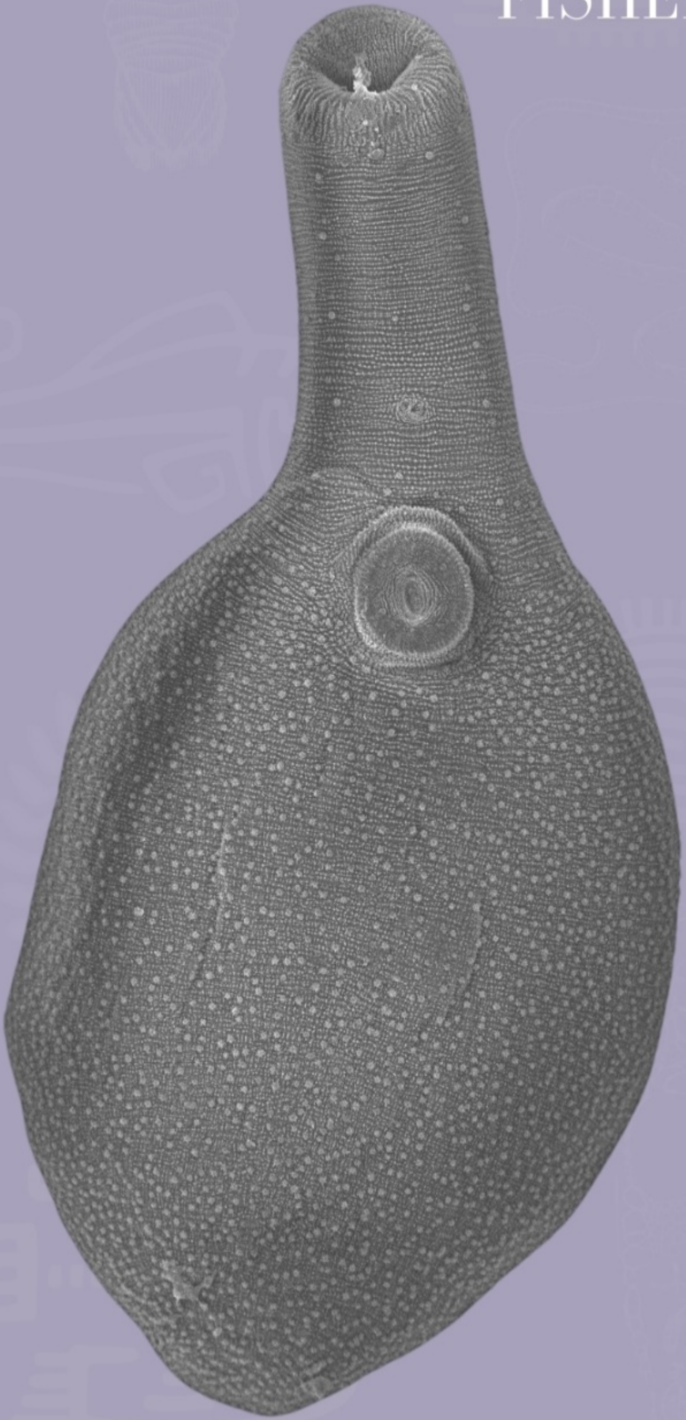
The red rainbowfish *Glossolepis incisa* is native to Indonesia and is one of the most popular species within the ornamental fish trade. The present study aimed to evaluate host-parasite interactions by imitating the keeping of this species as ornamental fish in standard household aquaria. In this study, a total of 100 red rainbowfish were imported from Indonesia and kept in four sixty-liter aquaria whereby 15 fish specimens were randomly sampled and examined for parasites on day 0 and during weeks (W) 1, 3, 5, 7, and 9. Due to the occurrence of fish mortalities, only seven fish were sampled on week 9. Standard procedures and methods were followed for fish dissection, parasite collection, and preservation. The infestation with ectoparasites remained fairly constant (Prevalence, P = 73.3 – 86.7%) during the trial except for W 9 when ectoparasites were absent. Similarly, the prevalence (P) for endoparasites was high from day 0 until W 5 (P = 73.3 – 86.7%) decreasing to a P of 53.3% during W 7 and a P of 42.9% during W 9. For ectoparasites, the highest intensity of infection was on W 7, with 148 specimens on fish and a mean intensity (MI) of 31.7, while for endoparasites an IF of 1 – 12 between W 1 and W5 and an MI of 5.3 for W 3 were reported. This study revealed that the parasites associated with fish imported from abroad can increase over time in an aquarium environment if not treated before being introduced into household aquaria. Supported by the DSI-NRF SARChI Chair (No.101054).

Thematic areas

6. PARASITES & FISHERIES



ORAL PRESENTATIONS

(Please note the name and institution shown in this list are those of the person presenting the talk, who may not be the first author; the complete author list including all institutional affiliations are shown with the full abstract)

1. ANISAKIDAE IN THE ENGLISH CHANNEL AND THE NORTH SEA: REVIEW OF THE LITERATURE, GAP IDENTIFICATION AND PRELIMINARY DATA. Duflot M. et al. Anses, Laboratory for Food Safety, Boulogne-sur-Mer, France
2. AFFECT OF A MAJOR RIVER RESTORATION EVENT ON ABUNDANCE AND DISTRIBUTION OF FISH PARASITES MAPPED BY WATER SAMPLING. Hallett S.L. et al. Department of Microbiology, Oregon State University, Corvallis, Oregon, USA
3. IMPACTS OF MYXOZOAN DISEASES IN SALMON WITHIIN AN URBAN-INFLUENCED WATERSHED. Lovy J. et al. U.S. Geological Survey, Western Fisheries Research Center, Seattle WA, USA
4. VIRULENCE AND PATHOLOGY OF EYE FLUKE TREMATODES, *Diplostomum* spp. AND *Tylodelphys* sp., INFECTING ENDANGERED LOST RIVER SUCKERS, *Deltistes luxatus*. Lovy J. U.S. Geological Survey, Western Fisheries Research Center, Seattle, WA, USA
5. UNCOVERING BIOMINERALIZATION IN MYXOZOA, MICROSCOPY, CHEMICAL ANALYSIS AND GENETIC DATA. Muller, M.I. et al. Department of Microbiology, Oregon State University, USA
6. ASSESSMENT OF THE METAZOAN PARASITES OF COMMERCIALLY VALUABLE FISH IN ICES AREA 6A. Osmond T. et al. Animal and Plant Sciences, School of Applied Sciences, Edinburgh Napier University. Scotland, UK
7. PARASITES: CASTING A BRIGHT LIGHT ON FISH MANAGEMENT AND ECOLOGY IN ICELANDIC WATERS. Randhawa H.S. Faculty of Life and Environmental Sciences, University of Iceland, Reykjavík, Iceland
8. EXPLORING HOW *Myxobolus cerebralis* AND *Tetracapsuloides bryosalmonae* DETERMINE THE OUTCOME OF RAINBOW TROUT CO-INFECTIONS BY QUANTITATIVE PROTEOMICS. Saleh M. Division of Fish Health, University of Veterinary Medicine, 1210 Vienna, Austria
9. INTRA-STOCK VARIABILITY IN THE STRUCTURE OF PARASITE ASSEMBLAGES OF ARGENTINE HAKE *Merluccius hubbsi* IN PATAGONIAN WATERS. Timi J.T. et al. Laboratorio de Ictioparasitología, Instituto de Investigaciones Marinas y Costeras, Fac. Cs. Ex. y Naturales, Universidad Nacional de Mar del Plata, Mar del Plata - CONICET. Argentina

POSTER PRESENTATIONS

(Please note the name and institution shown in this list are those of the person presenting the poster, who may not be the first author; the complete author list including all institutional affiliations are shown with the full abstract)

1. NEMATODA PARASITES FROM EUROPEAN HAKE (*Merluccius merluccius,* LINNAEUS, 1758) CAUGHT IN TWO AREAS OF THE ATLANTIC OCEAN (SOUTHWEST IRELAND AND THE BISCAY BAY). Atroch, F. et al. CIIMAR - Department of Biology, Faculty of Sciences, Porto University, Porto, Portugal
2. A COMPARISON OF THE METAZOAN PARASITES OF THE LIONFISH *Pterois volitans* (PISCES: SCORPAENIDAE) FROM YUCATAN PENINSULA, GULF OF MEXICO AND CARIBBEAN SEA. Centeno-Chalé O. A. et al. Centro de Investigación y de Estudios avanzados del instituto Politécnico Nacional Unidad Mérida. México
3. THE PARASITE COMMUNITY OF *Merluccius merluccius* AND *Sardinella aurita* FROM THE MEDITERRANEAN SEA. Muns-Pujadas, L., C. et al. Departament de Biologia Animal, de Biologia Vegetal i d'Ecologia, Universitat Autònoma de Barcelona, Cerdanyola del Vallès, 08193, Barcelona, Spain
4. UNUSUAL LOCALIZATION OF *Ligula intestinalis* PLEROCERCOIDS IN *Abramis brama*. Palíková M. et al. University of Veterinary Sciences Brno, Faculty of Veterinary Hygiene and Ecology, Department of Ecology & Diseases of Zoo Animals, Game, Fish and Bees, Brno, Czech Republic
5. OCCURRENCE OF PROLIFERATIVE KIDNEY DISEASE IN SALMONID WATERS OF THE CZECH REPUBLIC. Palíková et al. Mendel University in Brno, Faculty of AgriSciences, Department of Zoology, Fish Production, Hydrobiology and Apiculture, Zemědělská 1, 613 00 Brno, Czech Republic
6. *Nybelinia* sp. (CESTODA: TRYPANORHYNCHA) IN POUTING, *Trisopterus luscus* (LINNAEUS, 1758) FROM THE NORTHEAST ATLANTIC; EPIDEMIOLOGY, MORPHOLOGY AND MOLECULAR CHARACTERIZATION. Ramos P. et al. IPMA, I.P., Portuguese Institute for the Sea and Atmosphere, Lisboa, Portugal
7. PLEROCERCOIDS OF *Hepatoxylon* spp. (CESTODA: TRYPANORHYNCHA) PARASITIZING BLACK SCABBARFISH, *Aphanopus carbo* - QUALITY AND SAFETY EVALUATION. Santos M.J. et al. CIIMAR, University of Porto, Matosinhos, Portugal
8. RNA VIROME CHARACTERIZATION OF GNATHIID ISOPODS, A MARINE BLOOD-FEEDING ARTHROPOD. Hendrick GC et al. Department of Marine Biology and Ecology, Rosenstiel School of Marine, Atmospheric and Earth Science, University of Miami, Coral Gables, FL, USA

ORAL PRESENTATIONS

ANISAKIDAE IN THE ENGLISH CHANNEL AND THE NORTH SEA: REVIEW OF THE LITERATURE, GAP IDENTIFICATION AND PRELIMINARY DATA

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The Anisakidae life cycle involves zooplanctonic crustaceans, fish and/or cephalopods and marine mammals or piscivorous birds. A wide variety of commercially and ecologically important fish species may be infested. Reviewing the literature displayed a very large number of distribution studies. However, their comparison might be tricky due to important differences in methods, aims and species. The present work is part of the AniMode project that aims at describing the ecology of Anisakidae in the English Channel and North Sea. Indeed, this geographical area is of crucial importance for the fishing economy and industry in Europe. Moreover, from an ecological perspective, considering their wide distribution and potentially high infestation levels, the influence of Anisakidae on the marine ecosystem is to be considered for food web studies. The first step was to carry out a systematic review of the literature on the infestation levels of Anisakidae in all hosts but restricted to the studied geographical area. Specific research strings were designed for PubMed, Google Scholar and Scopus including the type of studies, the geographical area, the parasites and the hosts (fishes, crustaceans and marine mammals). This allowed identifying major gaps for important economic and/or ecological species such as cephalopods, zooplankton-feeding fish or flatfish. Epidemiological studies have been designed to cover these data gaps. Their objectives are to characterize distribution of Anisakidae in these hosts as well as to identify drivers, both biotic and abiotic of their variability. Preliminary data will be displayed on plaice and cephalopods.

AFFECT OF A MAJOR RIVER RESTORATION EVENT ON ABUNDANCE AND DISTRIBUTION OF FISH PARASITES MAPPED BY WATER SAMPLING

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After 100 years, the largest dam removal event in the world is almost complete in the Klamath River, Oregon/California (USA). The dams affected river flow and temperature, severed migration routes for anadromous fishes, and altered the host-parasite balance in the system, with consequent detrimental impacts on salmonid populations. How will dam removal affect waterborne parasites and their hosts, and thereby alter pathogen effects and disease in resurgent salmon populations? River reconnection means that both adult and juvenile anadromous salmonids will be exposed to novel pathogens in the upper basin, and resident upper basin native fishes will be exposed to pathogens associated with the new in-migrants. Mapping parasite distributions before and after dam removal is essential to assess risks of novel and known threats to fish health, and to empower managers with information on which to base decisions. We collected monthly water samples in tributaries and mainstem of the Klamath River, at 26 sites relevant to salmonid ecology. Collections spanned three years pre-dam removal (2021-2023), the removal year (2024), and will continue for another 3 years post dam removals. Molecular analysis of a subset of 0.2µm water samples for parasites *Ceratonova shasta, Parvicapsula minibicornis, Ichthiophthierius multifiliis*, *Nanophyetus salmincola* and the annelid *Manayunka occidentalis* detected all 5 in both a tributary and the mainstem above its confluence, with a unique pattern for each. Waterborne stages of *Cs* were most abundant. *Cs*, *Pm* and their annelid host were most abundant in the mainstem whereas *Im* and *Ns* were more abundant in the tributary.

IMPACTS OF MYXOZOAN DISEASES IN SALMON WITHIIN AN URBAN-INFLUENCED WATERSHED

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The Lake Washington watershed in central Puget Sound, Washington, USA, is a highly urbanized watershed. The watershed supports runs of three hatchery-supported anadromous salmon species. Global climate change and urban development have introduced thermal stressors and migration bottlenecks for the natural migration of salmon, which are reaching critical thresholds for salmon survival. This is apparent through a high degree of salmon "en route" mortality and prespawn mortality. Prespawning mortality has been noted to approach 20-30% in Chinook salmon and up to 50% in sockeye salmon, depending on year. Three myxozoan species have been detected in salmon within the watershed, including *Tetracapsuloides bryosalmonae*, *Parvicapsula minibicornis*, and *Ceratonova shasta*. In 2022, we noted a 100% prevalence of *Ceratonova shasta* in adult Chinook salmon returning to spawn at Issaquah Salmon Hatchery with 60% of these fish severely affected as seen by histopathology. Environmental DNA surveys to detect *C. shasta* spores has indicated a relatively high and persistent detection level in the Lake Washington Ship Canal, a migration corridor utilized by all salmon entering and exiting the watershed. In 2024, we conducted sentinel caging studies with Chinook salmon to identify temporal and spatial pathogen patterns and *C. shasta* infection hot spots. We will discuss these results in the context of aquatic habitats and possible mitigation efforts to protect salmon populations.

VIRULENCE AND PATHOLOGY OF EYE FLUKE TREMATODES, *Diplostomum* spp. AND *Tylodelphys* sp., INFECTING ENDANGERED LOST RIVER SUCKERS, *Deltistes luxatus*

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Lost River and short nose suckers, *Deltistes luxatus* and *Chasmistes brevirostris*, respectively, are critically endangered species that occur only in the Klamath Basin, Oregon, USA. Fisheries data demonstrates that their failed population recovery in Upper Klamath Lake is a result of poor juvenile survival preventing adult recruitment to the spawning population. Juvenile mortality is likely the result of numerous factors including water quality, habitat suitability, predation, and disease. Field studies in Upper Klamath Lake using age-0 surrogate species, including blue chub *Gila coerulea* and tui chub *Siphateles bicolor*, showed a declining trend in eye fluke prevalence and infection intensity between July and September, suggesting reduced survival in heavily infected fish. To test if eye flukes cause disease in endangered suckers, an experimental infection model was developed in captive propagated YOY Lost River suckers to evaluate the virulence of eye fluke trematode cercariae. Virulence of a species consistent with *Diplostomum pseudospathaceum* was shown to be acutely lethal to YOY suckers when challenged with doses between 500 to 1,000 cercariae / fish, with low mortality occurring when exposed to doses as low as 250 cercariae / fish. Testing the virulence of *Tylodelphys* sp. was complicated by snail co-infection with *Bolbophorus* spp. trematodes. Co-infection of these parasites were less acutely lethal to suckers, though induced chronic mortality following infection. The sequential infection and pathology related to these fluke species in experimentally infected suckers will be discussed.

UNCOVERING BIOMINERALIZATION IN MYXOZOA, MICROSCOPY, CHEMICAL ANALYSIS AND GENETIC DATA

Muller, M.I.[1]; Americus, B.E.[1]; Ibrahim. A.G.[2]; Russo, C.[3]; Lotan, T.[4]; Bartholomew, J.L.[1] & Atkinson, S.D.[1]

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Biomineralization is widespread in the biosphere and typically involves calcium, silicon and iron. Myxozoan spores (myxospores and actinospores) enable the waterborne transmission of the parasite between hosts. Whereas actinospores of many species are flexible, myxospores are highly compact, with rigid valve cells. Some studies have suggested that the hardening of myxosporean spore valves is achieved by secretion of chitin, and others have found evidence for silicon. We used transmission electron microscopy (TEM/SEM) with energy-dispersed x-ray spectroscopy to determine presence and localization of elements in myxozoan spores, and inductively coupled plasma mass spectroscopy (ICP-MS) to determine primary inorganic components. We used bioinformatics to search existing 'omics databases for *Ceratonova shasta*, *Henneguya salminicola* and *Myxobolus squamalis*, for known components of the "biomineralization toolkit" and related genes. ICP-MS showed that different species' myxospores have magnesium and calcium present in differing ratios, though magnesium was typically higher than calcium. Silicon, magnesium and calcium were evident in TEM/SEM and ICP-MS. Our data show that the myxozoan genomes do not have homologs to "biomineralization"-associated genes, particularly no genes associated with silicon-mineralized species. We analyzed the genomes of *C. shasta* and its vertebrate host, using a pipeline built in R and RepeatMasker to identify repetitive elements related to solute carrier genes for Si and Mg. We identified multiple genes related to Si and Mg in the fish datasets, which appeared to be copied as transposons in the transcriptomic data of the parasite and the infected host. We identified a fibrilin gene, but no chitin synthase.

ASSESSMENT OF THE METAZOAN PARASITES OF COMMERCIALLY VALUABLE FISH IN ICES AREA 6A

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In marine ecosystems, parasitic species exhibit considerable diversity. Parasites can benefit ecosystem communities by regulating predator populations and acting as biological indicators. Contrastingly, parasites can weaken fish populations and potentially impede stock recovery. This study assesses the metazoan parasites from four commercially valuable fish species on Scotland's west coast (ICES fisheries management area 6a) and evaluates their significance for fisheries management. The research focused on mackerel (*Scomber scombrus*), herring (*Clupea harengus*), anglerfish (*Lophius piscatorius*), and whiting (*Merlangius merlangus*). A total of 395 fish were collected and dissected from two demersal trawl surveys in 6a during 2022, consisting of 185 mackerel, 152 whiting, 23 anglerfish and 35 herring. Parasites were fixed in AFA, stained, and identified morphologically using microscopy and taxonomic keys. A total of 32 metazoan parasite species were identified, representing groups such as Digenea, Monogenea, Cestoda, Nematoda, Acanthocephala, Hirudinea, and Copepoda. Among these were three new digenean host records. Notably, two possible new species of bucephalid digeneans, likely of the genus *Prosorhynchus*, were found in whiting. Several parasite species identified during the study such as *Lacistorhynchus tenuis, Grillotia erinaceus, Anisakis simplex s.s* and *Corynosoma* sp. have previously been characterised as potential biological tags for stock discrimination in Scottish waters. The results identify parasites that could be utilised for zonal attachment stock discrimination, improving our understanding of stock structure in Scotland's economically important fisheries. In conclusion, incorporating parasite data into fisheries management plans for ICES area 6a could enhance policy decision-making and support sustainable fisheries management.

