BSPP annual scientific meeting

16th of December 2025

Zebrastraat

Zebrastraat 32

9000 Gent

ABSTRACT BOOK

Meeting program

09:30	Registration	
09:55	Welcome word (Carl de Trez, president)	
Session 1 - Chair: Philippe Van den Steen		
10:00	**Keynote 1: dr. John Gilleard** - DIAGNOSTICS, SURVEILLANCE, AND BEYOND: WHERE NEMABIOME SEQUENCING WILL TAKE US NEXT	
10:25	PETRELLIS G	IL-4 RECEPTOR SIGNALING REGULATES LUNG MACROPHAGES DURING HELMINTH COINFECTION RESULTING IN ENHANCED GAMMAHERPESVIRUS PERMISSIVENESS
10:40	PIEDFORT O	ENTERIC HELMINTH INFECTION IMPAIRS THE MEMORY T CELL RESPONSE TO A RECOMBINANT VESICULAR STOMATITIS VIRUS VECTOR VACCINE
10:55	Pitch ITM: Establishment Malaria consortium in Belgium	
11:00	Coffee break	
Session 2 - Chair: Sarah Hendrickx		
11:30	SADLER R	THE ROLE OF COMPLEMENT FACTOR 3 (C3) IN MALARIA-ASSOCIATED ACUTE KIDNEY INJURY
11:45	JACOBS Y	EARLY NEUTROPHIL RESPONSES UPON INFECTION WITH AFRICAN TRYPANOSOMES
12:00	DE CLEENE W	ELUCIDATING THE MOLECULAR BASIS FOR THE RECOGNITION OF HUMAN BASIGIN BY PLASMODIUM VIVAX TRYPTOPHAN-RICH ANTIGENS
12:15	1-minute poster pitches	
12:45	Lunch	
13:40	BSPP statutory meeting	
Session 3 - Chair: Benjamin Dewals		
14:00	**Keynote 2:dr. Susanne Hart** – ASCARIS: HOST INTERACTION AND BACTERIAL COINFECTIO	
14:25	ZENG L	DEVELOPMENT OF A CAMELID SINGLE-DOMAIN ANTIBODY-BASED ANTIGEN DETECTION ASSAY FOR THE PAN-SPECIFIC DIAGNOSIS OF ACTIVE HUMAN AND ANIMAL TRYPANOSOMA BRUCEI INFECTIONS
14:40	ÁLVAREZ-RODRÍGUEZ A	A CRISPR-CAS-BASED RECOMBINASE POLYMERASE AMPLIFICATION ASSAY FOR ULTRA-SENSITIVE DETECTION OF ACTIVE TRYPANOSOMA BRUCEI EVANSI INFECTIONS
15:55	TIRUNEH A	DEVELOPMENT, FIELD-TESTING, AND OPTIMIZING OF A DIAGNOSTIC TOOL TO QUANTIFY SOIL-TRANSMITTED HELMINTH LIFE STAGES IN PIT LATRINE SLUDGE IN JIMMA TOWN, ETHIOPIA
15:10	Coffee break	
Session 4 - Chair: Johannes Charlier		
15:40	**Keynote 3: dr. Cyril Hammoud** – LONG-TERM CHANGES IN WILDLIFE POPULATIONS: INSIGHTS FROM A META-ANALYSIS	
16:05	KATTENBERG E	HIGHLY MULTIPLEXED AMPLISEQ TARGETED NGS ASSAYS FOR MALARIA GENOMIC SURVEILLANCE IN AFRICA
16:20	MABILLE D	EVALUATING THE ANTITRYPANOSOMAL ACTIVITY AND MODE-OF-ACTION OF PYRAZOLOPYRIMIDINES
16:35	SHIGOLEY M	PARASITE DIVERSITY, PATHOLOGY, AND NEGLECT BY LOCAL STAKEHOLDERS IN NILE TILAPIA (OREOCHROMIS NILOTICUS) FROM UPPER TANA RIVER REGION, KENYA
16:50	DE BOCK S	ASSESSMENT OF INTERNAL AND EXTERNAL HELMINTH EGG CARRIAGE BY FLIES FOLLOWING EXPERIMENTAL EXPOSURE
17:00	Break / Award deliberation	
17:15	**Award session and closing remarks** (Avia-Gis, Huvepharma & Zoetis awards)	
17:30	End	

