

Oral Presentations:

WEDNESDAY, June 3rd, 2026 (13:00 to 16:00)

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A shark tapeworm reaches the Mediterranean: intestinal nodules and pathology associated with larval *Anthobothrium* sp. 1 in *Sardinella aurita*

Small pelagic fish play a central role in Mediterranean food webs and are increasingly recognized as key intermediate hosts for trophically transmitted helminths. However, life cycles and pathological impacts of larval cestodes in these hosts remain poorly documented. The round sardinella *Sardinella aurita* is a commercially important pelagic teleost with high trophic connectivity, linking planktonic prey to higher predators such as sharks, and thus represents a potential vector for shark tapeworms. Between 2015 and 2017, 401 specimens of *S. aurita* were collected from the Gulf of Tunis (central Mediterranean) and examined for larval cestodes. Parasites were studied using an integrative approach combining light microscopy, scanning electron microscopy, molecular analyses (LSU rDNA and COI), and histopathology. Larvae were identified as *Anthobothrium* sp. 1 sensu Jensen & Bullard, 2010. LSU rDNA sequences were identical to larvae and adults previously reported from teleosts and carcharhinid sharks in Gulf of Mexico, while COI sequences showed minimal intraspecific divergence. Infections were associated with conspicuous nodular lesions in the pyloric caeca, containing dense aggregations of plerocercoids. Histopathological examination revealed severe tissue alterations: mucosal atrophy, epithelial disorganization, muscular disruption, and marked inflammatory responses, despite sardinella acting as a regular second intermediate host. This study represents the first Mediterranean record of *Anthobothrium* sp. 1, extending its known trans-Atlantic distribution. By integrating parasite pathology within a food-web framework, our findings suggest that the complete life cycle of this shark tapeworm may occur in the Mediterranean and emphasize the ecological and health implications of parasite transmission through pelagic trophic pathways.

- O2. Jorina W. Riegert¹**, Bjoern C. Schaeffner², Harry W. Palm¹

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Diversity of Rhinebothriidea in Icelandic skates: New records and phylogenetic insights

The order Rhinebothriidea characterizes marine elasmobranchs as final hosts. They are characterized by distinctive scolex homologies, notably four bothridia on stalks. Erected on the basis of molecular evidence and morphology, the order currently includes more than 130 species in 27 genera and six families. Although distributed globally and even with few reports from Icelandic waters, rhinebothriideans have so far only been poorly documented from skates in that region. Eight skate species from waters west of Iceland were examined for rhinebothriidean tapeworms. Five taxa were recorded, including *Echeneibothrium bathyphilum* Campbell, 1975 and *Pseudanthobothrium hanseni* Baer, 1956. One species closely resembled *Echeneibothrium canadensis* Keeling and Burt, 1996 but showed a reduced number of loculi. Two further taxa (*Echeneibothrium* sp. A and sp. B) might

represent sibling or undescribed species based on the number and arrangement of loculi. New host records were established for *E. bathyphilum* in *Rajella bigelowi* Stehmann, 1978 and *Rajella fyllae* Lütken, 1887, and for *P. hanseni* in *Rajella bathyphila* Holt and Byrne, 1908. Ribosomal (partial 28S) and mitochondrial (COI) sequences were generated for selected taxa. Phylogenetic analyses revealed that specimens of *Pseudanthobothrium* fall within a clade with members of *Echeneibothrium*, with intergeneric genetic distances comparable to intrageneric variation, challenging current generic boundaries. A new project integrates morphological and molecular data from the North Atlantic and tropical Indo-Pacific, museum collections, and newly collected material of Rhinebothriidea. The aim is to establish reliable diagnostic characters and genetic thresholds for species boundaries, clarify phylogenetic relationships, and improve our understanding on host–parasite associations.

O3. Gabriel N. Ferreira¹, Bjoern C. Schaeffner², Peter D. Olson³, Haseeb S. Randhawa^{1,4}

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Parasite fauna of icelandic skates (Rajiformes: Rajidae): what is known, what is missing, and what do to next.

Fifteen skate species are known to occur in Icelandic waters. However, information on their parasites remains scarce. Recent records note that a total of 28 parasite species have been recorded from only three of these skate species, accounting for almost 70% of the total known parasite fauna of Icelandic chondrichthyans. Evidently, a vast majority parasites remain to be discovered. Our study aimed to expand this number. To this effect, we reviewed literature regarding chondrichthyan parasite species records in Icelandic surrounding waters and performed parasite assessments on some skate species. A total of 269 publications were examined for the review, 27 (10%) of which specifically referenced Iceland. Of these, 4 skate species included parasite records in Iceland. For our parasite assessments, a total of 101 individuals were examined. Ten skate species were identified, namely *Amblyraja radiata*, *A. hyperborea*, *Bathyraja spinicauda*, *Dipturus batis*, *D. intermedius*, *Malacoraja kreffti*, *M. spinacidermis*, *Rajella bigelowi*, *R. fyllae*, and *R. lintea*. Various parasites were recovered including the trematode *Otodistomum veliporum*, the nematode *Anisakis* sp., and seven cestode morphotypes from the genera *Echinobothrium* (1), *Rockacestus* (1), *Zyxibothrium* (1), *Echeneibothrium* (2), *Pseudanthobothrium* (1), and *Grillotia* (1). Future molecular work and parasite species (re-)descriptions will enable host specificity assessments. Our results raise the total number of Icelandic skate species assessed for parasites by 9, highlighting the need to investigate the remaining species for their parasites. This not only will enhance our knowledge on Icelandic marine parasites and their interactions with chondrichthyans but also provide a baseline for future research.