PARASITES: CASTING A BRIGHT LIGHT ON FISH MANAGEMENT AND ECOLOGY IN ICELANDIC WATERS

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Many marine fish species exhibit complex life cycles involving migrations across different life-history stages. These include the passive movement of larvae to juvenile-associated nursery grounds, migration of juveniles to the feeding grounds, and migration of adults to the spawning grounds. Fish from different populations or stocks might not overlap spatially or temporally during their respective migrations. As they disperse and migrate, they will acquire parasites endemic to the geographical areas used during their life cycle. Fish harbouring similar parasite communities are likely to have spent time in similar geographical areas. Therefore, parasites can be of potential use for stock identification. Marine ecosystems in Iceland are influenced by two major currents, the cold East Greenland Current to the north and the warm North Atlantic/Irminger Current to the south. Several marine species of commercial importance to Icelandic fisheries are found around Iceland with little suspected movement between warm and cold waters. However, given the lack of data and/or logistical difficulties associated with stock identification in Icelandic waters, most species are managed as single units. Failure to take stock structure into account can lead to biases in estimates of stock status and vulnerability, and impact on sustainability, community resilience, profitability, and conservation/biodiversity goals. Here, I share preliminary data demonstrating promise for parasites as potential biological tags for the identification of different populations of plaice, haddock, Atlantic wolffish, and cod in Icelandic waters. Furthermore, I will discuss my lab's approach to assessing the efficacy of parasite communities for stock identification relative to other techniques.

EXPLORING HOW *Myxobolus cerebralis* AND *Tetracapsuloides bryosalmonae* DETERMINE THE OUTCOME OF RAINBOW TROUT CO-INFECTIONS BY QUANTITATIVE PROTEOMICS

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This study aimed to investigate how the myxozoans *Myxobolus cerebralis, and Tetracapsuloides bryosalmonae* modulate the host proteome at the target organs (head cartilage and kidney) after single and co-infections. One group of fish was infected with *M. cerebralis (MC group)* and another group with *T. bryosalmonae (TB group).* After 30 days, half of the fish in each group were co-infected with the other parasite (MC+ group and TB+ group). The proteomic changes in the head cartilage and kidney of rainbow trout were then investigated 1- and 3-months post exposure (mpe) and the parasite numbers were determined in single and co-infection groups. In the head cartilage and kidney, numerous proteins were differentially regulated between the groups. The identified proteins were involved in proteasomal degradation, metabolism, host protection and host-parasite interactions. In the head cartilage, the parasite load increased in the MC+ group at 1 and 3 mpe as compared to the MC group, whereas the parasite count decreased in the TB+ group as compared to the TB group in the kidney, emphasizing that the primary infection controls the outcome of the subsequent infection. The results of the current study enhance our understanding of how myxozoan parasites modulate host responses in target organs, thereby determining the outcome of co-infections in rainbow trout. The study provides important insights into myxozoans evasion/invasion strategies, reveals novel traits of host-parasite interactions, and paves the way for the development of novel tools for the management of diseases caused by myxozoan parasites in aquaculture.

INTRA-STOCK VARIABILITY IN THE STRUCTURE OF PARASITE ASSEMBLAGES OF ARGENTINE HAKE *Merluccius hubbsi* IN PATAGONIAN WATERS

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The complex nature of the population structure in many marine fishes, even at intra-stock level, is being increasingly revealed by new assessment techniques, such as archival tags, genetic markers and otolith microchemistry. Such complexity can be reflected in the parasite assemblages they harbor. In the present work, parasites of *Merluccius hubbsi* were evaluated as indicators in that sense. The southern stock of *M. hubbsi* inhabits the Argentine Sea between the 41°S and 55°S, a region characterized by a latitudinal gradient of oceanographic conditions of approximately 1500 Km, that could have an impact on the structure of parasite assemblages. Eight samples from the southern stock (236 hakes), and one sample from a different stock (northern) were analyzed for parasites. A total of 34,350 metazoans, belonging to 32 taxa, were recovered. Long-lived species, mostly represented by larval cestodes, acanthocephalans and nematodes were selected as tags. These assemblages were analyzed by multivariate methods based on Bray-Curtis dissimilarity matrices, taking into account host sex and size. Significant differences in the structure and composition of parasite assemblages revealed clear latitudinal patterns in their similarity. This suggests a differential effect of environmental conditions on parasite populations harbored by hakes caught at the extremes of the distribution of the southern stock. Intra-stock differences in the parasitefauna should be considered carefully when parasite tags are used as tools for stock identification, when fish populations that occur over large or oceanographically heterogeneous areas are studied.

POSTER PRESENTATIONS

NEMATODA PARASITES FROM EUROPEAN HAKE (*Merluccius merluccius,* Linnaeus, 1758) CAUGHT IN TWO AREAS OF THE ATLANTIC OCEAN (SOUTHWEST IRELAND AND THE BISCAY BAY)

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European hake is very appreciated in the fish market and recognized as being usually heavily infected by *Anisakis* sp. The aim of this work was to know the distribution of the *Anisakis* spp. in fish from two different localities (Southwest of Ireland (SI) and Biscay Bay (BB) and evaluate its food safety. Fishes were collected during 2023/24 in SI (n=119; 59 eviscerated (EV) and 60 not eviscerated (NV)) and BB (n=118, 78 EV and 40 NV). The Nematodes were counted, and the food risk analyzed by parasitic indices. One belly flap (BF) was examined by UV-press method. 100% prevalence of nematode of the genera *Anisakis* was observed at both sampling sites. The mean intensity (MI) was 211.3 in the visceral cavity (VC) and 276.4 in the BF from SI and 223.3 - VC and 329.0 - BF from BB. The mean density was of 7.8 and 7.5 worms/g of muscle respectively. There was not significant difference in the BF intensity or density between SI e BB (H= 0.30; *p*= 0.58). Significant values were recorded at the density between EV and NV fishes in both localities (U=598.5and 416; *p*<0.0001). The immediately evisceration and mechanical cutting of all belly flaps on board should be mandatory, in order to reduce the migration of anisakids to the muscle. Due to the high intensity and density levels of infection detected, we recommend the freezing of the fishes at a temperature of -20ºC for 24 hours, to kill any viable parasites.

A COMPARISON OF THE METAZOAN PARASITES OF THE LIONFISH *Pterois volitans* (PISCES: SCORPAENIDAE) FROM YUCATAN PENINSULA, GULF OF MEXICO, AND THE CARIBBEAN SEA

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The lionfish *Pterois volitans* invaded the Gulf of Mexico and the Caribbean Sea in the 1980s. As a predator and due to the lack of enemies it threatens biodiversity, especially coral reef areas. However, is expected to harbor parasite species in invaded areas. In the Yucatán Peninsula, there is little data on the metazoan parasites of lionfish and their interaction with local parasite transmission. This study compares the lionfish metazoan parasites at localities of the Yucatan Peninsula the Gulf of Mexico and the Caribbean Sea. We collected 113 fish between 2011 and 2022 from Cozumel Island, Cabo Catoche, Alacranes reef, Cayo Arcas, Cayo Arenas reef, and in the eastern Yucatan Platform. We recovered 46 species of helminths (included in 26 families and 20 genera: 16 Digeneans, 12 Cestodes, 12 Nematodes, and six Acanthocephala). Species richness ranged from 2 to 24 and 2 to 690 parasites individuals. The lionfish participates as the final host of 16 parasite species and mostly as an intermediate, accidental, or paratenic host of 30 found in larval stage. The eastern Peninsula and Cozumel Island reported more parasite species, 24 and 21 respectively. Our results suggest that the helminth communities of P. volitans are richer in species number compared to reports in Veracruz (8 species), Northern Gulf: Florida, Carolina del Norte, Bahamas, and Bermuda (2-9 species), Mexican Caribbean: Contoy Island, Akumal and Xcalak (2-3 species), Caribbean: Jamaica, Belize, Panama, Puerto Rico, Saint Thomas, Turks y Caicos, Caiman Island (3-19 species). Research funded by Cinvestav-Mérida and SENER-CONACyT-201441.

THE PARASITE COMMUNITY OF *Merluccius merluccius* AND *Sardinella aurita* FROM THE MEDITERRANEAN SEA

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The parasite community of two important commercial fish species (*Merluccius merluccius* and *Sardinella aurita*), with special emphasis on zoonotic parasites has been studied in different areas of the Western (Catalan Sea) and Central Mediterranean Sea (Adriatic and Tyrrhenian Sea). For each fish species, internal organs from 20 specimens of each sampling point were completely inspected for parasites, and the rest were examined using a UV-press method. Parasites were identified by morphologic and molecular analyses. Overall, parasite fauna of *M. merluccius* (25 species) was richer than that of *S. aurita* (7 species). For *S. aurita*, the digenean *Aphanurus* sp. was the most prevalent and abundant parasite in the Western Mediterranean while the cestode *Anthobothrium* sp. was dominant in the Central Mediterranean. Zoonotic parasites were only detected in *M. merluccius* from the Central Mediterranean being *Anisakis pegreffii* as the predominant species. Significant differences in prevalence and abundance of nematodes were observed among regions, highlighting a higher proportion of *A. pegreffi* in the Adriatic Sea, while *Hysterothylacium* spp. displayed higher values in the Tyrrhenian and Catalan Seas. These differences in prevalence and abundance of nematodes in both fish species could be mainly explained by their different habitat and feeding behaviour, whereas the differences detected of nematodes species from *M. merluccius* in different geographical areas might be related to differences in the distribution of the intermediate and/or definitive hosts and environmental conditions. Fish from new areas of the Spanish coast (Western Mediterranean) will be examined and used for expanding the herein comparison and discussion.

UNUSUAL LOCALIZATION OF *Ligula intestinalis* PLEROCERCOIDS IN *Abramis brama*

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Ligula intestinalis (Cestoda: Diphyllobothriidea) is a widespread parasite with a life cycle that includes three hosts, namely crustaceans (Copepoda) and fish as intermediate hosts and piscivorous birds as final hosts. Plerocercoids are almost always found in the body cavity of the fish intermediate host. In this paper, we report two cases of ligulosis in the freshwater bream *Abramis brama* (Linnaeus, 1758) with an unusual location of plerocercoids. The fish were sampled in two water reservoirs in the Czech Republic. In the first case, a total of nine plerocercoids were found in the body cavity of the infected bream. One of the plerocercoids was partially located in the pericardial cavity, where it penetrated through the transverse septum. In the second case, the plerocercoid was located in the epaxial part of the musculus lateralis major of the infected bream. The plerocercoid was located horizontally above the peritoneal cavity in a 145 mm long cavern. While the occurrence of the plerocercoid stage of L. intestinalis in the musculature of cyprinids has been reported only sporadically, the present finding of plerocercoids of this cestode in the pericardial cavity of freshwater bream is the first report of the parasite in this location. Acknowledgement: project FVHE_Pikula_2024 ITA 24.

OCCURRENCE OF PROLIFERATIVE KIDNEY DISEASE IN SALMONID WATERS OF THE CZECH REPUBLIC

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Proliferative kidney disease (PKD) is an emerging parasitic disease, that causes high mortality in both farmed and wild freshwater salmonids in Europe and North America. It is expected that the spread of the agent and outbreaks of PKD will be more important in the future due to anticipated climatic changes assuming increasing water temperature. Recent outbreaks of PKD in Norway have demonstrated the potential of the disease to cause mass mortality of wild salmonid populations. The disease is also linked to long-term declines in the Swiss brown trout populations. The presence of the PKD agent in wild salmonid populations has been reported from many other European countries, including Austria, Finland, Denmark, Slovenia and even Iceland. The disease is caused by the myxozoan endoparasite *Tetracapsuloides bryosalmonae*. Two main strains of *T. bryosalmonae* have been described, North American and European. The life-cycle of the agent includes several species of freshwater bryozoans as invertebrate hosts and salmonids as vertebrate hosts. The aim of the presented study was to investigate the presence of *T. bryosalmonae* in brown trout from 62 locations of 42 streams/rivers in the Czech Republic. The monitored rivers belong to three catchment areas: the Morava (Dunaj) basin, the Odra basin and the Labe basin. In total, 787 fish were sampled. They were examined parasitologically and kidney samples were taken for the detection of *T. bryosalmonae* using PCR. The results so far demonstrate to a high prevalence of distribution of wild trout by the causative agent of PKD. Acknowledgement: This work was supported by the Czech Ministry of Agriculture of the Czech Republic (project NAZV QK 23020064).

Nybelinia sp. (CESTODA: TRYPANORHYNCHA) IN POUTING, *Trisopterus luscus* (LINNAEUS, 1758) FROM THE NORTHEAST ATLANTIC; EPIDEMIOLOGY, MORPHOLOGY AND MOLECULAR CHARACTERIZATION

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Trypanorhyncha species belonging to the genus *Nybelinia* have been reported with zoonotic potential. This work aimed to study the parasitic infection of *Nybelinia* sp. plerocercoids and assess their possible risk for consumers. Four seasonal pouting samples were carried out from North and South on the Portuguese coast (FAO zone 27) during 2023-2024. A total of 339 fish were analysed and 6,643 specimens of *Nybelinia* sp. were collected from the two main sites of infection, the musculature and the viscera. However, *Nybelinia* sp. plerocercus were also observed in the gill filaments at the base of the branchial arches in the Southern samples. This unusual site of infection, host gills lead to presume to be a distinct species infection. Although the parasite should not have marked pathological effects on this host fish, morphological and molecular characterizations were performed to assess its zoonotic potential.

PLEROCERCOIDS OF *Hepatoxylon* spp. (CESTODA: TRYPANORHYNCHA) PARASITIZING BLACK SCABBARFISH, *Aphanopus carbo* - QUALITY AND SAFETY EVALUATION

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The presence of Trypanorhyncha larvae in the visceral cavity and/or flesh of the teleost fishes, used as intermediate/paratenic hosts, can be unappealing to consumers. Although Trypanorhyncha larvae are harmless to humans, a fish heavily parasitized results in economic losses. This work aimed to evaluate the presence and infection levels of Trypanorhyncha tapeworms and their sites of infection in black scabbardfish, taxonomic and molecular identification and risk for consumers. During 2023-2024, five seasonal black scabbardfish samples in a total of 152 specimens were obtained from the Sesimbra area on the Portuguese coast (FAO zone 27). A parasitological search was performed in each fresh fish, and a few plerocercoids ($n = 9$) were found attached to the surface (mesenteries) surrounding the internal organs, such as the stomach, intestine, liver, and in the visceral cavity. These larvae were morphologically assigned to the genus *Hepatoxylon* (Sphyriocephalidae). Given the low prevalence of the plerocercoids and their presence in non-edible parts of black scabbardfish, which can be easily removed in evisceration before being marketed, we consider that their presence in this fish does not adversely affect its quality.

RNA VIROME CHARACTERIZATION OF GNATHIID ISOPODS, A MARINE BLOOD-FEEDING ARTHROPOD

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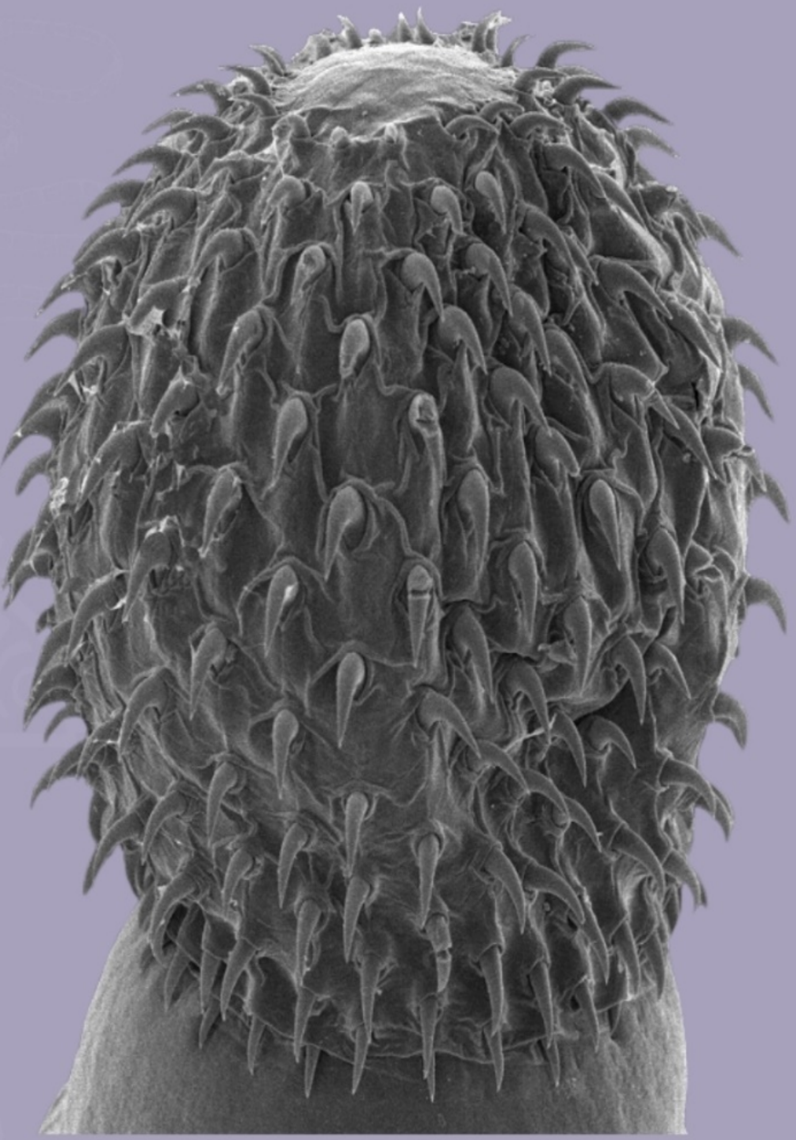
Gnathiid isopods are ubiquitous host-generalists in marine environments and are ecological analogs of ticks and mosquitoes. Gnathiids obtain a blood meal from a single host fish during each of three juvenile stages before metamorphosing into non-feeding adults. A variety of pathogens have been found within the larval stages of gnathiids. However, no previous study has characterized gnathiid-associated viruses. To address this issue, we conducted metatranscriptomic sequencing of 405 free-living gnathiids collected from lighted plankton traps from 4 sites in the western Atlantic and Gulf of Mexico. We identified 10 novel RNA viruses from 7 viral families with a variety of genome structures. Of note, four of these novel viruses from the families *Chuviridae* and *Spinareoviridae* were likely associated with vertebrate hosts, suggesting that gnathiids may be able to act as vectors transmitting viruses between fish, which warrants additional investigation. Additionally, we identified invertebrate host-associated viruses from *Rhabdoviridae, Nodaviridae, Iflaviridae, Phenuiviridae* and *Negevirus*. Overall, the presence of both fish and invertebrate-associated viruses highlights the potential role of gnathiids as viral transmission vectors within marine environments.