Poster Presentations

GOOSSENS E	EXCESSIVE MORTALITY IN THE CAPE BUFFALO UNDER HIGH ENVIRONMENTAL STRESS - THE ROLE OF TREMATODES AND INVASIVE SNAILS
ANTONOPOULOS A	NEMABIOME AND MIXED AMPLICON METABARCODING FOR SPECIES IDENTIFICATION AND ANTHELMINTIC RESISTANCE SURVEILLANCE: PRELIMINARY RESULTS FROM ON SITE SEQUENCING TRIAL IN GREECE AND POLAND
WIJTEN A	HARNESSING NANOBODIES TOWARDS POINT-OF-CARE TRYPANOSOMIASIS DETECTION
PRESENT C	EXPLORING ANTIGEN PRESENTATION ON BONE MARROW CELLS AFTER LEISHMANIA INFECTION
CRANSHOFF Y	RUXOLITINIB PROTECTS AGAINST MALARIA-ASSOCIATED ACUTE RESPIRATORY DISTRESS SYNDROME
BERGHMANS F	MOLECULAR BASIS FOR INFECTION AND QUIESCENCE OF LEISHMANIA IN THE BONE MARROW
SCHOTTE F	A SYSTEMATIC REVIEW OF AVAILABLE DETECTION METHODS FOR ANISAKID ALLERGENS IN FOOD PRODUCTS
GOES J	TOWARDS SUSTAINABLE WORM CONTROL: FIELD VALIDATION OF A DECISION SUPPORT TOOL FOR TARGETED TREATMENT OF GASTROINTESTINAL NEMATODES IN FIRST-SEASON GRAZING DAIRY CATTLE
DE MEULENAERE K	A PLASMODIUM KNOWLESI A1-H.1 TRANSCRIPTOME TIME COURSE FOCUSING ON THE LATE ASEXUAL BLOOD STAGES
ALI K	PROTEOMIC ANALYSIS AND IDENTIFICATION OF IMMUNOGENIC PROTEINS IN EXCRETORY/SECRETORY MATERIAL OF ASCARIDIA GALLI WORMS: TOWARDS RECOMBINANT-BASED SERODIAGNOSTIC ASSAYS FOR LAYING HENS
VAN DEN BROECK L	IN VIVO SELECTION OF A LEISHMANIA COSMID LIBRARY REVEALS CANDIDATE GENES INVOLVED IN SAND FLY TRANSMISSION
COOLS L	THE BIOINDICATION POTENTIAL OF PARASITIC FAUNA INFECTING MACROINVERTEBRATES IN AFRICAN WETLANDS
DE VOCHT L	IDENTIFICATION OF POTENT SINGLE-DOMAIN ANTIBODIES AGAINST THE MALARIA SPOROZOITE THROUGH SYNTHETIC SINGLE-DOMAIN ANTIBODY LIBRARIES CONTAINING UNCONVENTIONAL DIVERSIFICATION STRATEGIES
BRYS M	HIGH PREVALENCE OF CHORIOPTES BOVIS: AN IMPORTANT FACTOR IN CHRONIC PROGRESSIVE LYMPHEDEMA IN BELGIAN DRAFT HORSES
TOPIC M	DIVERSITY OF PARASITIC COPEPODS FROM ESTUARINE FISHES IN A SOUTH CAROLINA ESTUARY
ABAWARI MJ	EXPLORING THE CONTEXT AND OPPORTUNITIES FOR OPTIMIZING WATER, SANITATION AND HYGIENE FOR THE PREVENTION OF SOIL TRANSMITTED HELMINTHIASIS IN URBAN PRIMARY SCHOOLS: A PHOTOVOICE STUDY, ETHIOPIA
MONSIEURS P	DERMOTROPIC LEISHMANIA DONOVANI IN NEPAL: (RE-) EMERGENCE OF ‘PRUDENT’ PARASITES AND THREAT FOR ELIMINATION?