O4. Xaver Neitemeier-Duventester¹, Endang Wulandari Suryaningtyas², Alejandro López-Verdejo³, Francisco Esteban Montero³, Harry Palm¹

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Worms of the Devil - Trypanorhyncha fauna of Devil rays with a closer look on *Mobula mobular* (Bonnaterre, 1788) from Spain and *M. thurstoni* (Lloyd, 1908) from Indonesia.

The genus *Mobula* (Bonnaterre, 1788), which is distributed worldwide in tropical and temperate waters, contains eight species. Little is known about the parasite fauna of these planktivorous species. Only few studies of Trypanorhyncha from manta rays have been published to date. In 2025, a mass stranding of *M. mobular* (Bonnaterre, 1788) was observed on Spanish beaches. The reasons for this unusual event are unknown, but the parasite fauna of these rays was investigated in an attempt to find the causes for this tragedy. Several thousand cestode specimens were detected in the spiral valve and other organs of these rays. One new *Mobulocestus* Campbell and Beveridge, 2006 species was found and awaits description. Further identification work will probably reveal further so far undescribed Trypanorhyncha species. Earlier studies of two individuals of *M. thurstoni* (Lloyd, 1908) from the Lombok Strait in Bali, Indonesia, shed more light into the cestode fauna of this species. Already eight species of Trypanorhyncha could be identified, among them a new genus (*Archaenybelina* Suryaningtyas, Neitemeier-Duventester, Damriyasa, Frank, Haseli and Palm, 2025) including the two species *A. mimicricestus* Suryaningtyas, et al., 2025 and *A. pseudotetrabothrialis* Suryaningtyas, et al., 2025. One further new species, *Hemionchos arthanai* Suryaningtyas, Neitemeier-Duventester, Damriyasa, Haseli and Palm, 2025 was also identified. These studies demonstrate helped to better understand the trypanorhynch species diversity inside these interesting rays and also the morphological variability of armature patterns in *Hemionchos* species.

05. Harry W. Palm¹, Xaver Neitemeier-Duventester¹, Mohammad Haseli²

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Trypanorhynch cestodes from the Meguro Parasitological Museum, Japan

Deposited material of the cestode order Trypanorhyncha Diesing, 1863 in the Meguro Parasitological Museum, Tokyo, Japan, is identified. Because the majority of the material was collected either in Japanese waters, Western Pacific, or belongs to the Yamaguti collection of marine fish parasites from Hawaii, Central Pacific, we provide new data from a less studied tapeworm order and geographical region. Three new tentaculariid species are newly described, and *N. manazo* Yamaguti, 1952, *N. pintneri* Yamaguti, 1934 and *Pterobothrium hira* Yamaguti, 1952 are redescribed. New drawings and confocal laser scanning microscopy add further information on details of the armature and hook morphology. Information on a total of 55 trypanorhynch species, including 21 tentacularioids, 5 eutetrarhynchoids, 8 gymnorhynchoids, 16 lacistorhynchoids and 5 otobothrioids, is herewith provided for material of the Meguro Parasitological Museum collection. Registration numbers are given for trypanorhynch species deposited inside the Museum, mainly from the extensive collection of S. Yamaguti and S. Kamegai in Japan and Hawaii. Together with accepted records from the literature, so far 34 trypanorhynch species can be confirmed from Japanese and adjacent waters, including 13 tentacularioids, 3 eutetrarhynchoids, 6 gymnorhynchoids, 9 lacistorhynchoids and 3 otobothrioids. The high number of tentaculariids, oceanic and deep-water species makes the north-western Pacific unique among other parts of the world Oceans.

06. Masoud Nazarizadeh^{1,2}, Jan Štefka^{1,2}

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Beyond barcoding genes: Cryptic diversity and species delimitation in the *Ligula intestinalis* species complex (Cestoda: Diphylobothriidea) using genomic SNP and mitochondrial data

Ligula intestinalis (Cestoda: Diphylobothriidea) is a globally distributed parasite with a complex life cycle involving copepods as first intermediate hosts, planktivorous fish as second intermediate hosts, and fish-eating birds as definitive hosts. Although the parasite infects a wide range of hosts and occurs across multiple continents, species lineages within the *L. intestinalis* complex are morphologically very similar, making species boundaries difficult to identify using morphological

characters. To investigate potential cryptic diversity within this complex, we applied an integrative molecular species-delimitation framework using mitochondrial DNA (COI, Cyt b and ND1) and genome-wide SNP data obtained through ddRAD sequencing from samples collected across a broad geographic range. Species boundaries were assessed using several complementary delimitation approaches, including the Generalized Mixed Yule Coalescent model (GMYC), Bayesian Poisson Tree Processes (bPTP), Assemble Species by Automatic Partitioning (ASAP), and Bayes Factor Delimitation (BFD) under the multispecies coalescent model. Across methods and datasets, species-delimitation analyses consistently supported the presence of multiple independently evolving lineages within the *L. intestinalis* complex. Conservative interpretation of the results indicates the existence of at least ten candidate species distributed across different geographic regions and host groups. Despite the absence of clear morphological traits for both plerocercoids and adult worms, these lineages show strong genetic divergence, indicating extensive species diversity within the complex, with several taxonomically recognized, but hard to distinguish species (e.g. *L. alternans*, *L. pavlovskii*), and several cryptic species. These results highlight the importance of integrative genomic species-delimitation approaches for accurately defining species boundaries in morphologically conserved parasite taxa.