Thematic areas

7. FISH AND PARASITE CONSERVATION

(MINI-SYMPOSIUM)



ORAL PRESENTATIONS

(Please note the name and institution shown in this list are those of the person presenting the talk, who may not be the first author; the complete author list including all institutional affiliations are shown with the full abstract)

1. A PARTICIPATIVE APPROACH TO PRIORITISE ACTIONS FOR PARASITE RED LISTING. Gobbin T. et al. Hasselt University, Diepenbeek, Belgium
2. PARASITE BIOBLITZ IN A PROTECTED AREA: DIVERSITY ACROSS A FORESTED WETLAND TO TIDAL CREEK CONTINUUM IN SOUTH CAROLINA, USA. Kmentová N. et al. Hasselt University, Diepenbeek, Belgium
3. PARASITE BIOBLITZ: AN INTENSE, FOCUSSED, FIELD STUDY FOR BUILDING ECOSYSTEM KNOWLEDGE. Atkinson S.D. et al. Oregon State University, Department of Microbiology, Corvallis, Oregon, USA
4. EQUAL RIGHTS FOR PARASITES! Rubio-Godoy M. et al. Instituto de Ecología, A.C., Xalapa, Mexico
5. “PASTEURIZED” TILAPIA; DRASTIC MORTALITY OF *Gyrodactylus cichlidarum* DURING THE SPRING 2024 HEAT WAVE. Rubio-Godoy M. et al. Instituto de Ecología, Xalapa, Mexico
6. A NEW FRONTIER FOR FISH PARASITOLOGY: AQUATIC PARASITE CONSERVATION. Smit N.J. et al. North-West University, Potchefstroom, South Africa
7. CAPTIVE BREEDING OF THE CRITICALLY ENDANGERED EUROPEAN WEATHERFISH: A REFUGE FOR THE CONSERVATION-SENSITIVE PARASITE *Gyrodactylus fossilis*? Vanhove M.P.M. et al. Hasselt University, Diepenbeek, Belgium
8. WHAT ARE THE PROCESSES THAT DRIVE PARASITE ENDANGERMENT AND EXTINCTION? Wood C.L. University of Washington, Seattle, USA

POSTER PRESENTATIONS

(Please note the name and institution shown in this list are those of the person presenting the poster, who may not be the first author; the complete author list including all institutional affiliations are shown with the full abstract)

1. LOCAL EXTINCTION OF A PARASITE OF ANCHOVIES AND MAGELLANIC PENGUINS? THE EFFECT OF A WARMING HOTSPOT ON A “COLD” TREMATODE. Timi J.T. et al. Universidad Nacional de Mar del Plata-CONICET, Mar del Plata, Argentina

ORAL PRESENTATIONS

A PARTICIPATIVE APPROACH TO PRIORITISE ACTIONS FOR PARASITE RED LISTING

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Parasite red listing is in its infancy, and national red lists for parasites are lacking. The first challenge is the meagre data availability for metazoan parasites of animals that the IUCN SSC Parasite Specialist Group strives to assess. Indeed, parasites of medical importance to humans, or posing a problem to the health of domestic animals, are not covered by this young specialist group; hence, most of the target species are strongly understudied parasites. Moreover, procedures to formally assess more parasite species for inclusion in the IUCN Red List of Threatened Species might require optimisation and innovation of existing criteria. During a recently organised workshop on conservation and Red Listing of parasites, experts (either in parasitology or conservation) undertook a collaborative effort to determine priorities enabling the assessment of metazoan parasites of animals. We applied an adapted version of the Nominal Group Technique (NGT), a method of stakeholder elicitation aiming for a consensus. We covered five themes: (1) threats; (2) challenges of complex life cycles; (3) differences between global versus regional scales; (4) perceptions and ethics; (5) data availability and uncertainty. During a first, real-life round of NGT, for each theme, five priority challenges were determined. A second, online round was used to select an action to prioritise in response of each challenge. This structured approach enabled us to reach a consensus, supported by diverse experts with relevant backgrounds, on steps to be taken at the onset of the assessment of the conservation status of metazoan parasites of animals.

PARASITE BIOBLITZ IN A PROTECTED AREA: DIVERSITY ACROSS A FORESTED WETLAND TO TIDAL CREEK CONTINUUM IN SOUTH CAROLINA, USA

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The BioBlitz concept has become popular across taxonomic fields, attracting interest globally to increase knowledge of local biodiversity. However, large-scale application of BioBlitz events for parasites has not occurred due to the need for wide taxonomic expertise and in-field sample processing and microscopy. As a team of parasitologists with individual, complementary and methodologically aligned expertise, we adopted the concept of a BioBlitz as a ‘moonshot’-like endeavor and a proof-of-concept in our research field. Over ca. two weeks, we intensively screened fishes and various invertebrate taxa (annelids, crustaceans, snails, bivalves) for parasites, and sampled sediment and water for eDNA from four aquatic habitats: wetland, freshwater pond, brackish impoundment, and tidal creek at Stono Preserve (College of Charleston’s Foundation, South Carolina, USA) to cover ecosystem-level parasite diversity. Morphological and molecular identification of parasites collected revealed the presence of eight major parasite taxa (monogeneans, cestodes, digeneans, nematodes, copepods, myxozoans, flagellates, and leeches), several of which were new host and/or locality records with numerous host-parasite combinations. The finding of species new to science and numerous host-parasite combinations further supports that such short term and intensive surveys improve knowledge of parasite diversity, which is under-studied yet essential for deeper understanding of ecosystems at local and global scales.

PARASITE BIOBLITZ: AN INTENSE, FOCUSSED, FIELD STUDY FOR BUILDING ECOSYSTEM KNOWLEDGE

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Kendrick M.R. [6]; Kmentová N. [7,8]; Rothman G.K. [6]; Vanhove M.P.M. [7].

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A BioBlitz is an intense local effort to bring together experts and often lay participants to categorize biodiversity. This is typically undertaken in a single environment for macrobiota, which are observed easily and identified immediately on site. Inspired by the success of this approach, we undertook a parasite BioBlitz of fishes and invertebrates at an unexplored locality (College of Charleston's Stono Preserve, South Carolina, USA), to determine the feasibility and effectiveness of such an approach for parasites. The College's field station provided an essential controlled environment to facilitate parasite collections and record keeping. We successfully incorporated assistance from non- parasitologists and students for host collection and identification. In addition to traditional parasite discovery using dissection and microscopy, we incorporated environmental sampling of water and sediment. Our final data analyses will identify which approach is recommended for particular parasite taxa, as we discovered DNA evidence of parasite and potential host species that we did not observe directly using microscopy. We faced particular challenges and had to make enhancements to the BioBlitz concept to extend it to parasitology. These included: collection of small to microscopic biota, parasite diversity requiring additional experts, increased photographic capabilities. Furthermore, there was the need for post-Blitz funding and time for DNA data generation, taxonomy, and publication. Nevertheless, we demonstrated that a parasite BioBlitz can be effective for rapid discovery of the dimensions of parasite assemblages in a novel environment, and have developed suggestions for further improvements to this approach.

EQUAL RIGHTS FOR PARASITES!

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Lack of data to properly model key biological characteristics like abundance or distribution, seriously hinder comprehension of biodiversity patterns and their drivers — even for historically well-studied and charismatic organisms. Knowledge shortfalls are more extreme in the case of parasites, which are mostly part of the "hidden biodiversity" and generally have a bad reputation. However, being an extremely large portion of biodiversity and a fundamental part of ecosystems, failure to consider parasites is itself an information shortfall for conservation, and can result in important consequences not only for planning strategies to conserve biological diversity, but also to understand fully the patterns and processes that shape ecosystems. Parasites exhibit a marked duality: while some species are pathogenic and do compromise their host's survival (and human interests), the majority exert apparently negligible negative effects on their hosts and could be considered non-pathogenic; indeed, parasites are beneficial as they provide important ecosystemic functions and services. Using a comprehensive dataset of fish host-helminth parasites in Mexico as a case study, we review knowledge shortfalls relating to parasites, exemplifying their impacts — both positive and negative. A holistic appreciation of parasites should consider both their (many) beneficial and (a few, proven) detrimental impacts, something which could be operationally incorporated into conservation assessments and strategies (e.g., IUCN Green and Red Lists, respectively). Outreach and education are key to modify negative perceptions towards parasites, and to induce recognition of their importance for ecosystemic function and structure.

"PASTEURIZED" TILAPIA; DRASTIC MORTALITY OF *Gyrodactylus cichlidarum* DURING THE SPRING 2024 HEAT WAVE

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During spring 2024, a heat wave induced sustained water temperatures of 34 ºC during a week in Veracruz, Mexico. Serendipitously, we monitored *Gyrodactylus cichlidarum* infecting farmed tilapia during this pulse warming event and recorded a drastic decline of parasite populations over the following days. We subsequently established that parasites incubated *in vitro* at ca. 27 ºC survived up to 24 hours, while at ca. 30 ºC and 34 ºC, all worms died within 4–7 hours. Abnormal haptor structures were observed in parasites that developed and were born at a water temperature of 34 ºC. Under farming conditions, no unusual fish mortality was recorded, suggesting that pulse heat treatment may be an effective method to control *G. cichlidarum*, a recognized tilapia pathogen. N.B. in late summer 2024, parasites were back with a vengeance: 0.7 gram, four week-old tilapia fry harbored up to >50 worms/host, and 80% of the infected fish population died within a week. This study was supported by CONACYT grant CF-2023-G-362.

A NEW FRONTIER FOR FISH PARASITOLOGY: AQUATIC PARASITE CONSERVATION

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Global biodiversity has been in decline for several decades, marked by species extinctions and population losses that have cascading negative impacts on ecosystems. Despite the growing list of described species, much of the actual threatened biodiversity remains unknown, particularly among invertebrates, including the ones with a parasitic mode of life. Parasites, which may outnumber free-living species and constitute a significant proportion of ecosystem biomass, remain largely neglected in conservation efforts. The extinction of free-living host species often leads to co-extinction events, where parasite species may face extinction even prior to their host species. This presentation highlights the need to incorporate parasites into broader conservation agendas and management plans and practices. It provides an overview of the evolution of species conservation from a focus solely on free-living species to one that includes symbiont assemblages. A case study on chondrichthyan parasites will be presented that illustrates the critical role of parasites in ecosystem health and the importance of their conservation. The presentation also outlines future research directions to better understand and conserve aquatic parasites, advocating for their inclusion in biodiversity monitoring programs and conservation agendas. Addressing these gaps is essential for maintaining the integrity of natural systems and the biodiversity they support.

CAPTIVE BREEDING OF THE CRITICALLY ENDANGERED EUROPEAN WEATHERFISH: A REFUGE FOR THE CONSERVATION-SENSITIVE PARASITE *Gyrodactylus fossilis*?

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Despite its large Eurasian range and its global Red List status of Least Concern, in Flanders (Belgium), European weatherfish *Misgurnus fossilis* (Linnaeus, 1758) (Teleostei, Cobitidae) is a critically endangered freshwater fish. The conservation actions for this species in Flanders include a captive breeding program. In the hatchery, juvenile weatherfish suffered from massive infection by an ectoparasitic flatworm causing mortalities. The helminth was

identified as *Gyrodactylus fossilis* Lupu & Roman, 1956 (Monopisthocotyla, Gyrodactylidae). While this flatworm naturally occurs on this host species, this is its first report in Belgium. At high infection intensities *G. fossilis* seems a threat to *ex situ* conservation of *M. fossilis*. However, adult weatherfish maintained at lower densities in these aquaculture facilities show no visible signs of infection. This observation may make this captive breeding program in fact relevant to the conservation of this host-parasite combination. Indeed, following IUCN criteria, in 1997, the parasite species was proposed to be endangered in the Czech Republic, and critically endangered in Slovakia. *Gyrodactylus fossilis* is hence of conservation interest as a native parasite of *M. fossilis*, and it will be interesting to evaluate whether the captive breeding stock of *M. fossilis* can offer the possibility to sustain a population of *G. fossilis* with infection levels at which it is not harmful to its host. In case this is found to be practically feasible, we propose conservation efforts to also consider *G. fossilis* when reintroducing weatherfish in nature; discussion among stakeholders about a policy with regard to parasite conservation is required.

WHAT ARE THE PROCESSES THAT DRIVE PARASITE ENDANGERMENT AND EXTINCTION?

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Like other consumer groups, parasites can respond to global change pressures with increases, decreases, or no change in abundance, but it has been challenging to identify the conditions under which each of these outcomes will hold. In this talk, I will present an organizing framework for predicting parasite responses to global change. I propose that parasite responses are determined by four non-mutually-exclusive processes: whether the global change driver increases or decreases (1) host density, (2) contact rates between/among hosts, and (3) translocation of parasites/hosts to places outside their native range, and (4) whether parasite evolution can keep up with or capitalize on change wrought by the global change driver. This framework can be used to predict whether parasites will decrease or increase, but I will pay special attention to predictors of declining abundance, and therefore of parasite endangerment and extinction: declines in host density (e.g., loss of infection opportunities), declines in contact rates (e.g., phenological mismatch between hosts and parasites), translocation of hosts to places outside their native range (e.g., invasive species crowding out native hosts and parasites), and global change that occurs too rapidly for parasite evolution to keep pace. I will end with some thoughts on where parasite endangerment and extinction may be occurring most rapidly, to help prioritize research on parasite declines and extinctions.

POSTER PRESENTATIONS

LOCAL EXTINCTION OF A PARASITE OF ANCHOVIES AND MAGELLANIC PENGUINS? THE EFFECT OF A WARMING HOTSPOT ON A “COLD” TREMATODE

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In the northern Argentine Sea, the rise of ocean temperature has produced a tropicalization of demersal megafauna since 2013. This rapidly warming hotspot provides an excellent model to test whether fish parasites have increased, declined, or remained stable in the region. *Cardiocephaloides physalis* a parasite of penguins *Spheniscus magellanicus* as adult and suspected to parasitise anchovies *Engraulis anchoita* as larvae is here used to compare their occurrence and abundance between samples composed by 1752 fish of variable age caught at different latitudes during 1993-1995 and 2022 and between 20 juvenile birds and literature data. In the present work, the identity of metacercariae as *C. physalis* is confirmed genetically, as well as a net decline of population parameters of the parasite to its effective disappearance in anchovies from northern areas and to extremely low levels in fish from southern regions and penguins. After analysing possible causes for such changes in a scenario of rapid regional tropicalization, a direct effect of increasing temperature on parasites arose as the main causal candidate for the observed decline in their populations over the last decades. Beyond the biological and ecological consequences of global change on them, parasites offer excellent systems for measuring and monitoring such effects. The almost local extinction of *C. physalis* in a marine hotspot of global warming seems to be one of the first examples of such processes.

Thematic areas

8. FISH DISEASE & ZOONOSIS

ORAL PRESENTATIONS

(Please note the name and institution shown in this list are those of the person presenting the talk, who may not be the first author; the complete author list including all institutional affiliations are shown with the full abstract)

1. GENETIC AND BIOCHEMICAL CHARACTERISATION OF *Anisakis pegreffii* HSP90α AS A TARGET OF HOST DEFENCE STRATEGIES IN A FISH MODEL OF PARASITE TOLERANCE. Ayra-Pardo C. et al. CIIMAR, University of Porto, Matosinhos, Portugal
2. RESPONSES OF RAINBOW TROUT TO PARASITIC AND BACTERIAL PATHOGENS REVEAL DIFFERENTIAL INVOLVEMENT OF IMMUNOLOGICAL AND GENETIC FACTORS. Buchmann K. et al. Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Frederiksberg C, Denmark
3. LOCATION AND ELIMINATION OF *Anisakis simplex* LARVAE IN ATLANTIC HERRING *Clupea harengus*. Buchmann K. et al. Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Frederiksberg C, Denmark
4. THE EMERGENCE OF PROLIFERATIVE KIDNEY DISEASE IN AN OREGON SALMONID HATCHERY. Das N. et al. Department of Microbiology, 226 Nash Hall, Corvallis, OR, USA
5. *Anguilla anguilla* AND ITS TWO NEMATODE PARASITES, *Contracaecum rudolphii* A AND *Anguillicoloides crassus*: TALE OF SITE SPECIFICITY BY THE WORMS AND IMMUNE RESPONSE BY THE HOST. Dezfuli B. et al. Department of Life Sciences and Biotechnology, University of Ferrara, Italy
6. EMERGENCE OR UNDER REPORTED ZOONOTIC PARASITE *Clinostomum complanatum*? Duflot M. et al. Laboratory for Food Safety, Boulogne-sur-Mer, France
7. ANISAKIDAE INFESTATION LEVELS OF SEVEN FISH SPECIES COLLECTED AT THE RETAIL STAGE IN FRANCE: COMPARISON OF THE 2017 AND 2022 MONITORING PLANS. Gay M. et al. Laboratory for Food Safety, Boulogne-sur-Mer, France
8. SUSCEPTIBILITY PATTERNS OF SALMONID HOSTS TO *Tetracapsuloides bryosalmonae* INFECTION IN THE GREAT LAKES BASIN. Gorgoglione B. et al. Fish Pathobiology and Immunology Laboratory, Dept. Pathobiology and Diagnostic Investigation / Dept. Fisheries and Wildlife, Michigan State University, East Lansing, Michigan, USA
9. MICROBIAL COMMUNITY STRUCTURE IN A HOST-PARASITE SYSTEM: THE CASE OF PRUSSIAN CARP AND ITS PARASITIC CRUSTACEANS. Kashinskaya E. et al. Institute of Systematics and Ecology of Animals SB RAS, Novosibirsk, Russia
10. PARASITE-RELATED ISSUES IN AQUARIUMS: A NATIONWIDE QUESTIONNAIRE SURVEY TO ASSESS THE CURRENT SITUATION IN JAPAN. Katahira H. et al. School of Life and Environmental Science, Azabu University, Japan
11. TRANSCRIPTOME OF *Hirudinella ventricosa* (HEMIUROIDEA: HIRUDINELLIDAE): CATHEPSINS, TETRASPANINS AND MECHANISMS OF HOST IMMUNE MODULATION. Louvard C. et al. Water Research Group, Unit for Environmental Study and Management, 11 Hoffman St, Potchefstroom 2531, North-West, South Africa.
12. IMMUNE RESPONSE IN BLUEFIN TUNA INFECTED BY *Cardicola* spp. Nowak B. et al. School of Science, RMIT University, PO Box 71, Bundoora Victoria 3083, Australia
13. CONSUMPTION OF RAW FISH IN PORTUGAL AND FOOD SAFETY RISK ASSOCIATED. Santos M.J. et al. IPMA, I.P., Portuguese Institute for the Sea and Atmosphere, Lisboa, Portugal
14. DYNAMICS AND EPIDEMIOLOGY OF *Anisakis* spp. INFECTION IN SCABBARDFISH, *Aphanopus carbo* OFF THE ATLANTIC COAST OF PORTUGAL. Santos M.J. et al. IPMA, I.P., Portuguese Institute for the Sea and Atmosphere, Lisboa, Portugal
15. EXPERIMENTAL REPRODUCTION OF THE TREMATODE WHIRLING DISEASE CAUSED BY *Galactosomum nagasakiense*. Takeuchi D. et al. Aquaculture Research Institute, Kindai University, Wakayama, Japan
16. PISCES, PARASITES, AND PEOPLE: NAVIGATING THE NEXUS. Shamsi S. Gulbali Institute, Charles Sturt University, Australia

POSTER PRESENTATIONS

(Please note the name and institution shown in this list are those of the person presenting the poster, who may not be the first author; the complete author list including all institutional affiliations are shown with the full abstract)

1. A NEW RECORD OF POTENTIALLY ZOONOTIC *Contracaecum* LARVAE PARASITIZING TWO FRESHWATER FISHES FROM BRAZIL. Aguiar J.C.C. et al. Laboratory of Parasitology of Wild Animals, Division of Parasitology, São Paulo State University (Unesp), Institute of Biosciences, Botucatu, Brazil
2. BIODIVERSITY OF POUTING MACROPARASITES (*Trisopterus luscus* Linneaus, 1758) CAUGHT IN PORTUGUESE WATERS AND FOOD SAFETY. Atroch F. et al. CIIMAR, Department of Biology, Faculty of Sciences, Porto University, Porto, Portugal
3. LARVAL NEMATODES INFECTING CEPHALOPODS FROM NORTH EAST ATLANTIC AND MEDITERRANEAN SEA. Caffara M. et al. Department of Veterinary Medical Sciences, Alma Mater Studiorum Bologna University, Ozzano Emilia (BO), Italy
4. CAN HIGHLY INVASIVE MUSSELS ACT AS CARRIERS, OR HOSTS, OF MYXOZOAN PARASITES IN THE GREAT LAKES REGION? Gorgoglione B. et al. Dept. Pathobiology and Diagnostic Investigation/Dept. Fisheries and Wildlife, Michigan State University, East Lansing, MI, USA