GEENS R	TRYPTACKLE – TACKLING THE LIVESTOCK PARASITE TRYPANOSOMA CONGOLENSE BY TARGETING INVARIANT SURFACE GLYCOPROTEINS
GABRIEL S	INTEGRATED ANTHELMINTIC-BASED CONTROL OF TAENIA SOLIUM CYSTICERCOSIS/TAENIASIS, SOIL-TRANSMITTED HELMINTHIASIS AND SCHISTOSOMIASIS: SAFETY, EFFECTIVENESS, AND IMPLEMENTATION STRATEGIES: 3SI-CONTROL
ARAUJO S	IMMUNOLOGICAL MECHANISMS OF RESPIRATORY CO-INFECTIONS: THE IMPACT OF TRYPANOSOMES ON SECONDARY INFECTIONS CAUSED BY MAJOR LOWER RESPIRATORY TRACT PATHOGENS
ARAUJO S	UNVEILING GLIAL CELLS IN THE NASAL MUCOSA AS HOST CELLS FOR LEISHMANIA WITH POTENTIAL IMPLICATIONS IN DISEASE OUTCOMES
WONG S	ADAPTIVE CO-EVOLUTION IN VISCERAL LEISHMANIASIS: THE ROLE OF HOST MIF CYTOKINE AND PARASITE MIMICRY
VRANKEN N	FROM SLIDES TO BYTES: DIGITAL PARASITES INNOVATE EDUCATION AND PROMOTE AWARENESS
VAN ACKER L	DEVELOPMENT OF A COST-UTILITY MODEL FOR EPILEPSY MANAGEMENT: INTEGRATING IMMUNODIAGNOSIS FOR NEUROCYSTICERCOSIS DETECTION
MATOKA T	NGAL DIPSTICK AS A PROGNOSTIC MARKER FOR PEDIATRIC MALARIA-ASSOCIATED ACUTE KIDNEY INJURY IN A RESOURCE-LIMITED SETTING
MWANGI H	ROAD TOWARDS SUSTAINABLE ANTHELMINTIC USE IN GRAZING RUMINANTS: INSIGHTS FROM STAKEHOLDER ENGAGEMENT

DIVERSITY OF PARASITIC COPEPODS FROM ESTUARINE FISHES IN A SOUTH CAROLINA ESTUARY

Topić M.[1], Vanhove M.P.M.[1,3], Tkachenko M.[2], Kmentová N.[1,3]

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Copepods are one of the most diverse groups of aquatic organisms, with more than 15 000 accepted species. They can be found in a number of different freshwater and marine habitats. Parasitism has evolved independently in 14 copepod clades; currently, more than 6 000 species of parasitic copepods are known. These crustaceans can be found parasitizing on a range of fish taxa, and in a range of aquatic habitats, including transitional habitats like estuaries. In 2023, a parasite 'BioBlitz' project was conducted in the Stono Preserve, part of the Stono River estuary in South Carolina, USA. The aim of the project was to assess the diversity of different parasitic taxa in that area, and part of the project included sampling of fishes, in order to look into the diversity of fish parasites. For this project, 125 fish specimens of 12 genera (17 species) were caught and inspected for parasites; when it comes to parasitic copepods, members of only 3 genera (four species) were infected: *Fundulus* (*F. heteroclitus*, *F. majalis*), *Menidia* (*Menidia* sp.), and *Mugil* (*M. cephalus*). From these hosts, 18 parasitic copepods were collected and identified based on their morphology and genetic data (sequences of 28S and 18S rDNA, and mitochondrial COI marker). In our samples, we found four species of *Ergasilus* (Ergasilidae), and one per genus for *Bomolochus* (Bomolochidae), *Caligus* (Caligidae), and *Naobranchia* (Lernaeopodidae). From all screened hosts, *M. cephalus* hosted the highest number of species, with one species of *Bomolochus*, two *Ergasilus* species and one species of *Naobranchia* infecting this fish. The diversity of copepod parasites in the Stono Preserve corresponds to previously reported trends in estuarine habitats, with ergasilids as the most species-rich taxon. Furthermore, *Bomolochus* and *Ergasilus* species are new to science, but assessing the relationship of these species to other members of their respective families through molecular methods proves challenging, due to a pronounced gap in available molecular data.

Literature:

Bernot, J. P., Boxshall, G. A., & Crandall, K. A. (2021). A synthesis tree of the Copepoda: integrating phylogenetic and taxonomic data reveals multiple origins of parasitism. PeerJ, 9, e12034. DOI: 10.7717/peerj.12034

Boxshall, G. A., & Halsey, S. H. (2004). An introduction to copepod diversity. The Ray Society, Andover, UK.

