

Oral Presentations:

THURSDAY, June 4th, 2026 (13:00 to 15:00)

07. Anna J. Phillips¹

¹ Department of Invertebrate Zoology, National Museum of Natural History, Smithsonian Institution, Washington, DC, USA

Developing a baseline of diversity and specificity of avian cestodes in eastern North America

A major challenge for studying avian cestodes is accessing host specimens since birds are in decline worldwide due to human activity and climate change and collecting permits are becoming more difficult to obtain. The Smithsonian's National Museum of Natural History has a sizable collection of birds from Audubon's Lights Out program in Washington, DC; birds collected during migrations that died after striking windows. While not ideal for systematic study, morphological vouchers paired with genetic data of the worms from this opportunistic sampling of birds are being used to identify Operational Taxonomic Units (OTUs) and develop baseline data of host associations. These results will direct future collecting efforts to obtain high-quality cestode specimens for systematic description and characterization. In a preliminary study, at least five individuals of the six most common bird species were examined. Cestode prevalence was highest in Common Yellowthroat (*Geothlypis trichas*) and White-throated Sparrow (*Zonotrichia albicollis*), although surprisingly no Ovenbirds (*Seiurus aurocapilla*) were infected. Cestodes were more prevalent in Common Yellowthroat and Gray Catbird (*Dumetella carolinensis*) in the spring and White-throated Sparrow, Yellow-bellied Sapsucker (*Sphyrapicus varius*), and Song Sparrow (*Melospiza melodia*) in the fall. Genome skimming detected at least five OTUs of cestodes, all appearing to be members of either Dilepididae or Paruterinidae. This work maximizes the scientific knowledge gained from these birds in the spirit of the Extended Specimen Concept. Further, this research demonstrates how museums can work with participatory science programs to access otherwise difficult to obtain vertebrate specimens while facing the biodiversity crisis.

08. Jan Brabec¹, Masoud Nazariadeh¹, Tomáš Scholz¹, Roman Kuchta¹

¹ Institute of Parasitology, Biology Centre of the Czech Academy of Sciences, České Budějovice, Czech Republic

The early evolution of the Cestoda from the perspective of transcriptomes

Reconstructing the evolutionary history of tapeworms has been a longstanding challenge. Although combined analyses of nuclear ribosomal RNA genes and mitochondrial genomic data have progressively clarified relationships among major lineages, molecular phylogenetics of the group has seen little methodological advance over the past decade. Several deep nodes remain poorly resolved or unstable, including the phylogenetic position of the Caryophyllidea — the non-proglottised, monozoic tapeworms widely regarded as the earliest-diverging eucestode order — and the broader sequence of early divergences among non-proglottised, partially proglottised and bothriate lineages. Genome-wide data, now routinely applied to resolve deep divergences across the tree of life, have not previously been brought to bear on cestode phylogeny. Here we address this gap through transcriptome sequencing of representatives of all major basal cestode lineages and apply rigorous phylogenomic methods to produce the first transcriptome-based reconstruction of early cestode evolution, revealing genome-wide insights into the origins and diversification of the group's principal lineages.

O9. Kaylee S. Herzog^{1,2*} and Sara V. Brant²

¹Department of Biology, University of New Mexico, Albuquerque, NM, USA

² Museum of Southwestern Biology, University of New Mexico, Albuquerque, NM, USA

Highlighting the cestode holdings of the Museum of Southwestern Biology Division of Parasites

The Museum of Southwestern Biology Division of Parasites (MSBP) at the University of New Mexico houses the third-largest collection of parasites in North America. Established in 2011, the MSBP is steadily building a reputation as a world-class repository for parasite natural history specimens. The division's diverse holdings include helminth collections with notable strengths in mammal and seabird hosts from the Arctic and Antarctic; small mammal hosts from the desert Southwest, US; raptor hosts from the Midwest, US; and gastropod hosts from around the world. In total, the division holds over 10,000 cestode specimens preserved using a variety of methodologies (e.g., permanent slides for light microscopy, histological sections, formalin- and ethanol-persevered worms and host tissues) and encompassing a considerable breadth of ordinal diversity. Remarkably, over 70% of MSBP cestode holdings come directly from the life's work of Robert and Virginia Rausch. Many of these species, particularly those from high-latitude regions, are from hosts that are now considered threatened or endangered. As modern recollection of these hosts and their parasites becomes increasingly challenging or even impossible, access to historical specimens becomes ever more valuable. Here, we will highlight the various cestode specimens deposited in the MSBP, demonstrate how to search divisional holdings via the Arctos online collection management information system, and provide guidelines for requesting loans and depositing new specimens. Our goals are to encourage the use of MSBP specimens in ongoing research and to identify opportunities for the MSBP to meet the needs of the growing international community of cestode systematists.

O10. Fečová Z¹, Marková A¹, Orosová M¹

¹ Institute of Parasitology, Slovak Academy of Sciences, Hlinkova 3, 040 01 Košice, Slovakia

From Repeatome to Cytogenetics: Chromosomal Mapping of U1 snDNA, 5S rDNA and a Satellite DNA in *Caryophyllaeus laticeps* (Caryophyllidea)

Parasitic flatworms (Platyhelminthes), particularly cestodes, remain poorly studied cytogenetically, largely due to the limited number of species examined and the limited set of chromosomal markers available. The development of new markers using the RepeatExplorer2 approach provides an effective way to expand cytogenetic resources in this group. In this study, we combined bioinformatic, cytogenetic, and molecular approaches to characterise the repetitive DNA fraction of *Caryophyllaeus laticeps*. Repetitive elements were identified and quantified using RepeatExplorer2, a computational tool available on the Galaxy platform. The method performs unsupervised graph-based clustering of short next-generation sequencing reads to detect and classify repetitive elements, including transposable elements and tandem repeats, without requiring prior genome assembly, enabling their annotation and quantification even from low-coverage data. Our analysis showed that transposable elements represent the predominant component of repetitive DNA in the *C. laticeps* genome. Among Class I elements, Long Interspersed Nuclear Elements were the most abundant, followed by Long Terminal Repeat elements, including Ty3/Gypsy and Penelope. Selected abundant repeat families were subsequently mapped onto chromosomes using fluorescence in situ hybridisation (FISH), revealing predominantly dispersed hybridisation patterns. We identified three novel chromosome-specific markers: small nuclear U1 DNA, 5S ribosomal DNA, and a satellite DNA designated ClatSat14-167. Each marker hybridised to a single locus on a different chromosome pair, enabling reliable identification of three chromosome pairs. Expanding the repertoire of repeat-derived chromosomal markers and their mapping by FISH is an essential step toward expanding cytogenetic data and will be crucial for future comparative and evolutionary studies of tapeworm genomes.