5. HELMINTH PARASITE GUILD COMMUNITY IN *Mugil cephalus, Pomadasys macracanthus* AND *Galeichthys peruvianus* IN PUERTO EL MORRO (GUAYAQUIL – ECUADOR): THE IMPACT OF CLIMATE CONDITIONS ON ICHTHYOZOONOTIC RISK. Iannacone J.A. et al. Facultad de Ciencias Biológicas, Grupo de Investigación "One Health", Universidad Ricardo Palma (URP), Lima – Perú
6. ULTRASTRUCTURE OF MICROBIOTA OF TYPEWORMS TEGUMENT USING SCANNING AND TRANSMISSION ELECTRON MICROSCOPY. Kashinskaya E. et al. Institute of Systematics and Ecology of Animals SB RAS, Novosibirsk, Russia
7. MICROBIAL COMMUNITY STRUCTURE ASSOCIATED WITH *Coregonus lavaretus* AND CESTODES PARASITIZING THEIR DIGESTIVE TRACT. Kashinskaya E. et al. Institute of Systematics and Ecology of Animals SB RAS, Novosibirsk, Russia
8. MOLLIES AND GILTHEAD SEABREAMS AS NOVEL MODEL ORGANISMS FOR ANISAKID RESEARCH: EXPERIMENTAL INFECTIONS AND HISTOLOGICAL EXAMINATION OF THE INFECTION PROCESS IN SAILFIN MOLLY. López-Verdejo A. et al. Marine Zoology Unit, Cavanilles Institute of Biodiversity and Evolutionary Biology, University of Valencia, C/Catedrático José Beltrán 2, 46980 Paterna, Spain
9. INVESTIGATING THE HOST-PARASITE GENETIC ARCHITECTURE AND IMMUNE RESPONSE IN HUMAN ANISAKIASIS IN ITALY CAUSED BY *Anisakis pegreffii*. Mattiucci S. et al. Department of Public Health and Infectious Diseases and University Hospital "Policlinico Umberto I", "Sapienza University of Rome", 00185 Rome, Italy
10. SEASONALITY OF *Anisakis* spp. LARVAE INFECTION OF SCABBARDFISH, *Aphanopus carbo* OFF THE ATLANTIC COAST OF PORTUGAL. Ramos P. et al. IPMA, I.P., Portuguese Institute for the Sea and Atmosphere, Lisboa, Portugal
11. OCCURRENCE OF PARASITES IN FISH FINGERS. Ramos P. et al. IPMA, I.P., Portuguese Institute for the Sea and Atmosphere, Lisboa, Portugal
12. INFECTION OF *Enteromyxum leei* IN CULTURED STARRY FLOUNDER (*Platichthys stellatus*). Shin S.P. & Kim S.Y. Department of Aqualife Medicine, Kongju National University, Yesan, 32439, Republic of Korea
13. THE GUT MICROBIOTA OF *Cystidicola farionis* PARASITIZED THE SWIM BLADDER OF THE CHARR *Salvelinus schmidti* IN KRONOTSKOE LAKE (KAMCHATKA, RUSSIA). Solovyev M. et al. Institute of Systematics and Ecology of Animals of SB RAS, Novosibirsk, Russia
14. *Crassicauda* LARVAE (NEMATODA: HABRONEMATIDAE) IN ARGENTINE HAKE, PORBEAGLE AND ARGENTINE SQUID: A ZOONOTIC THREAT? Timi J.T. et al. Laboratorio de Ictioparasitología, Instituto de Investigaciones Marinas y Costeras, Fac. Cs. Ex. y Naturales, Universidad Nacional de Mar del Plata, Mar del Plata,-CONICET. Argentina
15. IDENTIFICATION OF CYMOTHOID ISOPODS PROBABLY RESPONSIBLE FOR MASS MORTALITY OF HATCHERY-REARED PACIFIC BLUEFIN TUNA *Thunnus orientalis* JUVENILES AFTER TRANSFER TO SEA CAGES. Umeda K. et al. Fisheries Technology Institute, Japan Fisheries Research and Education Agency, Japan

ORAL PRESENTATIONS

GENETIC AND BIOCHEMICAL CHARACTERISATION OF *Anisakis pegreffii HSP90α* AS A TARGET OF HOST DEFENCE STRATEGIES IN A FISH MODEL OF PARASITE TOLERANCE

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Anisakis spp., parasitic nematodes found in marine fish, pose a significant risk to food safety and public health. European hake (*Merluccius merluccius* L.), a common food fish in the EU, is a favoured host of *Anisakis* spp., representing a considerable health concern. In our study, we found a 100% prevalence of *Anisakis* worms in the visceral cavities of 20 European hake specimens, with *A. pegreffii* and *A. simplex* being the most common species. Despite this, Fulton's condition factor (k-factor), a measure of fish health, was not significantly impacted by the parasite burden, suggesting that European hake may exhibit tolerance to *Anisakis* infestation. In addition, the *A. pegreffii* heat shock protein 90 alpha (ApHsp90α) was identified as a potential dominant antigen in the hake's immune response via colony immunoblotting, using hake serum as the primary antibody. Interestingly, the *ApHsp90a* sequence corresponded to a truncated form at the C-terminal end. The qPCR analysis revealed high *ApHsp90a* expression in L3 larvae of both *A. simplex* and *A. pegreffii*, indicating its significance in host-parasite interactions. A His-tagged fusion of the truncated ApHsp90α protein (6xHis-tApHsp90α) was produced in *Escherichia coli* and purified using immobilised metal ion affinity chromatography (IMAC). The recombinant 6xHis-tApHsp90α protein was then characterised by SDS-PAGE and Western blotting. The biological significance of the truncated ApHsp90α in the parasite's life cycle and infection process is discussed in relation to its potential role in immune evasion and stress response.

RESPONSES OF RAINBOW TROUT TO PARASITIC AND BACTERIAL PATHOGENS REVEAL DIFFERENTIAL INVOLVEMENT OF IMMUNOLOGICAL AND GENETIC FACTORS

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We exposed under controlled conditions (separate trials) disease free rainbow trout (*Oncorhynchus mykiss*) to one parasite (*Ichthyophthirius multifiliis*) and four bacterial pathogens (*Aeromonas salmonicida, Yersinia ruckeri, Vibrio anguillarum, Flavobacterium psychrophilum*). Rainbow trout experimentally exposed to the five different pathogens reacted differently in terms of immune pathways and genome sections involved. The parasitic ciliate targeting gills of the fish host elicited a combined innate and adaptive response in gills, whereas central organs (spleen, liver) of the fish mainly activated innate immune factors. In contrast, the bacterial pathogens penetrated the external mucosa and targeted the internal organs resulting in activation of genes encoding both innate and adaptive factors. Microarrays depicting specific genome regions of rainbow trout involvement in innate resistance to infections showed that different genetic factors determine resistance to different pathogens. Rainbow trout chromosome 16 and 17 are involved in resistance to *I. multifiliis*, whereas chromosome 21 and 25 are involved in resistance to *V. anguillarum* and *F. psychrophilum*, respectively. The intricate immunogenetic network involved in host responses against parasites will be discussed.

LOCATION AND ELIMINATION OF *Anisakis simplex* LARVAE IN ATLANTIC HERRING *Clupea harengus*

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We describe the location of anisakid third stage larvae in Atlantic herring *Clupea harengus* L. caught in the North Sea in August 2023. We further demonstrate how industrial processing (mechanical gutting, removal of entrails, head, tail, hypaxial anterior musculature and vertebral column) reduces the overall infection and worm load in the musculature. The isolated anisakid larvae were identified as *Anisakis simplex* sensu stricto by a combination of morphometrics and molecular methods (PCR of rDNA and mtDNA, sequencing, BLAST analysis). As a baseline we examined freshly caught and ungutted herring and showed a positive correlation between host size (fish length and weight) and infection level. The overall prevalence of infection was 84 %, the mean intensity 11.3 (range 1-38 parasites per fish) and the abundance 9.52. The main part of the overall worm population was associated with stomach and pyloric caeca in the body cavity (77 %) and only 5 % was found in the musculature. The prevalence of muscle infection was 28 % and the mean intensity 1.6 (range 1-5) parasites per fish and abundance 0.44 parasites per fish. In order to assess the effect of industrial processing on worm occurrence in the fish we examined herring, from exactly the same batch, but following processing. This included removal of organs in the body cavity, cutting the lower part of the hypaxial segment but leaving the right and left musculature connected by dorsal connective tissue. Five out of these fish carried one larva (prevalence 7.5%, mean intensity 1, abundance 0.07 larvae per fish), and these worms were located in the ventral part of the anterior musculature (2), in the central part of the anterior musculature (2) and one larva in the central part of the caudal musculature. The industrial processing reduced the overall occurrence (abundance) of worms in the fish from 9.52 to 0.07 (136 times reduction) and the occurrence in the musculature from 0.44 to 0.07 (6.28 times reduction). The overall prevalence was reduced from 84 % to 7.5 % (11.2 times reduction). Muscle infection prevalence fell from 28 % to 7.5 % (3.7 times reduction). The importance of fish handling and processing for consumer safety is discussed.

THE EMERGENCE OF PROLIFERATIVE KIDNEY DISEASE IN AN OREGON SALMONID HATCHERY

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Proliferative Kidney Disease (PKD) is of great economic and ecological concern for cultured salmonids in Europe and North America. Though the causative myxozoan parasite, *Tetracapsuloides bryosalmonae* (*T. bryo*), is native to Oregon (USA), only four occurrences of *T. bryo* infections had been recorded in the state's fish hatcheries over the past 25 years, all between 1994 and 2001. That was until 2020, when a PKD outbreak caused severe mortality of juvenile Chinook salmon *(Oncorhynchus tshawytscha)* at a hatchery on the McKenzie River. To describe the parasite's regional epidemiology, we commenced a multifaceted monitoring program. Monthly from May 2023 to March 2024, water samples from the hatchery inflow, raceways and outflow were collected and analyzed for waterborne parasite stages via qPCR, and kidney tissue from both Chinook salmon and steelhead trout *(Oncorhynchus mykiss)* was sampled for histology and PCR. This increased surveillance revealed that the onset of fish exposure to waterborne *T. bryo* spores occurs in early June, and the first kidney infections are detectable in mid-July. Though infection prevalence reached 80% or higher in both species, disease signs were observed only in Chinook salmon, as evidenced by severe granulomatous inflammation of the kidney. Degree day analyses indicate that only the Chinook salmon met the established time and temperature thresholds to develop clinical PKD (~30 days ≥15°C), which may explain these disparate infection outcomes. As salmonids are moved among hatcheries and stocked around the state, these data can immediately help inform management decisions to mitigate losses from this temperature-dependent parasitic disease.

Anguilla anguilla AND ITS TWO NEMATODE PARASITES, *Contracaecum rudolphii* A AND *Anguillicoloides crassus*: TALE OF SITE SPECIFICITY BY THE WORMS AND IMMUNE RESPONSE BY THE HOST

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A total of 42 *Anguilla anguilla* was sampled in Cannevië lagoon (Northern Adriatic Sea, Italy) and examined for endoparasitic helminths. Twenty-six eels (67%) harboured third-stage larvae (L3) of *Contracaecum rudolphii* A and the intensity of infection ranged from 1 to 100 parasites per fish. The larvae were encysted in the serosa (primarily on the external surface of the rectum) as conspicuous granulomas, appearing as white nodules. Each granuloma was arranged in a tri-layer, formed by a series of concentric whorls; the outer layer contained macrophages, macrophage aggregates, and mast cells (MCs) scattered among fibroblasts. The middle layer was rich in MCs and fibroblasts and the inner layer, closest to the parasite larva, consisted mainly of dark epithelioid cells, some of which were necrotic. Twenty-five eels (59.5%) harbored *Anguillicoloides crassus* in their swim bladders and the intensity of infection was from 1 to 13 adult nematodes per organ. In heavily infected swim bladders hyperplasia, cellular swelling, and abundant vacuolization in the apical portion of the gas gland cells was noticed. Numerous MCs and several macrophage aggregates were observed in the mucosal layer of the parasitized organ. Infection of the eel swim bladder by the nematode impairs organ function, compromising the success of the eel spawning migration. This study revealed that fifteen eels (35.7%) harbored both species of nematodes and high site specificity of infection was encountered. Indeed, concerning *C. rudolphii* A, the innate cellular response of eel has a chronic inflammatory character and keeps the nematode larvae arrested in a state allowing both host tolerance and parasite survival.

EMERGENCE OR UNDER REPORTED ZOONOTIC PARASITE *Clinostomum complanatum*?

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Over the last two decades, the diffusion of new eating habits and the increase of fish products demand has led to a rising risk for consumers due to food-borne parasitic zoonoses. *Clinostomum* Leidy, 1856 are digenetic trematodes widely distributed in the world. They are present, at the larval stage, in numerous freshwater fish. One of the most distributed species of this genus, *Clinostomum complanatum*, is zoonotic and may induce pharyngitis or laryngitis in humans following the consumption of raw fish infected by the larvae. Until now, these parasites were mainly reported in America and Asia. Their occurrence in Europe was restricted to the Danube basin and the North-East of Italy. The present project tracks the distribution of these parasites from European perch (*Perca fluviatilis*) in French ecosystems. Batches of wild perch from different localizations were collected from December 2020 to September 2023. Fish were dissected, and metacercariae were isolated and characterized from a molecular perspective. Infection levels were calculated. Prevalence per batch varied between 0 and 80 %. Comparison of generated sequences with available data of literature confirmed the presence of *C. complanatum* in France. This survey constitutes the first mapping of *C. complanatum* in French freshwater ecosystems. As these parasites are zoonotic, these findings emphasize the importance of monitoring and controlling the presence of *C. complanatum* in aquatic environments to minimize the risk of infections and ensure food safety. Moreover, further and broader samplings of diverse species with abiotic parameters associated are needed to understand in detail the distribution of these parasites.

ANISAKIDAE INFESTATION LEVELS OF SEVEN FISH SPECIES COLLECTED AT THE RETAIL STAGE IN FRANCE: COMPARISON OF THE 2017 AND 2022 MONITORING PLANS

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Anisakidae are nematodes found in many seafood products frequently consumed in France. These parasites may induce digestive and/or allergic pathologies in humans following the consumption of infested seafood. The objective of the monitoring plans of 2017 and 2022 was to estimate the levels of infestation by these parasites in fish available on the market, whatever their presentation to the end consumer, and consequently, to contribute to the evaluation of consumer exposure. The goal of the 2022 monitoring plan was to update the previous assessment conducted during the 2017 monitoring plan. The targeted species for both plans were selected based on results of epidemiological studies: megrim, saithe, blue ling, ling, monkfish, whiting, and hake. Infestation levels (prevalence and intensity) obtained with non-destructive detection methods (used by professionals) and a destructive and exhaustive detection method were compared to estimate the progress made by the industry and assess consumer exposure. Out of the 205 analyzed and interpretable samples in 2017, 42.93% were positive by naked-eye observation, 47.80% were positive by inspection on a light table, and 62.93% were positive by observation using the press/UV method. Out of the 197 samples analyzed and interpretable in 2022, 28.93% were positive by naked-eye observation, 29.95% were positive by inspection on a candling table, and 59.39% were positive by observation using the press/UV method. Therefore, a decrease in the number of samples found infested by naked eye observation was recorded between the two plans, while the number of samples found infested by the press/UV method remained stable.

SUSCEPTIBILITY PATTERNS OF SALMONID HOSTS TO *Tetracapsuloides bryosalmonae* INFECTION IN THE GREAT LAKES BASIN

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The geographic distribution of the myxozoan *Tetracapsuloides bryosalmonae* (Malacosporea) in North America is being reconsidered, following our recent discovery that this parasite is infecting multiple salmonid species in North America. Despite it may cause Proliferative Kidney Disease (PKD), a severe chronic lymphoid immunopathology, we keep finding low parasite burdens and asymptomatic fishes. Based on studies on European hosts, juveniles of Rainbow Trout, have been traditionally considered the most susceptible hosts to suffer PKD, and cannot propagate T. *bryosalmonae* life cycle (occurrence of histozoic extrasporogonic sporulation). Instead, Brown Trout have been considered a more infection tolerant host, able to propagate *T. bryosalmonae* life cycle (coelozoic sporogony in renal tubules). Considering the higher parasite strain diversity and wider range of salmonid species in North America, the traditional PKD susceptibility paradigm should be reconsidered. We comparatively examined histological preparations toward the definition of susceptibility/tolerance patterns in freshwater-adapted salmonids from the Great Lakes region. The occurrence of histozoic and coelozoic *T. bryosalmonae* stages was searched in PCR positive specimens of migratory Chinook and Coho Salmon, and Rainbow and Brown Trout. Due to the low parasite burden (10^3/10^5/g kidney), and lack of PKD, the histological identification of parasitic stages was challenging. A new immunohistochemistry protocol was optimized using a new antibody specific to the parasite, confirming that both sporogonic and extrasporogonic stages of *T. bryosalmonae* are occurring in these species. These findings revealed that all these Great Lakes salmonids act as tolerant or partially susceptible hosts and can propagate the parasite life cycle.

MICROBIAL COMMUNITY STRUCTURE IN A HOST-PARASITE SYSTEM: THE CASE OF PRUSSIAN CARP AND ITS PARASITIC CRUSTACEANS

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The present study aimed to investigate the microbial community of skin mucus of infected and uninfected Prussian carp *Carassius gibelio* (Linnaeus 1758) caused by parasitic crustaceans (*Argulus foliaceus* and *Lernaea cyprinacea*) in an eutrophic lake with parallel studying of associated microbiota of the parasites and environmental compartments. Prussian carp and their ectoparasites were collected in the area of Malye Chany Lake in west Siberia (Russia, 54°36’56.3”N, 78°12’5.9”E). Associated microbiota of skin of Prussian carp and ectoparasites were investigated by sequencing of the V3, V4 hypervariable regions of 16S rRNA using Illumina MiSeq sequencing platform. In the microbial community associated with the parasitic crustaceans, along with representatives of the normal microbiota, there were identified microorganisms that could be potential agents of infectious diseases in fish (*Flavobacterium* sp., *Aeromonadaceae* sp., *Corynebacterium* sp. and *Streptococcus* sp.). Each parasite is characterized by a specific structure of its associated microbiota, which may indicate their role as vectors of different infectious diseases. Significant perturbation of the dominant microbiota of skin mucus of unhealthy fish in comparison with healthy fish was registered (ADONIS, $p \leq 0.05$). Results from these studies indicate that ectoparasites have the potential to alter skin microbiota, which can play a possible role in transmission of secondary bacterial infection in fish, caused by pathogenic bacteria.

PARASITE-RELATED ISSUES IN AQUARIUMS: A NATIONWIDE QUESTIONNAIRE SURVEY TO ASSESS THE CURRENT SITUATION IN JAPAN

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Aquariums fulfill significant functions in public recreation, education, conservation, and scientific research. To maximize these societal benefits, it is essential to provide enrichment and maintain stable rearing conditions for the organisms in their care. However, these organisms are constantly exposed to the risk of pathogen introduction, primarily because aquariums often depend on specimens sourced from the wild. Once a pathogen is contaminated into an aquarium system, the potential for mass mortality of the displayed organisms becomes a serious concern. In Japan, despite the widespread presence of aquariums, detailed information regarding losses remains insufficiently shared, leading to countermeasures that rely heavily on the individual expertise of staff members. To address this issue, we conducted a nationwide survey with a specific focus on parasitic diseases, aiming to organize and standardize their occurrence and the control measures. The survey was sent to 125 aquariums by mail, spanning the period from December 2022 to February 2023. Responses were received from 64 aquariums (51.2%), of which 62 (49.6%) were valid. The frequency of parasite outbreaks was once a month (30.6%), followed by once every two to three months (29.0%). Parasitic diseases were usually treated by the aquarium keeper (76.6%), while veterinary care was limited (11.7%). In total, 325 cases of major parasitic diseases were reported, with marine and freshwater white spot diseases by protozoan ciliates and Capsalid monogenean infections being the most common.