De Buron, I., Hill-Spanik, K. M., Atkinson, S. D., Vanhove, M. P. M., Kmentová, N., Georgieva, S., Díaz-Morales, D.M., Kendrick, M.R., Roumillat, W.A., & Rothman, G. K. (2025). ParasiteBlitz: Adaptation of the BioBlitz concept to parasitology. Journal of Helminthology, 99, e39. DOI: 10.1017/S0022149X25000197

Walter, T.C., & Boxshall, G. (2025). World of Copepods Database. Accessed at: https://www.marinespecies.org/copepoda (28 October 2025). DOI:10.14284/356

Diversity of parasitic copepods from estuarine fishes in a South Carolina estuary

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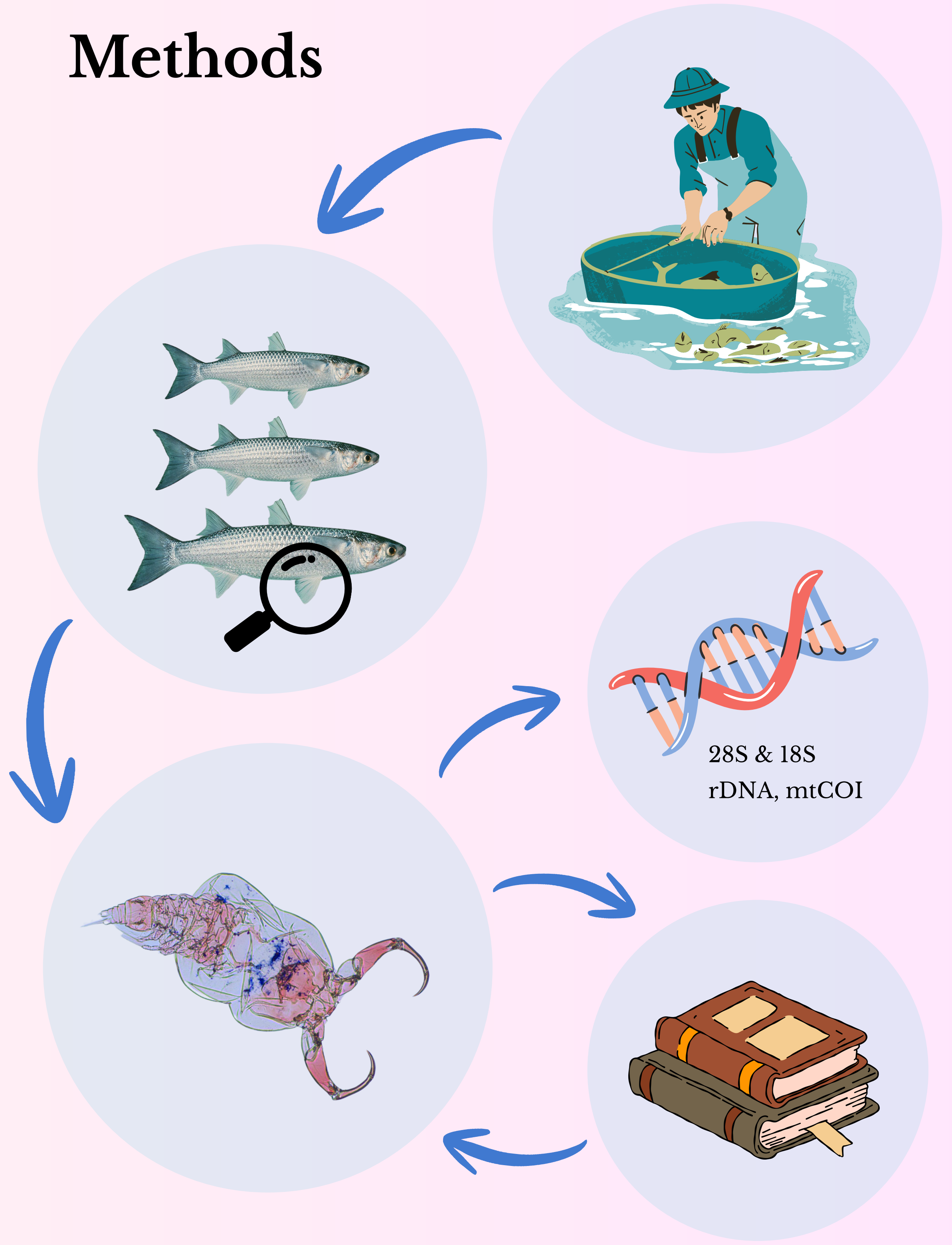
About (parasitic) copepods

- Diverse group of aquatic organisms; more than 15 000 accepted species (the World of Copepods database)
- Inhabiting different freshwater and marine habitats
- Parasitism evolved independently in 14 clades of copepods; more than 6 000 recognized species of parasitic copepods