TRANSCRIPTOME OF *Hirudinella ventricosa* (HEMIUROIDEAIUROIDEA: HIRUDINELLIDAE): CATHEPSINS, TETRASPANINS AND MECHANISMS OF HOST IMMUNE MODULATION

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Although omics studies have greatly improved our understanding of the physiology and evolution of the Digenea (Trematoda), they have focused almost exclusively on terrestrial pet-, human- and cattle pathogens. As digeneans are far more taxonomically diverse in marine fishes than on land, our current knowledge of digenean genomes and transcriptomes does not reflect the physiological, ecological and evolutionary diversity of the Digenea. Especially, the gene-expression patterns linked to host immune modulation remain almost unstudied for fish digeneans. Species of the superfamily Hemiuroidea are major parasites of commercially important pelagic fishes, e.g. scombrids. In our study, we assembled and investigated the *de novo* transcriptome of *Hirudinella ventricosa* (Pallas, 1774) (Hemiuroidea: Hirudinellidae), a prominent stomach parasite of the high-value wahoo fish, *Acanthocybium solandri* (Cuvier) (Scombriformes: Scombridae). The non-redundant transcriptome assembly enabled the prediction of several proteins essential in host-parasite interactions, e.g. nutrient acquisition from the host and response to oxidative stress, with some proteins shared with terrestrial trematodes. We focused especially on cathepsin-type peptidases (currently under characterisation) for their crucial role in host immune evasion and modulation in other host-parasite systems, and on tetraspanin transmembrane proteins for their role in immune-detection avoidance. We expect our phylogenetic analyses to offer novel insights into the evolution of both cathepsins and tetraspanins in mammal- *vs* fish-infecting trematodes, and our other downstream analyses (e.g. characterisation of biochemical pathways *via* KEGG, orthology inference *via* OrthoFinder) to inform the molecular mechanisms of interactions between marine digeneans and their fish hosts.

IMMUNE RESPONSE IN BLUEFIN TUNA INFECTED BY *Cardicola* spp.

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Bluefin tunas are commercially important species worldwide. Introduction of quotas and catch reduction resulted in the development of ranching and farming bluefin tuna industries. One of the main health problems during farming in sea cages are infections by Aporocotylid blood flukes. Three species have been reported from bluefin tunas: *Cardicola forsteri, Cardicola opisthorchis and Cardicola orientalis*. Here, based on a number of our studies, we review Southern bluefin tuna and Pacific bluefin tuna responses to the infection by different life stages of the flukes, including adults and eggs and discuss how the immune response is affected by changes in tuna husbandry practices, for example by the introduction of praziquantel as a treatment against the blood flukes. We explore effects on an infection on immune gene expression, and on humoral immune response, including specific antibody response as well as on cellular immune response, for example increased pigmented macrophage centres. Potential species-specific responses (both at host and parasite level) will be highlighted. As these studies have been done in a commercial environment, we will outline their limitations.

CONSUMPTION OF RAW FISH IN PORTUGAL AND FOOD SAFETY RISK ASSOCIATED

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The zoonotic parasites may cause serious problems in terms of food safety. Raw fish consumption increases these problems, and knowing its pattern will help us to mitigate them. In the present work, we aim to determine what are the food behaviors of the consumers in Portugal, to evaluate the offer of raw food at Asian restaurants, and to evaluate if the most consumed fish species represent a risk to food safety. The tendency reported was: that people consumed 10% of raw fish, around 6 Kg/per person/year, preferring to go to restaurants to eat it, but also to do it at home. Surveying the Asian/Japanese restaurants we found that the most popular dishes were nigiri, sashimi, and temaki, the fish species often used were salmon, tuna, and white fish (that can be numerous species). For the Portuguese consumers, the top 5 fish species more consumed raw were: salmon, tuna, cod fish, hake, and sardine. Of those species, the most dangerous is by far hake, since it is a wild fish usually heavily infected. Salmon and cod are not dangerous, since the first is an aquaculture fish negligibly infected, while cod is eaten salted which inactivates eventual worms. This can explain the reduced numbers of Anisakiasis reported in Portugal so far, with only 3 recent cases. However, the tendency can change shortly since young generations are more and more prone to eat raw food, and their food habits are changing.

DYNAMICS AND EPIDEMIOLOGY OF *Anisakis* spp. INFECTION IN SCABBARDFISH, *Aphanopus carbo* OFF THE ATLANTIC COAST OF PORTUGAL

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The black scabbardfish, *Aphanopus carbo* (Ac) is a fish species of significant commercial value. To evaluate the dynamics and epidemiology of *Anisakis* larvae infection in Ac from Sesimbra, were compared the infection parameters between samples with no statistically significant differences in weight and length of Ac captured in 2005-2006 (n=81) with those from 2023-2024 (n=118), caught in the same region at the Northeast Atlantic coast of Portugal (FAO zone 27, sub-zone IX). Adult Ac specimens were obtained seasonally and the body cavity and visceral organs were examined for the presence of *Anisakis*. The prevalence and mean intensity of *Anisakis* infection were determined. Comparisons between the two time periods, with approximately 20 years between them, showed statistically significant differences in infection intensity, with notable high-intensity values in 2023-2024 (501.41 ± 470.99 worms per host against 187.72 ± 295.29 worms per host) in 2005-2006. The increasing intensity values of *Anisakis* larvae highlight the potential health risk of consuming raw or undercooked Ac and underscore the need for enhanced health control measures and increased consumer awareness. The *Anisakis* species recorded were *A. simplex* s.s. and *A. pegreffii* for both periods. Further studies are needed to evaluate potential etiological factors associated with the significant increase in the parasitic intensity of *Anisakis* in Ac during the studied period.

EXPERIMENTAL REPRODUCTION OF THE TREMATODE WHIRLING DISEASE CAUSED BY *Galactosomum nagasakiense*

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The trematode whirling disease, caused by *Galactosomum nagasakiense,* has been reported in various marine fishes in Japan. Infected fish exhibit characteristic whirling behavior at the water surface and eventually die unless consumed by the definitive host, the black-tailed gull. Typically, only a single metacercaria, rarely two or three, is found in the brain of diseased fish, though the mechanism behind the behavioral changes remains unknown. The recent discovery of the first intermediate host, the cerithiid snail *Cerithium dialeucum*, has enabled experimental infections in the laboratory. In this study, cercariae from infected snails were introduced to multiple fish species through oral gavage, intraperitoneal or cephalic injections, self-feeding, and cohabitation with snails. Cercarial injection into the head resulted in the highest establishment of metacercariae (up to 100%) in the brain, followed by intraperitoneal injection and oral gavage. Metacercariae were detected in the brain as early as 1-hour post-introduction. Experimental infections resulted in high metacercarial loads, reaching up to 74 worms, a level not observed in natural infections. Infected fish exhibited the whirling symptoms approximately 6 weeks post-introduction, successfully reproducing the disease. The metacercariae in diseased fish had a cyst diameter of over 500 µm, suggesting that the behavioral changes are linked to their development. This system provides a valuable model for developing control measures and investigating the behavioral modifications caused by brain-infecting trematodes.

PISCES, PARASITES, AND PEOPLE: NAVIGATING THE NEXUS

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Fish, parasites, and people share a complex relationship that connects aquatic ecosystems, human health, and economic stability. This presentation examines the roles of fish as hosts, parasites as pathogens, and humans as both consumers and stakeholders, focusing on the challenges posed by zoonotic parasitic infections to aquaculture, wild fisheries, and public health. Case studies will include well-known parasites like anisakids and less-studied ones such as *Eustrongylides* spp. and *Kudoa* spp. The talk also addresses the differing challenges faced by developing and developed countries in managing fish-borne parasitic diseases, highlighting the need for a global approach in our interconnected world. Developing nations often struggle with limited resources for monitoring and control, while developed nations face declining expertise, leaving them vulnerable to emerging diseases. By exploring these issues, the presentation emphasizes the importance of collaboration, knowledge sharing, and policy alignment to tackle the shared burden of parasitic diseases. Ultimately, it calls for integrated strategies to balance the needs of fish, parasites, and people, ensuring sustainable aquaculture, healthy ecosystems, and safe food supplies for a growing global population.

POSTER PRESENTATIONS

A NEW RECORD OF POTENTIALLY ZOONOTIC *Contracaecum* LARVAE PARASITIZING TWO FRESHWATER FISHES FROM BRAZIL

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Two fish species, *Astyanax lacustris* (n = 26) and *Geophagus brasiliensis* (n = 28), were collected at two sampling sections of the Pardo River, in the municipality of Botucatu, state of São Paulo, Brazil, and surveyed for parasites. White nematodes lacking sexual organs were found encysted in the intestine serosa, heart, and fatty tissue. Ecological parameters such as prevalence, mean abundance, and mean intensity of infection were calculated for each host species from each locality. Morphological analysis indicated that the worms were L3 larvae of the genus *Contracaecum*, which was confirmed by molecular analyses of cytochrome c oxidase subunit 2 (COX2) and large subunit ribosomal RNA (28S) genes that placed the larvae within a well-supported clade of Neotropical and Panamanian *Contracaecum* species containing sequences of *Contracaecum jorgei* and some, but not all, sequences identified as *Contracaecum multipapillatum*. Our findings suggest that *C. jorgei* is synonymous with some previously identified *C. multipapillatum* lineages, indicating that the latter species is currently non-monophyletic with separate lineages in the Palearctic and Nearctic regions. This novel record of a species of *Contracaecum* parasitizing fishes in the Pardo River provides new insight into the phylogeny of this genus, which is believed capable of zoonotic infection, though there are no documented human cases in the Americas. Future research will be necessary to confirm or refute the monophyly of this clade. Financial support: FAPESP 2020/05412-9, 2022/04715-3; CNPq 311635-2021-0, 140871/2017-9 and CAPES 88887.976117/2024-00.

BIODIVERSITY OF POUTING MACROPARASITES (*Trisopterus luscus* Linneaus, 1758) CAUGHT IN PORTUGUESE WATERS AND FOOD SAFETY

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The knowledge of parasite biodiversity of marine fishes is essential to assess the risk of parasitic species with zoonotic potential becoming emergent. This work aimed to study the parasitic biodiversity of pouting (*Trisopterus luscus* Linneaus, 1758) and their possible zoonotic potential. The macroparasites of pouting were analysed in two sets of fishes, one from the North (Porto) n=119, and the other from the South (Lisbon), n= 120, both off the Portuguese coast (FAO zone 27). The fish were caught in sets of around 30 per season, during the year 2023/24. The parasites found were isolated, and identified and the infection levels determined. A total of 8,792 parasites were counted, 4,236 in the North (13 taxa) and 4,556 in the South (8 taxa), with a parasitic similarity of 57%, 6 taxa in common (Monogenea (*Diclidophora* sp.); Digenea (*Stephanostomum* sp.; *Hemiurus* sp.); Cestoda (*Grillotia* sp.; *Nybelinia* sp.) and Copepoda (*Lernaeocera lusci*)). The *Nybelinia* sp. showed the highest coefficient of dominance (d=0.65 and d=0.83). According to the intracommunity component, *Nybelinia* sp. was shown to be a central taxa with prevalence (%)= 91 and 82 for the North and South and total intensity of 2,843 and 3,800 parasites, respectively. The presence of the *Nybelinia* sp. and the local infection, the muscle, may generate an alert regarding the zoonotic potential, since there are some records of other species of Trypanorhyncha with zoonotic potential. However, more studies need to be carried out to understand if indeed this species can be potentially zoonotic.

LARVAL NEMATODES INFECTING CEPHALOPODS FROM NORTH EAST ATLANTIC AND MEDITERRANEAN SEA

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The occurrence of zoonotic parasites, such as Anisakid nematodes, in commercially important cephalopod species is often overlooked. This study investigates the prevalence, tissue distribution, and species composition of anisakids in three squid species belonging to the family Ommastrephidae, namely *Illex coindetii*, *I. illecebrosus* and *Todaropsis eblanae*. From November to December 2023, a total of 238 squids have been sampled from 4 FAO areas. Mantle and internal organs were inspected by the naked eye, to detect Anisakid nematodes following national and European Regulations, but also by the UV-Press method. All the recovered nematodes were identified by PCR-RFLP of the ITS rDNA. Out of 238 examined squids, 53 (22.2%) showed L3 larvae of nematodes of the families Anisakidae and Raphidascaridae: 45.3% in mantle, 39.6% in viscera and 15.1% in both tissues. Visual inspection detected nematodes only in 16 squids (6.7%), while 37 squids (15.5%) exhibited nematodes under UV-press examination and only 6 squids (2.5%) showed nematodes by both methods. Our investigation revealed the presence of both zoonotic (*A. simplex* and *A. pegreffii*) and non-zoonotic (*Lappetascaris* sp. and *Hysterothylacium* sp.) nematodes. It's noteworthy that the squid species examined in our study are frequently consumed raw as sushi or undercooked, raising concerns about public health risks. The preliminary results of our study contribute to the growing body of research on the presence of zoonotic Anisakids in cephalopods marketed in Italy. Furthermore, our data underline the need to establish an official diagnostic method, as visual inspection alone proved to be insufficiently sensitive.

CAN HIGHLY INVASIVE MUSSELS ACT AS CARRIERS, OR HOSTS, OF MYXOZOAN PARASITES IN THE GREAT LAKES REGION?

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The Great Lakes basin was recently invaded by Zebra (*Dreissena polymorpha*) and Quagga (*D. bugensis*) mussels. Reproducing and growing fast, they widespread across large and small lakes and rivers in North America, threatening local freshwater environments and fisheries. They can bio-accumulate substances and microorganisms that can become harmful for animals and people relying on these freshwater ecosystems. The myxozoan *Tetracapsuloides bryosalmonae* (Malacosporea) propagates through a two-host lifecycle and may cause Proliferative Kidney Disease (PKD) in salmonids. Infected freshwater bryozoans, moss filter-feeding organisms, release waterborne malacospores that can be infectious to susceptible salmonids. The reproducibility of *T .bryos* life cycle is enhanced by warmer water temperatures, environmental and host susceptibility conditions. We recently confirmed the presence of *T. bryos* in several salmonid species and bryozoans across the Great Lakes region. Freshwater mussels are filter-feeder invertebrates that are often found sharing the same substrates with several bryozoan species, which also grow on their shells. We collected Zebra and Quagga mussels from rivers and lakes around Michigan, to assess whether they may be acting as vectors or hosts for *T. bryos*. Whole organisms and selected internal organs (e.g., gills, digestive glands) are screened for *T. bryos* detection by PCR, followed by histological evaluation of relevant samples. Defining the possibility of detecting myxozoan parasites from freshwater mussels will determine if they could be used as bioindicators to detect this regulatory fish pathogen and provide further insights on how the parasite life cycle may be completed. This study is relevant towards understanding the impact that invasive mussels may have on people using lacustrine and riverine systems for commercial fisheries and aquaculture, and even for recreation purposes.

HELMINTH PARASITE GUILD COMMUNITY IN *Mugil cephalus, Pomadasys macracanthus* AND *Galeichthys peruvianus* IN PUERTO EL MORRO (GUAYAQUIL – ECUADOR): THE IMPACT OF CLIMATE CONDITIONS ON ICHTHYOZOONOTIC RISK

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Mugil cephalus, *Pomadasys macracanthus* and *Galeichthys peruvianus* represent some of the most consumed marine resources in Puerto el Morro (Guayaquil, Ecuador). This fishing village has a culture of holding fairs dedicated to the consumption of fish, especially the so-called mullet fair *(M. cephalus),* which takes place once a year and is consumed in different preparations. During the period from January to June 2021, 550 individuals were examined among three species of fish (n = 550). This study aimed to determine the prevalence (P), mean intensity (MI) and mean abundance (MA). Five helminths' species were collected, nematodes *Cullanus sp., Procamallanus sp,* and acanthocephalan *Floridosentis mugilis* (adult stage), and nematodes *Contracaecum sp,* (L3) and *Hysterothylacium sp.* (L4). In *M. cephalus* (n = 160): *Contracaecum* sp, (L3) (P = 6.88%, MI = 1.27, MA = 0.09) and *F. mugilis* (P = 39.38%, MI = 7.02, MA = 2.76). In *P. macracanthus* (n = 185): *Hysterothylacium* sp, (L4) (P = 0.67%, MI = 1, MA = 0.01), *Cucullanus* sp (P = 0.54%, MI = 1, MA = 0.01), *Procamallanus* sp. (P = 2.16%, MI = 1.25, MA = 0.03) and *F. mugilis* (P = 0.54%, MI = 1, MA = 0.01). In *G. peruvianus* (n = 205): *Cucullanus* sp. (P = 0.49%, MI = 1, MA = 0.005) and *F. mugilis* (P = 0.98%, MI = 0.67, MA = 0.01). Seasonal effects in parasite prevalence were observed, between January to March period we found high prevalences in compare to April to June period, even some parasites even disappeared. Perhaps because more intense rain was reported in the first months of the year and the temperature increases, affecting the population dynamics of the fish studied their predator-prey relationships and consequently parasite transmission dynamics. *Contracaecum sp,* and *Hysterothylacium sp.* represent a zoonotic risk

ULTRASTRUCTURE OF MICROBIOTA OF TYPEWORMS TEGUMENT USING SCANNING AND TRANSMISSION ELECTRON MICROSCOPY

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Bacterial associations with tapeworms are especially interesting because this group of Platyhelminthes lacks all elements of a digestive system except absorption. It is known that the external surfaces of tapeworms are composed of a multifunctional syncytial tegument performing digestive-absorptive functions which are similar in structure and function to the brush border of the intestines of vertebrates. To make advances toward a deeper understanding of the tapeworm's microbiome organization we approved an approach based on serial washing of bacterial cells from the tegument of cestodes via shaking of the whole parasite in buffers and their transfer through a series of those buffers. Ultrastructural description of the presence of bacteria on the tegument surfaces was done using scanning and transmission electron microscopy. By SEM, there was the typical highly dense arrangement of long, remarkably flexible filamentous microtriches revealed throughout the strobila. The TEM images shows that the tegument is composed of an external anucleate cytoplasmic layer (distal syncytial cytoplasm) covered with numerous long slender filamentous microtriches interspersed with individual spiniform microtriches. Using scanning and transmission electron microscopy, it was found that the tegument of cestodes was covered with numerous and diverse bacteria. These bacteria colonized both the apical and deep parts of the microtriches, as well as were associated with the cytoplasmic membrane of the tegument. This work was partially supported by the Russian Science Foundation, project no. 23-74-10101.

MICROBIAL COMMUNITY STRUCTURE ASSOCIATED WITH *Coregonus lavaretus* AND CESTODES PARASITIZING THEIR DIGESTIVE TRACT

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Sympatric pair of whitefish that inhabits Teletskoye Lake in the Altai Mountains (West Siberia, Russia) have a different trophic specialization. *Coregonus lavaretus pravdinellus* feeds on zooplankton, whereas the diet of *C. l. pidschian* is based on benthic prey. The study aimed to identify composition and structure of microbial community of the digestive tract of sympatric pair of whitefish from Teletskoye Lake and their parasites *Proteocephalus* sp. Fish and cestodes were collected in the north part of Lake Teletskoye (51.79 N; 87.30E). Microbial communities associated with the cestodes *C. l. pidschian* and *C. l. pravdinellus* were studied using next-generation high-throughput sequencing of the 16S ribosomal RNA genes. The dominant phyla in associated microbiota of the cestodes extracted from intestine of *C. l. pidschian* and *C. l. pravdinellus* were represented by Proteobacteria and Tenericutes, respectively. At the genus level the microbiota of cestodes parasitizing the intestine of *C. l. pidschian* were dominated by *Rickettsiella*, *Mycoplasma*, and unclassified bacteria from Aeromonadaceae and Enterobacteriaceae families. The microbiota of cestodes parasitizing the intestine of *C. l. pravdinellus* were dominated by *Mycoplasma* and *Acinetobacter*, respectively.

The study of host–helminth–microbiota interactions is essential to clarify the mechanism of their relationship and understand possible potential to alter host homeostasis. This work was supported by the Russian Science Foundation, project no. 23-74-10101.

MOLLIES AND GILTHEAD SEABREAMS AS NOVEL MODEL ORGANISMS FOR ANISAKID RESEARCH: EXPERIMENTAL INFECTIONS AND HISTOLOGICAL EXAMINATION OF THE INFECTION PROCESS IN SAILFIN MOLLY

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Anisakis spp. (Nematoda, Anisakidae) are parasites known for their economic and health impacts, as their third larval stage infects various fish species, many of which are of commercial interest. To study how this infection develops, we propose new fish model organisms for experimental studies on *Anisakis* and other fish pathogens, as alternatives to the commonly used model *Danio rerio*. For this purpose, the sailfin molly (*Poecilia latipinna*, due to its easy adaptation to seawater) and the gilthead seabream (*Sparus aurata*) were tested. Preliminary susceptibility challenges in mollies showed successful infections with *Anisakis simplex* s.l. larvae. Two infection methods, "oral ingestion" and "orogastric inoculation", were evaluated in both fish species. Results demonstrated successful infections with both methods. Additionally, the study examined the chronology of the infection process, histological changes, and encapsulation patterns in the infected fish. This comprehensive study highlights the suitability of the sailfin molly as a model organism for experimental studies on anisakid infections and provides valuable insights into the infection dynamics and host-parasite interactions. Further research in this field could contribute to the development of effective prevention and control measures for anisakid infections, thereby reducing the health risks associated with fish consumption. This work has been financed by the Spanish Ministry of Science and Innovation with funding from the European Union NextGenerationEU project [ThinkInAzul, PRTR-C17·I1] and from Generalitat Valenciana to the project REMEDISA-ICHTHYOPARASITES [GVA-THINKINAZUL/2021/029]; and the European Union's Horizon 2020 Research and Innovation Programme under the Marie Skłodowska-Curie grant agreement No 101027941 (ABT).

INVESTIGATING THE HOST-PARASITE GENETIC ARCHITECTURE AND IMMUNE RESPONSE IN HUMAN ANISAKIASIS IN ITALY CAUSED BY *Anisakis pegreffii*

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Anisakis pegreffii is one of the most causative agents of human anisakiasis. A study was carried out on past and novel cases of anisakiasis occurred in Italy during the years 2013–2023, with the following aims: *i)* genotyping the parasite from different clinical cases (i.e. gastric GA, intestinal IA and gastro-allergic anisakiasis GAA); *ii)* genotyping the human HLA; *iii)* investigating patients IgE immune response. The study included patients with larval finding during endoscopy or post-surgical removal of granuloma (N=17), as well as those patients showing chronic urticaria (CU) symptoms and other allergic disorders after fish consumption (N=50). For genetic/molecular identification, DNA was extracted from each larva removed from the above cited cases. Genetic analysis was carried out by sequence analysis of the mtDNA *cox*2 gene and genotyping at nuclear SSRs DNA loci. HLA-DRB1, HLA-DQA1 and HLA-DQB1 of the patients were genotyped by ImmunoCOR kit. Sera were tested by IgE response in WB and ELISA assays. Genetic findings revealed that all the GA, IA and GAA cases were due to *A. pegreffii*. The larvae causing GA showed a particular heterozygote genotype at a certain DNA-SSR locus and homozygous at another polymorphic locus. A certain IgE-WB hypersentization to *A. pegreffii* was detected in the sera of patients, who showed specific alleles at the HLA loci, compared to negative control patients. Investigating the genetic architecture of both the parasite species and the human host in anisakiasis may provide knowledge in understanding the evolutionary aspects of the pathogenesis of this fish-borne zoonosis.

SEASONALITY OF *Anisakis* spp. LARVAE INFECTION OF SCABBARDFISH, *Aphanopus carbo* OFF THE ATLANTIC COAST OF PORTUGAL

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The black scabbardfish, *Aphanopus carbo* (Ac) is a deep-sea fish species with important commercial value. This study evaluated the seasonality of *Anisakis* larvae infection in Ac sampled from the Sesimbra region, Northeast Atlantic coast of Portugal (FAO zone 27). Seasonal differences in the parameters of infection and the relationship with the seasonality of host parameters (length and weight) were evaluated. A total of 123 adult Ac specimens were obtained seasonally and the visceral cavity and organs were examined for the presence of *Anisakis*, revealing a 100% prevalence year-round. There was no significant seasonality for intensity of infection and the values recorded ranged from 649.73 in summer and 373.45 in spring throughout the year. Similarly, no significant seasonal variations were observed in fish weight and length, with the highest mean weight recorded in autumn (2111.50±577.45 g [1095-3090]) and the lowest in summer (1749.17±346.16 cm [1220-2845]). The highest mean length was observed in spring (113.09±10.24 cm [103.1-162.7]) and the lowest in autumn (108.79±5.23 cm [103.0-118.7]). The consistently high number of parasites throughout the year underscores the potential health risks of consuming raw or undercooked black scabbardfish, the need for enhanced health control measures, and increased consumer awareness.

OCCURRENCE OF PARASITES IN FISH FINGERS

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Fish fingers (Ff) are known for their sensory characteristics and convenience, making their consumption popular in family meals all over the world. The presence of parasites in Ff threatens their quality and safety, leading to a rising risk for consumers due to parasitic zoonosis. Parasitological research was carried out on a survey of 35 brands of Ff of European hake, North Pacific hake, Alaska pollock, Atlantic salmon, and minced fish, in a total of 1,518 units. The presence of the myxosporean *Kudoa* sp. was registered in 15 Ff brands, whose constitution included hake. The presence of cysts and spores of *K. thyrsites* and *K. paniformes* was observed, either alone or simultaneously (5 brands). In seven Ff brands, the presence of *Kudoa* spores was observed in more than 50% of the sample, ranging from 68.88% to 86.96% and in three of these samples, Ff showed flesh liquefaction. L3 *Anisakis* larvae (n=7) were identified in five Ff brands whose composition was European hake. The presence of *Trypanorhyncha* cestode was also recorded. Despite the presence of zoonotic parasites, the consumption of Ff doesn't constitute a hazard due to the high temperatures at which they are usually cooked, which contributes to making them inviable. Monitoring the frozen storage temperature of Ff also counteracts the parasite viability and inhibits the activity of the enzymes they produce. However, the presence of *Anisakis* larvae in 60% Ff samples with minced fish, warns of the need for further sanitary control of fish intended for Ff production.

INFECTION OF *Enteromyxum leei* IN CULTURED STARRY FLOUNDER (*Platichthys stellatus*)

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Enteromyxum leei has been identified as the causative agent of emaciation disease in a wide range of marine fish hosts. In this study, we aimed to determine the effect of parasitic infection with *Enteromyxum* species on starry flounder cultured in aquaculture farms on Jeju Island in Republic of Korea. To identify myxosporeans found in the intestine of cultured starry flounder, the 18S rDNA gene of the parasite was sequenced. To reveal the effect of parasitic infection on starry flounder, the intensity of parasitic infection was measured using quantitative PCR, and the condition factor of the fish was measured and analyzed statistically. In addition, histological changes depending on the intensity of parasitic infection were investigated. The partial 18S rDNA of myxosporeans showed 100% similarity with *E. leei*. The statistical analysis showed that high-intensity *E. leei* infection significantly decreased the condition factor of the starry flounder. However, the pathogenicity of *E. leei* to starry flounder is low, considering its mortality and clinical signs. The developmental stage of *E. leei* was observed clearly in high intensity (CT < 23) of the parasite infection group.

THE GUT MICROBIOTA OF *Cystidicola farionis* PARASITIZED THE SWIM BLADDER OF THE CHARR *Salvelinus schmidti* IN KRONOTSKOE LAKE (KAMCHATKA, RUSSIA)

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The aim of the present study was to analyze the bacterial diversity associated with the gut and body of *Cystidicola farionis* parasitizing the swim bladder of the different morphs of the nosed charr *Salvelinus schmidti*. *C. farionis* from the nosed charr *S. schmidti* were collected in the littoral zone of Kronotskoe Lake. Associated microbiota of *C. farionis* and swim bladder of the nosed charr were investigated by sequencing of the V3, V4 hypervariable regions of 16S rRNA using Illumina MiSeq sequencing platform. The common dominant microbiota of the gut and body of nematode were represented by *Aeromonas*, *Pseudomonas*, *Shewanella*, and *Yersinia*, while the associated microbiota of the swim bladder of the nosed charr was dominated by *Acinetobacter*, *Cetobacterium*, *Pajaroellobacter*, *Paracoccus*, *Pseudomonas*, *Shewanella*. By comparing the associated microbiota of nematode parasitizing the different morphs of the nosed charr, the difference in richness estimates (number of OTUs and Chao1) were revealed between the N1g and N2 morphs. For the first time, the microbial communities of the nematode gut and body, as well as microbiota of the swim bladder of charr were

analyzed using a next-generation sequencing approach. Moreover, increasing our knowledge of gut-associated microbiota of fish nematode parasites will help to elucidate more details of microbe-parasite relationships.

Crassicauda LARVAE (NEMATODA: HABRONEMATIDAE) IN ARGENTINE HAKE, PORBEAGLE AND ARGENTINE SQUID: A ZOONOTIC THREAT?

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The genus *Crassicauda* (Habronematidae) comprises 14 species of parasitic nematodes infecting several tissues and cavities of different cetaceans. Recently, Spirurina type X larvae, characterized by having two large tubercules at the tail tip and known as causative agents of creeping eruption in humans, were identified as members of this genus by genetic analyses. In humans, the main source of infection for this zoonosis are squids, although these larvae have been reported in the viscera of several fish species. In the Atlantic Sudoccidental, larvae identifiable morphologically as belonging to *Crassicauda* were found in samples of 712 Argentine squid *Illex argentinus*, 260 Argentine hake *Merluccius hubbsi* and 1 porbeagle *Lamna nasus* at relatively high prevalences. Sequencing of the mt-cox1 gene confirmed the identity of these larvae as belonging to *Crassicauda*. The K2P genetic distances considering all six species of *Crassicauda* available in GenBank, were at the level of interspecific differences, not allowing the identification at specific levels of the larvae. Furthermore, whereas larvae from hakes and squids resulted in conspecific, those found in the porbeagle were identified as a different species. Despite the zoonotic nature of other species, the microhabitats recorded (stomach wall of fishes and mantle cavity of squids) reduce the risk to consumers to a minimum, additionally, because both hake and squid are commercialized frozen and consumed cooked.

IDENTIFICATION OF CYMOTHOID ISOPODS PROBABLY RESPONSIBLE FOR MASS MORTALITY OF HATCHERY-REARED PACIFIC BLUEFIN TUNA *Thunnus orientalis* JUVENILES AFTER TRANSFER TO SEA CAGES

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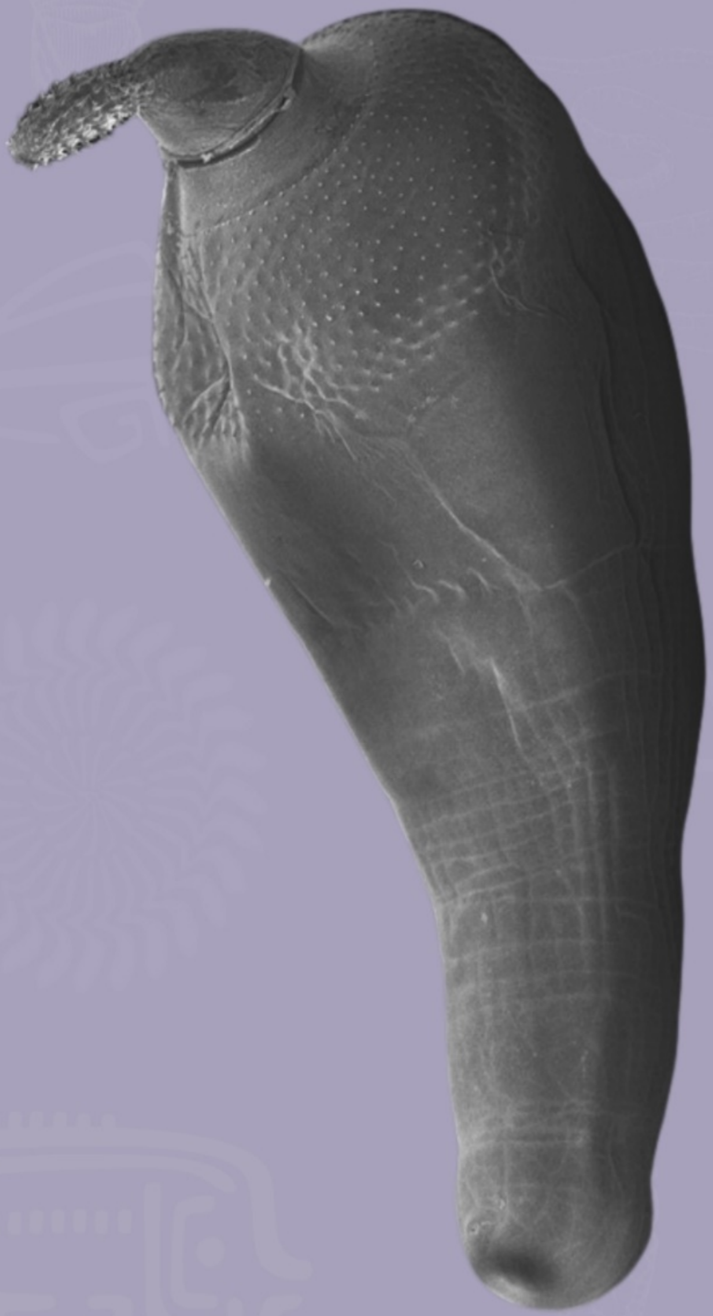
Hatchery-produced Pacific bluefin tuna (PBT) *Thunnus orientalis* juveniles experienced mass mortality after being transferred to sea cages in a cove on Kakeromajima Island, Kagoshima Prefecture, Japan, in July 2022. Although no obvious pathogens were found in the dead fish, mancae and juveniles of cymothoid isopods were highly prevalent in the branchial cavity of the few surviving PBT juveniles. The gills of the PBT juveniles were severely damaged, such as partial loss of gill filaments and discoloration indicating anemia. We identified two species of cymothoid parasites based on their mitochondrial DNA sequences. Most parasites had cytochrome c oxidase subunit 1 (COI) and 16S rDNA sequences similar to those of *Norileca indica*, while some were identified as *Ceratothoa carinata*. Adult cymothoids were not found in the PBT juveniles but in the bigeye scad *Selar crumenophthalmus* caught around the PBT farming cages. The adults were morphologically and molecularly identified as *N. indica*. Therefore, it is likely that the mancae and juveniles of the cymothoids accidentally infested the PBT juveniles after they were released from adult parasites in wild natural hosts, such as *S. crumenophthalmus*, living in the same area. This is the first record of *N. indica* in Japan and the northernmost record of this species. To our knowledge, this is the first report of mass mortality in PBT juveniles caused by parasitic isopods. Our study would be the first step in developing measures to avoid the damage caused by the parasites.

Thematic areas

9. ACANTHOCEPHALA WORKSHOP



ORAL PRESENTATIONS

(Please note the name and institution shown in this list are those of the person presenting the talk, who may not be the first author; the complete author list including all institutional affiliations are shown with the full abstract)

1. ARE ACANTHOCEPHALANS THE ONLY ONES WITH A PARASITIC LIFESTYLE IN SYNDERMATA? TRACKING DOWN PARASITIC ROTIFERS IN EARTHWORMS. Alama-Bermejo, G. et al. Fish Health Division, University of Veterinary Medicine, Vienna, Austria
2. PHYLOGENOMICS OF ACANTHOCEPHALA: INSIGHTS FROM NOVEL TRANSCRIPTOMES. Brabec, J. et al. Institute of Parasitology, Biology Centre of the Czech Academy of Sciences, České Budějovice, Czechia
3. PATHOGENICITY OF ACANTHOCEPHALAN LARVAE IN CRUSTACEANS AND ADULTS IN FISH: DIFFERENCES IN HOST RESPONSES ARE RELATED TO PARASITE SPECIES. Dezfuli, S.B. et al. Department of Life Sciences and Biotechnology, University of Ferrara, Italy
4. ESTIMATION OF METAL IMPACT AND BIOMARKER RESPONSES IN ACANTHOCEPHALANS AS POTENTIAL INDICATORS OF ENVIRONMENTAL POLLUTION. Filipović Marijić, V. et al. Division for Marine and Environmental Research, Ruđer Bošković Institute, Zagreb, Croatia.
5. A SURVEY OF 21 NEOECHINORHYNCHID FISH ACANTHOCEPHALANS AT THEIR TYPE LOCALITIES. Fleming M.B. & Reyda F.B. Biology Department and Biological Field Station, State University of New York at Oneonta. New York, USA
6. A PHYLOGEOGRAPHIC STUDY OF TWO POLYMORPHID SPECIES (ACANTHOCEPHALA) DISTRIBUTED SYMPATRICALLY IN THE NEARCTIC REGION. García-Varela, M. et al. Departamento de Zoología, Instituto de Biología, Universidad Nacional Autónoma de México, Avenida Universidad 3000; Ciudad Universitaria; C.P. 04510; Ciudad de México. México
7. ACANTHOCEPHALANS IN THE PARASITIC WORMS COLLECTION OF THE NATURAL HISTORY MUSEUM, LONDON. Hernández-Orts J.S. & García-Gallego A. Natural History Museum, London, United Kingdom.
8. EMERGING WAVE OF CORYNOSOMIASIS IN HOKKAIDO, NORTHERN JAPAN. Katahira, H. et al. School of Life and Environmental Science, Azabu University, Japan
9. THE GENOMES OF THE ACANTHOCEPHALANS *Oncicola* sp. AND *Floridosentis mugilis*. Martinek, I.N. et al. Institute of Parasitology, Biology Centre of the Czech Academy of Sciences, České Budějovice, Czech Republic
10. ACANTHOCEPHALANS IN A TROPHC CONTEXT: STABLE ISOTOPES OF CARBON AND NITROGEN PROVIDE INSIGHTS INTO HOST-PARASITE TROPHIC INTERACTIONS. Nachev, M. et al. Department of Aquatic Ecology and Centre for Water and Environmental Research (ZWU), University of Duisburg-Essen, Essen, Germany
11. KARYOTYPES AND CYTOGENETIC MAPPING OF RRNAS AND HISTONE H3 GENES IN THREE SPECIES OF THE GENUS *Acanthocephalus* (PALAEACANTHOCEPHALA). Orosová M. & Marková A. Institute of Parasitology, Slovak Academy of Sciences, Hlinkova 3, 040 01 Košice, Slovakia
12. PHYLOGENETIC ANALYSIS OF NORTH AMERICAN SPECIES OF FAMILY NEOECHINOHYNCHIDAE. Reyda F. B. et al. Biology Department and Biological Field Station, State University of New York at Oneonta. New York, USA
13. FIRST FINDINGS ON METAL-BINDING PROTEINS IN ACANTHOCEPHALA FROM THE TRANSCRIPTOME OF *Dentitruncus truttae*. Šariri, S. et al. Division for Marine and Environmental Research, Ruđer Bošković Institute, Zagreb, Croatia
14. ACANTHOCEPHALANS AND POLLUTANTS AFFECT PHYSIOLOGICAL RESPONSES OF AMPHIPODS USED IN ECOTOXICOLOGY. Sures B. et al. Department of Aquatic Ecology and Centre for Water and Environmental Research (ZWU), University of Duisburg-Essen, Essen, Germany