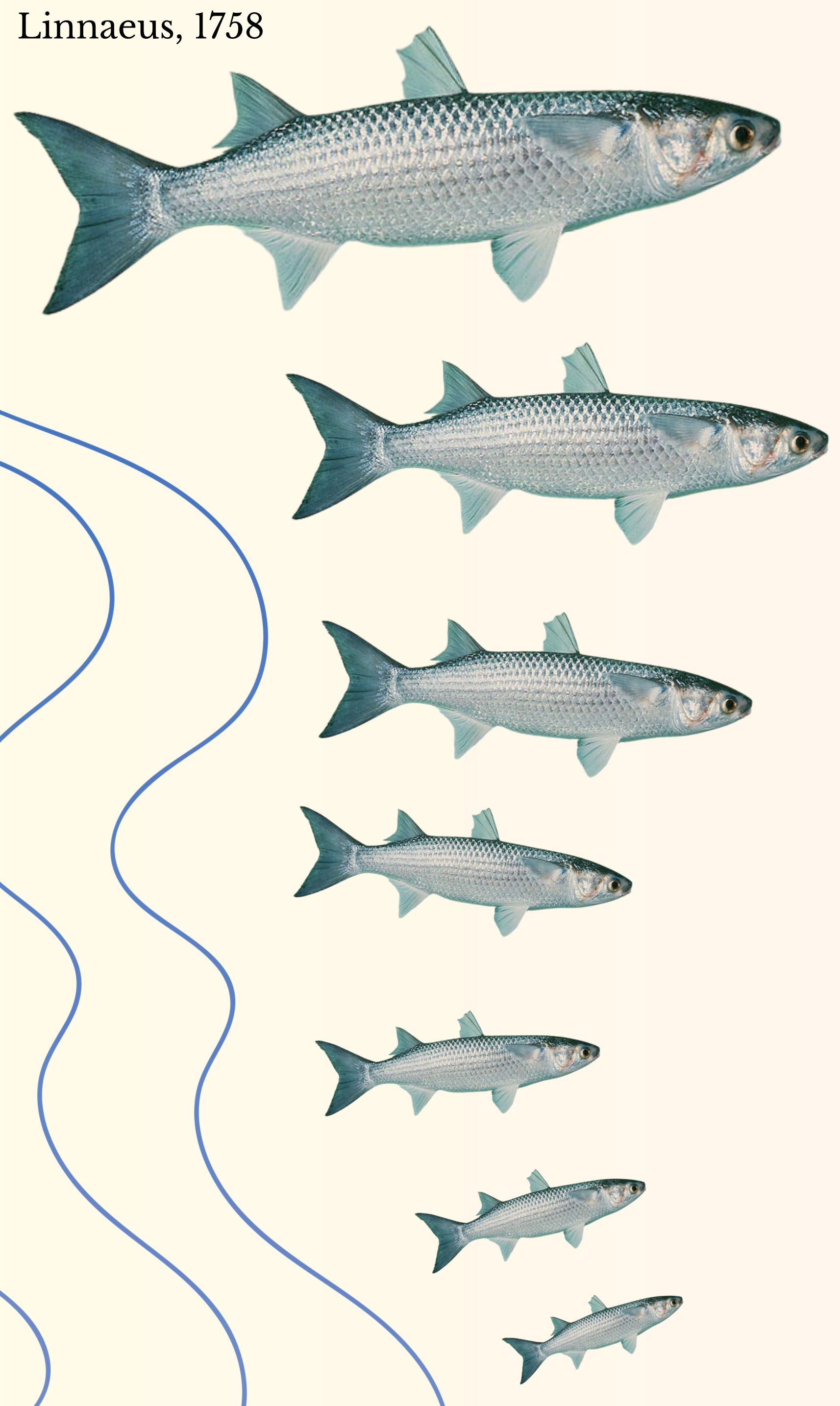
Parasite BioBlitz project

- Conducted in 2023 in the Stono Preserve, South Carolina, USA
- Intense survey of aquatic habitats in order to assess the parasite diversity
- Four connected habitats: wetland, pond, impoundment, creek
- Estuarine fishes sampled for parasites, including parasitic copepods