POSTER PRESENTATIONS

(Please note the name and institution shown in this list are those of the person presenting the poster, who may not be the first author; the complete author list including all institutional affiliations are shown with the full abstract)

1. MOLECULAR CHARACTERIZATION AND PHYLOGENY OF *Pomphorhynchus* sp. PARASITIZING LEVANTINE SCRAPER (*Capoeta damascina*) FROM LAKE HULA, ISRAEL. Davidovich N. et al. Israeli Veterinary Services, Bet Dagan, Israel
2. UNDER THE SURFACE: ACANTHOCEPHALAN PARASITES AS BIO-INDICATORS OF ELEMENT ACCUMULATION IN MARINE ECOSYSTEMS. Erasmus, A. et al. Water Research Group, Unit for Environmental Sciences and Management, North-West University, Private Bag X6001, Potchefstroom 2520, South Africa
3. LINKING ADULTS AND CYSTACANTHS OF A NEW SPECIES OF *Rhadinorhynchus* LÜHE, 1911 (ACANTHOCEPHALA: RHADINORHYNCHIDAE) FROM PACIFIC COASTS OF MEXICO BY USING MORPHOLOGICAL, ECOLOGICAL, AND MOLECULAR DATA. Grano-Maldonado M.I. et al. Facultad de Ciencias del Mar, Universidad Autónoma de Sinaloa, Av. Claussen s-n, Mazatlán, Sinaloa, México
4. CONTRASTING ACANTHOCEPHALAN INFECTIONS IN NATIVE VS. NON-NATIVE CRAYFISH INTERMEDIATE HOSTS. Hill-Spanik K.M. et al. SC Dept. of Natural Resources, Marine Resources Research Institute, Charleston, SC, USA
5. BIOGEOGRAPHY OF GUILD POPULATION OF *Andracantha* sp. SCHMIDT, 1975 (ACANTOCEPHALA, POLYMORPHIDAE) IN CHARACIDS (OSTEICHTHYES: CHARACIDAE) OF EL ORO PROVINCE, ECUADOR: LATITUDINAL GRADIENT OF POPULATION DYNAMICS. Iannacone J. et al. Laboratorio de

Zoología, Facultad de Ciencias Biológicas, Grupo de Investigación "One Health", Universidad Ricardo Palma (URP), Lima – Peru

6. *Profillicolis altmani* AND *Corynosoma australe* IN NORTHERN HUMBOLDT CURRENT SYSTEM: EFFECTS OF EL NIÑO-SOUTHERN OSCILLATION (ENSO) ON NEGLECTED ICHTHYOZOONOSES IN PERU. Iannacone J. et al. Laboratorio de Zoología, Facultad de Ciencias Biológicas, Grupo de Investigación "One Health", Universidad Ricardo Palma (URP), Lima – Peru
7. PHYLOGENETIC STUDY OF ACANTHOCEPHALA BASED ON MITOCHONDRIAL GENOMES, INCLUDING JAPANESE SPECIES. Kita Y. et al. Graduate School of Science, Hokkaido University, Sapporo, Japan
8. SATELLITOME OF THREE *Acanthocephalus* SPECIES: SEARCHING FOR NEW CYTOGENETIC MARKERS. Orosová M. et al. Institute of Parasitology, Slovak Academy of Sciences, Hlinkova 3, 040 01 Košice, Slovakia

ORAL PRESENTATIONS

ARE ACANTHOCEPHALANS THE ONLY ONES WITH A PARASITIC LIFESTYLE IN SYNDERMATA? TRACKING DOWN PARASITIC ROTIFERS IN EARTHWORMS

Alama-Bermejo G.[1]; Bartonicek Z.[2,3,4]; Martinek I.[2]; Brabec J.[2]; Devetter M.[5] & Hernández-Orts J.S.[2,3]

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The group Syndermata includes rotifers or wheel animals (>2100 species) and acantocephalans or thorny-headed worms (1300 species), an exclusively parasitic lineage. Interestingly, this is not the only time that a parasitic lifestyle has been acquired in the Syndermata: few species of rotifers, like the ones belonging to the genera *Albertia* and *Balatro* (Monogononta: Dicranophoridae), are found as endoparasites in the guts of earthworms (Annelida: Lumbricidae) and gastropods. Comparative morphological and genomic studies between these parasitic rotifers and their free-living relatives will provide first insights on their transition and adaptations to parasitism. We collected 289 earthworms (*Aporrectodea longa*, *A. caliginosa*, *Eiseniella tetraedra*) from Newport, Wales (n = 209) and Cudham, London, England (n = 80) between 2023 and 2024. Individual earthworm intestines were dissected for the presence of rotifers, detecting two species *Albertia vermicularis* and *Balatro calvus* (prevalences 3.6-7.5%). For morphological and molecular comparison, free-living, closely related *Encentrum* spp. were collected from soil around České Budějovice, Czechia. Sequence data for nuclear (18S and 28S rDNA) and mitochondrial (cox1) genes were generated for the first time to evaluate the phylogenetic affinities of these parasitic rotifers with free-living dicranophorids. Phylogenetic analyses placed *A. vermicularis* as a sister lineage to *B. calvus* with strong nodal support. The clade formed by both parasitic species was placed as sister to a clade of free-living dicranophorids *Encentrum* spp. These first results not only shed light on the diversity and host associations of parasitic rotifers but also provide a framework for subsequent planned studies on the evolution of parasitism within the Rotifera. Financial support was provided by the Czech Science Foundation (project 23-05733S).

PHYLOGENOMICS OF ACANTHOCEPHALA: INSIGHTS FROM NOVEL TRANSCRIPTOMES

Brabec J.[1]; Alama-Bermejo G.[2], Barrena M.A.[3,4], Blasco-Costa I.[5], Flores V.R.[6], García-Varela M.[7], Gomez-Puerta L.A.[8], Hernández-Mena D.I.[7], Kibet C.[1], Kuchta R.[1], Martinek I.[1], Míguez-Lozano R.[9], Montero F.E.[9], Oceguera-Figueroa A.[7], Panti-May J.A.[10], Reyda F.[11], Schaeffner B.C.[12], Streicher J.W.[13], Valmaseda-Angulo M.[9] & Hernández-Orts J.S.[1,13]

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Thorny-headed worms (Acanthocephala) represent a diverse monophyletic group of endoparasites that likely originated from a free-living rotifer-like ancestor. Due to their status as non-human parasites and non-model organisms, the phylogenetic relationships within Acanthocephala have traditionally been investigated using limited genomic data, focusing mainly on mitochondrial protein-coding and nuclear ribosomal RNA genes. In this study, we present 40 newly sequenced acanthocephalan transcriptomes, belonging to the classes Archiacanthocephala (2 species), Eoacanthocephala (10 species) and Palaeacanthocephala (21 species), representing a broad sampling of the group's diversity. Using these data, we construct a supermatrix of protein-coding genes to resolve the evolutionary history of

Acanthocephala with genome-wide information. To ensure the accuracy of our analysis, we manually inspect individual single-protein candidate homolog trees for the presence of paralogs, minimizing phylogenetic noise. We also evaluate and address compositional heterogeneity and other sources of systematic error to improve the robustness of our phylogenetic inferences. Our phylogenomic framework aims to resolve unclear or contradictory positions of major lineages of acanthocephalans and provide a robust estimate of their evolutionary tree. Financial support was provided by the Czech Science Foundation (project 23-05733S).

PATHOGENICITY OF ACANTHOCEPHALAN LARVAE IN CRUSTACEANS AND ADULTS IN FISH: DIFFERENCES IN HOST RESPONSES ARE RELATED TO PARASITE SPECIES

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This study describes light microscopy and ultrastructure of the interface between *Echinogammarus stammeri* (Amphipoda), *Asellus aquaticus* (Isopoda) and *Cypria reptans* (Ostracoda) from the River Brenta naturally infected with the larvae of, respectively, *Pomphorhynchus laevis*, *Acanthocephalus anguillae* and *Neoechinorhynchus rutili*. Fully developed larvae of each species occupy the crustacean's hemocoel and displace its internal organs. In *E. stammeri*, *P. laevis* larvae establish intimate contact with the internal organs and hemocytes of the host. In *A. aquaticus*, a transparent acellular envelope covers each *A. anguillae* larva within the crustacean hemocoel. Intact isopod hemocytes were observed mainly on the outermost edge of the envelope around each *A. anguillae* larva. In *C. reptans*, *N. rutili* larvae were surrounded by some ostracod hemocytes. Light microscopy was also used to compare the pathogenicity of adult acanthocephalans in their fish hosts, also from the River Brenta. *N. rutili* penetrated only the surficial zone of the intestinal wall of *Gasterosteus aculeatus* and induced only slight inflammation. *A. anguillae* contacted the mucosal folds of *Squalius cephalus* intestine, causing damage by destroying the mucosal layer and inducing moderate inflammation. In *Barbus barbus*, penetration of *P. laevis'* long neck through the intestinal wall resulted in intense inflammation and, within the capsule around the bulb and proboscis, numerous mast cells and collagen fibres were encountered. The pathogenicity of adult acanthocephalans is attributed to the depth of worm penetration. Accordingly, among these three acanthocephalan parasites of fish, *P. laevis* penetrates the deepest and thus induces the most intense response in its adult host.

ESTIMATION OF METAL IMPACT AND BIOMARKER RESPONSES IN ACANTHOCEPHALANS AS POTENTIAL INDICATORS OF ENVIRONMENTAL POLLUTION

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In recent decades, the interrelation between parasites and contaminants has gained interest, especially in aquatic ecotoxicology. The novel field, Environmental Parasitology, investigates linkage between contamination and parasitism, including application of acanthocephalans as indicators in environmental risk assessment. Fish intestinal parasites, acanthocephalans, lack digestive system and depend on micronutrients from their host, including essential metals, which are absorbed from the fish intestine together with toxic elements, in concentrations usually orders of magnitude higher than those of the commonly used indicator organisms (fishes, bivalves, crustaceans). Accordingly, attempts have been made to utilize acanthocephalans as bioindicators of metal exposure. Estimation of metal exposure in Croatia was conducted at the reference and anthropogenically influenced sites in the karst Krka River, using *Dentitruncus truttae* from brown trout (*Salmo trutta*). Metal levels (measured by ICP-MS) confirmed higher efficiency of metal accumulation in *D. truttae* than in the fish intestinal tissue, especially for toxic elements (Cd, Pb, Tl). Metallothioneins (MT), biomarkers of metal exposure (measured electrochemically by DPV), in *D. truttae* were comparable to *Pomphorhynchus laevis* and *Echinorhynchus* sp. from other Croatian rivers and were in the range of 0.77–3.23 mg g^{-1}, while total proteins, biomarkers of general stress (measured spectrophotometrically), were in the range of 80-130 mg g^{-1}. The metal distribution within cytosolic proteins (measured by HPLC/ICP-MS) was comparable to that of fish and specific for certain metals, like binding of Cd and Cu to MT. Acanthocephalans also showed spatial differences in metal and biomarker levels, confirming their application as valuable bioindicators of water quality.

A SURVEY OF 21 NEOECHINORHYNCHID FISH ACANTHOCEPHALANS AT THEIR TYPE LOCALITIES

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Acanthocephalans are integral parts of ecosystems and can damage host populations. But many species in the USA have not been studied since being originally described; and most have not yet been analyzed using DNA sequencing. This survey builds on previous efforts to obtain numerous species of *Neoechinorhynchus* at their type localities in the USA. The focus here is on survey work to obtain the other north American genera of Family Neoechinorhynchidae for further study. That work resulted in acquisition of *Tanaorhamphus longirostris* (Van Cleave, 1913) Van Cleave 1919 and *Gracilisentis gracilisentis* (Van Cleave, 1913) Van Cleave 1919 from Gizzard shad (*Dorosoma cepedianum*) from Illinois; *Octospiniferoides chandleri* Bullock, 1957 from Eastern mosquitofish (*Gambusia holbrooki*) from Florida; *Floridosentis mugilis* (Machado-Filho, 1951) Bullock, 1962 from White mullet (*Mugil curema*) from coastal Florida; *Atactorhynchus verecundus* Chandler, 1935 from Texas; *Paulisentis fractus* Van Cleave & Bangham, 1949 from Ohio; *Octospinifer macilentus* Van Cleave, 1919 from New York and Virginia (but not at its type locality in Michigan). Efforts to obtain specimens of *Eocollis arcanus* Van Cleave, 1947 from its type locality in southern Illinois were unsuccessful in spite of having examined 312 centrarchid fishes. Between our own survey efforts and specimen donations from collaborators we now have study sets of specimens of most species and all genera of neoechinorhynchid acanthocephalans that occur in the USA. These specimens are being utilized for molecular phylogenetic and morphological analyses. This collection will be ultimately deposited in publicly accessible museum collections, thereby enhancing taxonomic infrastructure of this important group.

A PHYLOGEOGRAPHIC STUDY OF TWO POLYMORPHID SPECIES (ACANTHOCEPHALA) DISTRIBUTED SYMPATRICALLY IN THE NEARCTIC REGION

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Polymorphidae is a family of acanthocephalans parasite of aquatic birds and marine mammals distributed worldwide. The species *Pseudocorynosoma constrictum* is a typical parasite of ducks, whereas *Polymorphus brevis* is a parasite of herons distributed sympatrically in freshwater bodies in the Nearctic region. Both species use amphipods as intermediate hosts. However, *P. brevis* uses a broad spectrum of freshwater fishes (paratenic hosts) to complete its life cycle. In the current research, sequences of the cytochrome *c* oxidase subunit 1 (*cox 1*) from mitochondrial DNA from adults and cystacanths were generated to several populations of both species along their distribution in the Nearctic region. The haplotype network of both species are like start-shaped, with low haplotype diversity, and high values of fixation index, F_{st} among populations, indicated high genetic flow among the populations and it could be due for the migration of the definitive hosts.

ACANTHOCEPHALANS IN THE PARASITIC WORMS COLLECTION OF THE NATURAL HISTORY MUSEUM, LONDON

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The Parasitic Worms Collection of the Natural History Museum is one of the largest and most comprehensive collections of parasitic worms in the world. Established in the first half of the 19th century, the collection comprises over 600,000 specimens stored in alcohol in 20,000 jars and 180,000 slides of terrestrial and marine platyhelminths, parasitic nematodes, nematomorphs and acanthocephalans from around the world. It is particularly rich in type (~30% of the collection) and voucher material and includes specimens from important historical collections and expeditions. As of August 2024, the collection contains more than 5,000 acanthocephalans stored in alcohol and 711 slides of 329 taxa (277 identified to species level) of 10 orders and 27 families. Type specimens of 59 species (holotypes of 13 taxa) are deposited in the collection; 31 are acanthocephalans of teleosts, 2 of reptiles, 14 of birds and 12 of mammals. Here we give an overview of the Acanthocephala section of the collection and the work the museum is doing to preserve the material and ensure the process of transcribing information about the specimens into publicly accessible databases. Information is also provided on the procedures for depositing specimens, loans and the guidelines for research visitors.

EMERGING WAVE OF CORYNOSOMIASIS IN HOKKAIDO, NORTHERN JAPAN

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Zoonotic disease caused by *Corynosoma villosum*, an intestinal parasite of the Steller sea lion, has recently been identified in Hokkaido, northern Japan. This parasite uses coastal marine fish as paratenic hosts, and human infections are thought to result from consuming raw fish or through cross-contamination via cookware. Once inside the human body, the parasite can sometimes penetrate the intestinal wall and remain latent until it reaches maturity, causing inflammation, ulcers, or, in severe cases, intestinal obstruction. Infections in the small intestine are particularly difficult to detect and treat due to their deeper location, requiring advanced endoscopic techniques, unlike infections in the stomach or large intestine. The recent rise in infection cases is likely due to the expanding distribution and increasing population of pinniped mammals, including the Steller sea lion, which serve as definitive hosts of the genus *Corynosoma*, in the waters surrounding Hokkaido. Additionally, changes in human dietary patterns, such as the increased consumption of previously underutilized raw fish species, have likely led to a greater exposure to infection sources. In response, we have been working to identify these sources, assess the infection status in the definitive host mammals, and develop a diagnostic method. This presentation will outline the progress made in these efforts.

THE GENOMES OF THE ACANTHOCEPHALANS *Oncicola sp.* AND *Floridosentis mugilis*

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Acanthocephala is a large lineage of obligate parasites closely related to the epibiotic Seisonidae and the predominantly free-living rotifers (Monogononta, Bdelloidea). This close relationship has made this group, collectively called Syndermata, a model for studying adaptations associated with a parasitic lifestyle. However, the only available acanthocephalan genome to date is that of the palaeoacanthocephalan fish parasite *Pomphorhynchis laevis*. We present the draft genomes of the archiacanthocephalan *Oncicola* sp. and the eoacanthocephalan *Floridosentis mugilis*. Specimens of *Oncicola* sp. were collected from the small intestine of a white-nosed coati (*Nasua narica*) in Campeche, Mexico, in 2018; specimens of *F. mugilis* from the white mullet (*Mugil curema*) in Veracruz, Mexico, in 2024. For both species, genomic DNA was isolated from single specimens using a CTAB (cetyltrimethylammonium bromide) protocol. From one isolate of *Oncicola* sp 1.45 Mio long reads using Oxford Nanopore's MinION and 661.9 Mio paired-end short reads (150bp) using Illumina TruSeq DNA Nano. ONT and Illumina data were decontaminated individually before combining data assemblies to produce the most comprehensive assembly. A preliminary assembly resulted in a genome of 512Mb length in 6082 fragments with an N50 of about 324.7kb. For *F. mugilis* a single female specimen yielded 4.24 Mio high quality reads using Oxford Nanopore's PromethION. Transcriptomes derived from single specimens of both species extracted from the same host animal were used for further quality control of the assembly.

ACANTHOCEPHALANS IN A TROPHC CONTEXT: STABLE ISOTOPES OF CARBON AND NITROGEN PROVIDE INSIGHTS INTO HOST-PARASITE TROPHIC INTERACTIONS

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Stable isotope analysis of carbon and nitrogen can deliver valuable insights into trophic interactions between organisms. While this approach is widely used for studying the trophic interactions between free-living organisms, fewer studies focused on parasites and their associated hosts. Moreover, parasitic infections may alter the isotopic composition of hosts, leading to significant differences between infected and non-infected individuals. However, stable isotope composition is rarely studied in parasites, including acanthocephalans. Here, we studied the stable isotope composition in an isopod (*Asellus aquaticus*) - cystacanth (*Acanthocephalus* sp.) host-parasite system in a seasonal manner (spring, summer, autumn and winter) to determine the trophic position of larval acanthocephalans in relation to their host, over the course of the year. We also examined non-infected *A. aquaticus* to resolve potential isotopic differences between infected and non-infected conspecifics. Results were compared with data, which we obtained for European chub (*Squalius cephalus*) infected with *Acanthocephalus anguilae* as well as with data on *Pomphorhynchus tereticollis* from its amphipod intermediate host and definitive host, *S. cephalus*, to investigate isotopic shifts during trophic transmission of acanthocephalans. Our findings revealed species-specific fractionation patterns between acanthocephalans and their hosts. Infection with *Acanthocephalus* sp. caused isotopic fractionation between infected and non-infected isopods, whereas no isotopic differences were observed in amphipods infected with *P. tereticollis*. Both acanthocephalan species exhibited isotopic shifts during transfer from intermediate to definitive hosts, highlighting the complex dynamics of host-parasite trophic interactions.