Methods



Mugil cephalus
Linnaeus, 1758

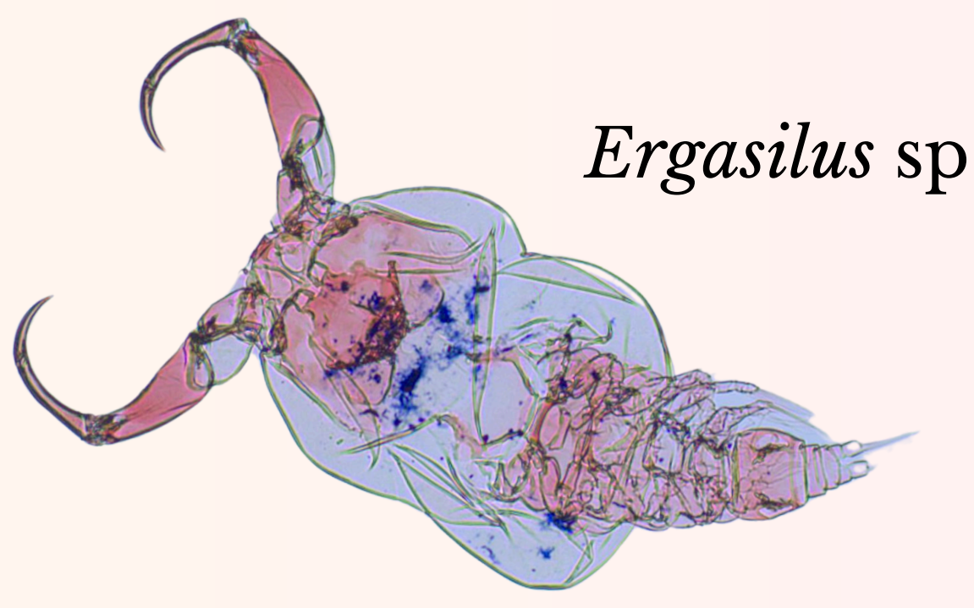


Preliminary results of the study

- 125 fishes (12 genera, 17 species) caught and inspected for parasites
- 18 parasitic copepods collected, from four host species: *Fundulus heteroclitus*, *Fundulus majalis*, *Menidia* sp., *Mugil cephalus*
    - Parasitic copepods belonging to families Bomolochidae (*Bomolochus* sp.), Caligidae (*Caligus* sp.), Ergasilidae (four species of *Ergasilus*), and Lernaeopodidae (*Naobranchia* sp.)
    - Among the molecular data collected from parasitic copepods (Table 1), we found seven distinct 28S haplotypes, three 18S haplotypes and one COI haplotype

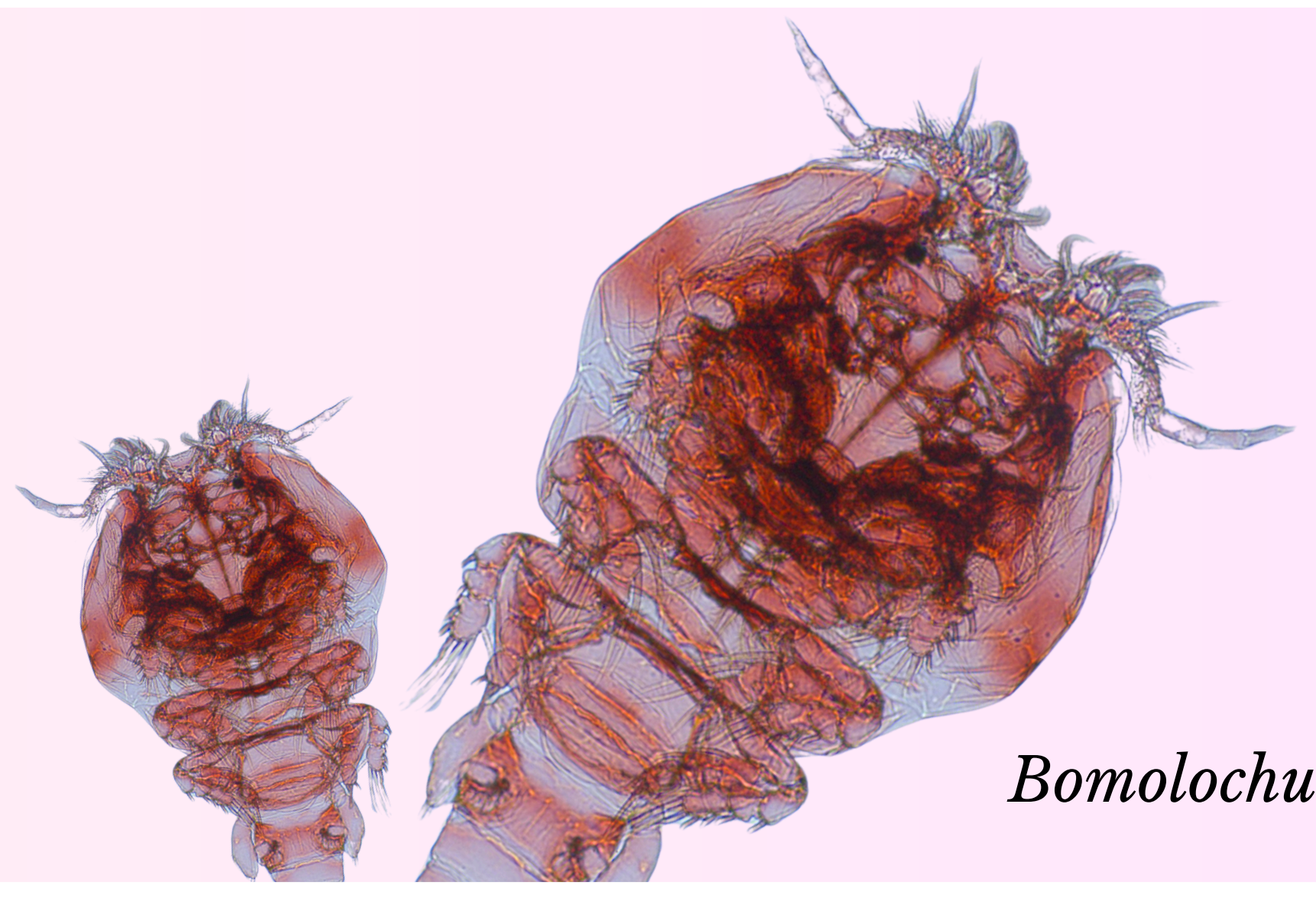
Table 1. Parasitic copepods found, their hosts, and the sequences of genetic markers obtained from parasitic copepods in this study.

Parasitic copepod	Host	Genetic marker sequenced
Bomolochus sp.	*Mugil cephalus*	28S rDNA
Caligus sp.	*Fundulus majalis*	28S rDNA
Ergasilus sp. 1	*Mugil cephalus*	28S rDNA
Ergasilus sp. 2	*Mugil cephalus*	28S & 18S rDNA
Ergasilus sp. 3	*Fundulus majalis,* *Fundulus heteroclitus*	28S & 18S rDNA
Ergasilus sp. 4	*Menidia* sp.	28S & 18S rDNA
Naobranchia sp.	*Mugil cephalus*	28S rDNA, mtCOI



Ergasilus sp. 1

Ergasilus sp. 2



Bomolochus sp.

Conclusions

- Diversity found corresponds to previously reported trends in estuaries
    - Ergasilidae as the most species-rich taxon
    - New species found (Bomolochidae, Ergasilidae)
- Pronounced gap in available molecular data
- Parasite BioBlitz as an effective approach to uncovering diversity of parasitic copepods

Literature:

- Walter, T.C., & Boxshall, G. (2025). World of Copepods Database. Accessed at https://www.marinespecies.org/copepoda on 2025-12-10. DOI:10.14284/356
- Bernot, J. P., Boxshall, G. A., & Crandall, K. A. (2021). A synthesis tree of the Copepoda: integrating phylogenetic and taxonomic data reveals multiple origins of parasitism. PeerJ, 9, e12034. DOI: 10.7717/peerj.12034
- De Buron, I., Hill-Spanik, K. M., Atkinson, S. D., Vanhove, M. P. M., Kmentová, N., Georgieva, S., Díaz-Morales, D.M., Kendrick, M.R., Roumillat, W.A., & Rothman, G. K. (2025). ParasiteBlitz: Adaptation of the BioBlitz concept to parasitology. Journal of Helminthology, 99, e39. DOI: 10.1017/S0022149X25000197

If you find parasitic copepods irresistible and want to talk about the work of our lab on them feel free to contact me!

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See also:

And mini version of the poster:

UHASSELT
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CMK CENTRE FOR ENVIRONMENTAL SCIENCES UHASSELT
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Sea Grant Inside Sea Grant
natural sciences .be
NRF National Research Foundation of Korea
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Belgian Society of Parasitology & Protistology