KARYOTYPES AND CYTOGENETIC MAPPING OF RRNAS AND HISTONE H3 GENES IN THREE SPECIES OF THE GENUS *Acanthocephalus* (PALAEACANTHOCEPHALA)

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Standard cytogenetic analysis and chromosomal mapping of the genes for 18S and 5S rRNAs and histone H3 were performed in species of the genus *Acanthocephalus*. Conserved karyotypes with 2n = 7/8 (♂/♀) but different chromosome morphology were observed in all species. FISH with 18S rDNA probe identified a single locus on the sex chromosome in *A. lucii* and *A. ranae*, while three loci were identified in *A. anguillae*, which are exclusively autosomal. FISH showed that the 5S rRNA genes are located in the distal region of pair 3. Interestingly, FISH with probe H3 identified a cluster on chromosome no. 1 in *A. lucii*, a scattering of this sequence in the genome of *A. anguillae* and no detectable hybridization signal in *A. ranae*. The observed variability in the distribution of histone H3 genes could be related to the presence of transposable elements in the H3 sequences of *A. anguillae*, which are responsible for the spread of histone repeats in the genome of the species. In *A. ranae*, it is plausible that the copy number of H3 gene units is below levels detectable by the FISH method. The variation in the number/size/position of major rDNA sites indicates a change in chromosomal rDNA distribution that could involve structural rearrangements, unequal crossing-over and transposition. In contrast, the conserved number and position of minor rDNA clusters appears to be an ancient pattern common to all species studied. These results provide new information on the chromosomal organization and diversification patterns of repetitive DNA families in Acanthocephala species. This study was supported by the Scientific Grant Agency of the Ministry of Education, Science, Research and Sport of the Slovak Republic and the Slovak Academy of Sciences (VEGA No. 2/0093/23).

PHYLOGENETIC ANALYSIS OF NORTH AMERICAN SPECIES OF FAMILY NEOECHINOHYNCHIDAE

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Acanthocephalans are integral parts of ecosystems and can damage host populations. But many species in the USA have not been studied since being originally described; and most have not yet been analyzed using DNA sequencing. The key objective of this project is to increase our understanding of features of Family Neochinorhynchidae, a diverse group of ~150 acanthocephalans of fish and turtles that consists of nearly 20 genera worldwide in which *Neoechinorhynchus*—its most diverse genus—is known to be paraphyletic. The approach is to compare species of the 9 neoechinorhynchid genera that occur in the United States using morphological data, with a focus on hook morphology, in the context of a phylogenetic analysis. The phylogenetic analysis presented here is based on nuclear DNA from the internal transcribed spacer (ITS) and large ribosomal subunit (LSU) regions of >30 species in Family Neoechinorhynchidae from fish from the USA and Canada with representatives from South America, Europe, and Asia after several years of field work. Our results demonstrate that, as shown previously, *Neoechinorhynchus* is paraphyletic given that two different neoechinorhynchid genera from fishes nest within a clade of species of *Neoechinorhynchus* from fishes from the USA. We also found evidence of paraphyly of Neoechinorhynchidae in that the tenuisentid *Paratenuisentis ambiguous* nests within a clade of neoechinorhynchid genera. Potential pattrens of morphological character evolution, including hook morphology, are discussed in the context of the phylogenetic analysis.

FIRST FINDINGS ON METAL-BINDING PROTEINS IN ACANTHOCEPHALA FROM THE TRANSCRIPTOME OF *Dentitruncus truttae*

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The ability of acanthocephalans to accumulate high concentrations of toxic metals and serve as bioindicators of metal pollution is increasingly recognized. However, the molecular mechanisms of metal homeostasis in these parasites remain unclear as there has been only one genomic study on Acanthocephala species *(Pomphorhynchus laevis*) to date. In the present study, the transcriptome of the freshwater species *Dentitrunces truttae* was assembled *de novo* and analyzed for metal-binding proteins (MBPs). The MBPs were characterized using the PFAM database and MeBiPred software and compared between two acanthocephalans, evolutionarily and lifestyle similar species. Of the entire proteome of *D. truttae*, 14.5 % of the protein sequences were characterized as metal-binding by MeBiPred. According to the PFAM database, most of them were associated with the binding of Zn (mainly zinc finger proteins), comparable to only reported data for *P. laevis*. Phylogenetic analysis of metalloproteases (zinc-binding), iron-sulfur group (iron-binding) and nickel-binding ureases/hydrogenases showed that the analyzed sequences are quite conserved in all selected taxonomic groups, with a particularly high conservation in Acanthocephala and Rotifera. Considering only the specific PFAM groups of proteins known to be involved in metal binding, most *D. truttae* proteins belonged to the PF00005 group (ABC transporters). The protein sequences that could not be described with the PFAM database were divided into three different clusters characterized by a high preference for binding Zn and Cu. Overall, this study represents the first draft of the entire transcriptome of *D. truttae* and provides a basis for further studies on metal homeostasis in Acanthocephala.

ACANTHOCEPHALANS AND POLLUTANTS AFFECT PHYSIOLOGICAL RESPONSES OF AMPHIPODS USED IN ECOTOXICOLOGY

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In a series of exposure studies, we examined how conventionally treated wastewater and environmentally relevant concentrations of the herbicide metazachlor affect the physiological responses of the amphipod *Gammarus fossarum*, infected with the acanthocephalan *Polymorphus minutus* and microsporidians. Responses were measured by mortality rates, biomarker concentrations or activities, and overall locomotor activity. Before sublethal exposure tests with metazachlor, we conducted acute immobility and lethality (EC_{50} and LC_{50}) tests. While *P. minutus* enhanced chemical stress tolerance in *G. fossarum*, microsporidians did not. Acanthocephalan-infected gammarids exhibited significantly higher locomotor activity compared to uninfected ones when exposed to metazachlor, although the herbicide itself had no direct impact on locomotion. Similarly, after exposure to conventionally treated wastewater or river water, *P. minutus* infected gammarids showed increased locomotor activity compared to uninfected individuals. Biomarker responses were primarily directed against chemical exposure but were significantly modulated by parasitic infections in several cases. Our results demonstrate that parasite infections can influence ecotoxicological test outcomes, potentially skewing evaluations of environmental contaminants. Locomotor activity in *G. fossarum* was mainly driven by *P. minutus* infections, while molecular biomarker changes were linked to chemical exposure but influenced by parasites. We recommend that future ecotoxicological assessments consider parasitic infections as a key factor to ensure accurate evaluations of pollutant effects on non-target species.

POSTER PRESENTATIONS

MOLECULAR CHARACTERIZATION AND PHYLOGENY OF *Pomphorhynchus* sp. PARASITIZING LEVANTINE SCRAPER (*Capoeta damascina*) FROM LAKE HULA, ISRAEL

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Acanthocephalans of the genus *Pomphorhynchus* Monticelli, 1905 are primarily intestinal parasites of fish in freshwater ecosystems. Their morphological identification is often challenging due to high intraspecific variability. In this study, we document the first occurrence of an unidentified *Pomphorhynchus* species in the Levantine scraper (*Capoeta damascina*) from Lake Hula, a freshwater body located in the Syrian–African Rift Valley in northeastern Israel. In April 2024, 27 Levantine scrapers were examined for acanthocephalans. Seven juvenile specimens of *Pomphorhynchus* sp. were recovered from the body cavity of four Levantine scrapers (prevalence: 14.8%; intensity: 0.9 worms per fish). DNA was extracted from six isolates, and partial fragments of the mitochondrial *cox*1 gene were amplified and sequenced. These newly generated sequences were aligned with published sequences of *Pomphorhynchus* spp. from several European countries available in GenBank. Phylogenetic analyses using maximum likelihood (ML) and Bayesian inference (BI) based on the *cox*1 dataset revealed that the specimens from Israel formed a distinct clade, sister to a clade containing representatives of *Pomphorhynchus tereticollis* from various European countries, although with low statistical support. Our findings suggest that the specimens of *Pomphorhynchus* from Levantine scrapers should be further examined using an integrative taxonomic approach to determine whether they represent a potential new species in Israel. Finally, further analyses of a larger number of fish species from Lake Hula are required to identify the definitive hosts of this putative new species.

UNDER THE SURFACE: ACANTHOCEPHALAN PARASITES AS BIO-INDICATORS OF ELEMENT ACCUMULATION IN MARINE ECOSYSTEMS

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Elemental exposure resulting from anthropogenic activities in proximity to the marine environment has major impacts on ecosystem health and functioning. A better understanding of ecosystem functioning can be obtained by considering all aspects including the parasites infecting these systems. Parasites (specifically endoparasitic worms) have been reported as promising sentinels for element accumulation, however, there are limited studies for marine environments. This study aimed to determine the elemental concentrations in two marine fish, *Diplodus hottentotus* and *Chelon richardsonii*, and their associated intestinal acanthocephalans. Fish were collected in the infratidal zone at the coastal town of Chintsa and Groot River estuary along the east coast of South Africa, respectively. Five *D. hottentotus* were infected with *Longicollum* sp., while *C. richardsonii* were infected with *Neoechinorhynchus* sp. Fish were dissected and fish and acanthocephalan tissue were frozen for element analysis. A subsample of acanthocephalans was fixed for morphological and molecular identification. Element concentrations were measured in host muscle and liver tissue, as well as in acanthocephalans. Parasite-host element accumulation ratios ranged from 0.04 (Cu) for *Neoechinorhynchus* sp.-*C. richardsonii* in liver to 542 (Cd) for *Longicollum* sp.-*D. hottentotus* in muscle. Data indicate that non-essential elements accumulated significantly higher concentrations in acanthocephalans than their associated host tissue, while concentrations were generally higher in the marine *D. hottentotus* than in the estuarine *C. richardsonii.* The euryhaline character trait of *C. richardsonii* plays a vital role in the bioavailability of elements, which should be considered along with different dietary sources of elements in these host systems.

LINKING ADULTS AND CYSTACANTHS OF A NEW SPECIES OF *Rhadinorhynchus* LÜHE, 1911 (ACANTHOCEPHALA: RHADINORHYNCHIDAE) FROM THE PACIFIC COAST OF MEXICO BY USING MORPHOLOGICAL, ECOLOGICAL, AND MOLECULAR DATA

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During parasitological surveys of marine fishes and zooplankton on the North Pacific coasts of Mexico, 28 Gafftopsail pompano (*Trachinotus rhodopus*) and 50 mysids (*Metamysidopsis frankfiersi*) were found to be infected with adults and cystacanths (larval) of an acanthocephalan respectively. Hologenophores and photogenophores were used to sequence the small (SSU) and large (LSU) subunits of ribosomal DNA and cytochrome c oxidase subunit 1 (*cox 1*) from mitochondrial DNA. Phylogenetic analyses of the new SSU, LSU, and *cox 1* sequence plus published sequences, identified as *Rhadinorhynchus* sp. from the coasts of Mexico form an independent lineage that is recognized herein as a new species, *Rhadinorhynchus pacifica* n. sp. The new species is morphologically distinguished from the other 38 congeners by having a cylindrical long proboscis armed with 16–18 longitudinal rows bearing 12 hooks each. The ecological information obtained through parasites, plus the genetic evidence confirm that the Gafftopsail pompano (*T. rhodopus*) serves as the definitive host appropriate of *Rhadinorhynchus pacifica* n. sp. and that mysid (*M. frankfiersi*) serves as the intermediate host. The current records also reveal that *Rhadinorhynchus pacifica* n. sp., distributed along the Mazatlán coast in northern Mexico reaching to Oaxaca coast in southern Mexico and this distribution corresponds with the Mexican Coastal Current, which extends from the Gulf of Tehuantepec in Oaxaca to the entrance to the Gulf of California.

CONTRASTING ACANTHOCEPHALAN INFECTIONS IN NATIVE VS. NON-NATIVE CRAYFISH INTERMEDIATE HOSTS

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The introduction of new hosts to an environment can alter native host-parasite interactions. We compared acanthocephalan infections of two sympatric crayfish, the native *Procambarus troglodytes,* and its introduced sister species *P. clarkii,* collected in September 2023 and February 2024 in a South Carolina wetland (USA). Cystacanths were identified morphologically and molecularly as polymorphids (*Ibirhynchus dimorpha* and one newly described species). Sex of crayfish did not affect infection parameters. Infection by *I. dimorpha* occurred in both crayfish species. Prevalence was similar between the two crayfish in either month, but significantly lower in February (40.5% (17/42) and 12.5% (4/32) in *P. clarkii* vs 40.7% (11/27) and 4.5% (1/22) in *P. troglodytes*, in September and February, respectively). Mean intensity of infection by *I. dimorpha* was higher in *P. clarkii* (5.9 ± 1.62) than in *P. troglodytes* (1.5 ± 0.26) with no difference between months within each crayfish. In contrast, the new polymorphid was only found in the introduced crayfish, only in September, and always with *I. dimorpha* (11.9% prevalence (5/42); mean intensity 3.2 ± 1.96). This represents the first report of polymorphids in the native *P. troglodytes* and in *P. clarkii* outside of its native range. Although it is unclear if either polymorphid was introduced, the dynamics of these acanthocephalans' lifecycles is clearly impacted by the introduced crayfish as it serves as a host to both species.

BIOGEOGRAPHY OF GUILD POPULATION OF *Andracantha* sp. SCHMIDT, 1975 (ACANTOCEPHALA, POLYMORPHIDAE) IN CHARACIDS (OSTEICHTHYES: CHARACIDAE) OF EL ORO PROVINCE, ECUADOR: LATITUDINAL GRADIENT OF POPULATION DYNAMICS

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We reported, for the first time, *Andracantha* sp. (cystacanths and immature specimens) in freshwater fishes from Ecuador, 148 individuals were examined among three species of fishes of family Characidae (n = 148): *Eretmobrycon* sp. (n = 58)*, Astyanax* sp. (n = 33) and *Rhoadsia* sp. (n = 57). This study aimed to determine the prevalence (P), abundance (A) and geographic distribution along 12 rivers of El Oro Province in Ecuador (sample points). The parasite is present in seven of the twelve rivers sampled. Latitudinal gradient of guild population of *Andracantha* sp. was observed from high prevalence and abundance in fish intermediate and/or paratenic host in south rivers to low ecological indicators in north rivers of El Oro. Different prevalence and abundance between sample points and host fishes was probably relation with different trophic ecology as diet composition and feeding strategies patterns along geographic gradients and probably was influenced by the distribution of piscivorous birds, fishes and aquatic invertebrates that serve as definitive, paratenic and intermediate hosts. El Oro rivers are characterized by the presence of heavy metals, so we could consider that these helminths could be sentinel indicators of contamination and diversity.

Profilicollis altmani AND *Corynosoma australe* IN NORTHERN HUMBOLDT CURRENT SYSTEM: EFFECTS OF EL NIÑO-SOUTHERN OSCILLATION (ENSO) ON NEGLECTED ICHTHYOZOONOSES IN PERU

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"Ceviche" (raw crustaceans and fishes) consumption is widespread among Peruvian population and represent an ichthiozoonotic risk. Cystacanths and inmature stages of acanthocephalans (infectious stage) have been found parasitizing a wide diversity of teleost fishes and crustaceans, and could infect humans due to low host specificity are those capable of switching from one host species to a distantly related one. *Profilicollis altmani* and *Corynosoma australe* are zoonotic acanthocephalans that have been reported in Northern Humboldt Current System. *C. australe* life cycle comprises a community trophic structure of benthic amphipods as intermediate hosts, teleostean fishes (20 marine fish species were reported in Peru) as paratenic hosts, and pinnipeds (*Otaria byronia* was reported in Peru) as definitive hosts, but they have also been found parasitizing cetaceans and waterfowl, include terrestrial mammals as accidental hosts (*Canis lupus familiaris* and *Lycalopex culpaeus* were reported in Peru). *P. altmani* life cycle comprises sand crabs (*Emerita analaga* was reported in Peru) as intermediate hosts and marine birds as definitive hosts (*Larus belcheri*, *Leucophaeus modestus*, *Leucophaeus pipixcan* and *Himantopus mexicanus* were reported in Peru), but they have also been found parasitizing cetaceans and waterfowl, include sea otters as accidental hosts (mice, rats, hamsters, cats and dogs were reported as experimental host in Peru). El Niño-Southern Oscillation impact in biotic (water temperature, salinity, nutrients, sea level and current conditions) and biotic factors (species composition of competitors and predators, migratory patterns, behavior, diet and prey selectivity) indirectly impacts in prevalence and abundance of ichthyozoonotic parasites in Peru.

PHYLOGENETIC STUDY OF ACANTHOCEPHALA BASED ON MITOCHONDRIAL GENOMES, INCLUDING JAPANESE SPECIES

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Recent advances in molecular phylogenetic research in acanthocephalans have been remarkable, leading to significant revisions of the traditional morphology-based classification system and reconsideration of taxonomic traits. However, the branching order among higher taxa remains unclear in many respects, posing challenges for understanding the evolutionary history of morphological and ecological diversification in acanthocephalans. One key reason for this is the limited availability of DNA data, such as the complete mitochondrial genome. In this study, we determined the complete mitochondrial genomes of eight acanthocephalan species collected from Japan and reconstructed phylogenetic trees using protein-coding gene sequences (both amino acids and DNA sequences). While our phylogenetic analysis produced al well-supported tree overall, there remains a lack of complete mitochondrial genome data for species in the families Rhadinorhynchidae and Transvenidae, highlighting the need for future research.

SATELLITOME OF THREE *Acanthocephalus* SPECIES: SEARCHING FOR NEW CYTOGENETIC MARKERS

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Acanthocephalan parasites are often understudied in various scientific fields, and satellitome and cytogenetic studies are no exception. Species of the genus *Acanthocephalus* are known for their very small chromosomes with similar morphology, which makes karyotyping a challenge. In this study, we performed the first satellitome analysis of three *Acanthocephalus* species to identify species- and chromosome-specific satellite sequences (satDNA) that could serve as cytogenetic markers. RepeatExplorer2 revealed notable differences between species, with *A. anguillae* having the highest proportion of repeats annotated as satellite and ribosomal DNA, correlating with previous findings of increased AT-rich heterochromatin and rDNA loci in this species. Moreover, *A. anguillae* showed a clear dominance of one repeat class, whereas the other species had more balanced ratio of repeats. Comparative analysis also revealed some differences between the sexes, with the male genomes showing a higher proportion of satDNA in all species studied. This could be due to the lower satDNA content in the X chromosome compared to the autosomes, resulting in lower satDNA content in females (two X chromosomes). Using fluorescence in situ hybridization, five satellites in *A. anguillae*, two in *A. lucii* and six in *A. ranae* were successfully mapped to chromosomes. Each satellite showed clustered hybridization signals at distinct chromosomal locations, allowing accurate identification of specific chromosomes and homologous pairs. These satellites proved to be valuable chromosomal markers for karyotyping. In addition, the absence of hybridization signals on the supernumerary chromosomes of *A. anguillae* and *A. lucii* supports the hypothesis that they arose recently in these species. This study was supported by the Scientific Grant Agency of the Ministry of Education, Science, Research and Sport of the Slovak Republic and the Slovak Academy of Sciences (VEGA No. 2/0093/23) and Slovak Academy of Sciences grants for PhD students (APP0452).

XI International Symposium on Fish Parasites

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Pérez-Ponce de León G., Aguirre-Macedo L., García-Varela M., Grano-Maldonado M.I., Guillen-Hernández S., Rodríguez-Santiago M.A., Rubio-Godoy M., Vidal-Martínez V. & Iannacone J. 2025. Abstract Book, XI International Symposium on Fish Parasites, ISFP XI-2025, *"Fish Health, Parasites and Biodiversity Conservation"*, January 20th-24th, 2025, Mérida, Yucatán, México. The Biologist (Lima), 2025, Vol. 23, ene-jun. Suplemento Especial 1: S1-S156.

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