The 100th Annual Meeting of the American Society of Parasitologists



ASP thanks the following individuals & organizations for their generous suppport:

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Thanks to Everyone Who Helped Make this Meeting Possible ...

The American Society of Parasitologists gratefully acknowledges the following for their support, sponsorship, and hard work in putting together this year's annual meeting.

ASP Local Organizing Committee

Kelli Sapp (ksapp@highpoint.edu)
Herman Eure (eure@wfu.edu)
Regina Joice Cordy (cordyrj@wfu.edu)
Skylar Hopkins (skylar_hopkins@ncsu.edu)
Vickie Hennings (em@editorialmanager.com)

Scientific Program Officers

Susan Perkins & Kirsten Jensen (amsocparasit.meetings@gmail.com)

American Society of Parasitologist's Discrimination Policy

Statement of Policy: In accordance with the bylaws of the American Society of Parasitologists (ASP), the Society will afford an environment free from discrimination, harassment, and retaliation. The ASP will not tolerate actions, statements, or contacts that discourage the free expression and exchange of scientific ideas. This includes unequal treatment or harassment of any person based on their age, gender, gender identity or expression, marital status, sexual orientation, race, color, national or ethnic origin, religious identifications, beliefs or practices, disabilities, veteran status, or any other reasons or expressions that are unrelated to their scientific merit. Harassment, sexual or otherwise, shall be considered as a form of misconduct and violators will be subject to disciplinary actions, including expulsion from a society function or from the society itself.

Definition of Sexual Harassment: Sexual harassment refers to unwelcome sexual advances, requests for sexual favors, and other verbal or physical conduct of a sexual nature. Sexual harassment does not refer to occasional compliments of a socially acceptable nature. It refers to behavior that is not welcome, is personally offensive, debilitates morale, and therefore, interferes with a collegial atmosphere. The following are examples of behavior that, when unwelcome, may constitute sexual harassment: sexual flirtations, advances, or propositions; verbal comments or physical actions of a sexual nature; sexually degrading words used to describe an individual; a display of sexually suggestive objects or pictures; sexually explicit jokes; unnecessary touching. What is perceived as acceptable to one person may be unwelcome by another. Those who have positions of authority or higher rank should be aware that others may be reluctant to outwardly express objections or discomfort regarding unwelcome behavior or language.

Other Types of Harassment: Remarks and behaviors based on other protected characteristics are also unacceptable to the Society. These include stereotyping, slurs, derogatory jokes or statements, and any hostile or intimidating acts.

Policy Scope: This policy applies to all attendees and participants at ASP meetings and functions, including social functions, tours, or off-site activities during the course of meetings and functions, and includes all members, guests, staff, contractors, and exhibitors.

Reporting an Incident: If any individual covered by this policy believes that they have experienced or witnessed harassment or bullying they should contact the Society's designated individual (**Dr. Ashleigh Smythe, smytheab@vmi.edu)**. No complainant will be required to discuss any incident with a respondent; no respondent will be required to discuss any incident with a complainant. All individuals (complainant or respondent) may bring an accompanying individual of their choice with them for support at any point when they discuss the matter with the Society's designated individual, or during any course of an ensuing investigation.

Because allegations of discrimination, harassment and misconduct are sensitive matters with the potential to negatively impact the reputation of individuals, institutions, and/or our Society, confidentiality and discretion throughout the process is expected from all parties involved and is assured from the ASP's designated individual and all involved in the investigation.

Regardless, a complainant may speak in confidence with the Society's designated individual without involving an official report, an investigation or a respondent. All complaints that are received will be treated seriously, and will be addressed promptly if that is the wish of a complainant. Any incidents of sexual assault should be immediately reported to the police. Note that many local and regional governments also consider a variety of behaviors to be reportable crimes regardless of the wishes of the complainant, respondent or of the Society.

Investigation: Following the official report of an incident, the Society's designated individual, in consultation with ASP Council, will name an impartial investigator; usually an elected officer or Council member, and the respondent will be promptly notified. No one who has a conflict of interest with respect to the complainant or respondent will serve in this role. A complainant will be asked to file a formal written complaint; the respondent will be notified immediately and prior to any discovery procedures. A respondent will be invited to respond to the complaint and allowed to bring evidence. The Council of ASP reserves the right to interview other individuals as witnesses at its own discretion. The investigator is allowed to seek counsel if they are in doubt as to how to proceed.

When the investigation is complete, the findings will be communicated to the elected officers, as well as both to the complainant and respondent. Those officers without a conflict of interest will decide on appropriate disciplinary actions.

Retaliation: The Society will not tolerate any form of retaliation against individuals who report an incident, against those who are subject to a complaint, nor against those who participate in an investigation. Retaliation will be considered a form of discrimination in and of itself and offenders will be subject to disciplinary action, up to and including ejection from the Society.

Disciplinary Action: If an individual harasses, retaliates, or knowingly makes a false claim, they will be subject to disciplinary action. These actions might range from a verbal warning to a request to leave the meeting or function without refund of fees and a reporting of the incident to the person's employer. Should repeated complaints, patterns of inappropriate behavior, or other events emerge, the Society's by-laws permit its Council to exclude and eject members through a process that has no appeal.

Appeal & Questions: Should any person be dissatisfied with the result of an investigation or disciplinary action, they may appeal to the President of the Society, or to the highest-ranking officer without a conflict of interest. Questions concerning the policy can be directed to an ASP officer or the ASP designated individual.

Program & Abstracts

Welcome!!

We would like to welcome you to the 100th Annual Meeting of the American Society of Parasitologists (ASP).

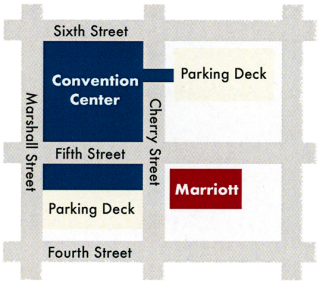
The ASP is a diverse group of approximately 500 scientists from industry, government, and academia who are interested in the study and teaching of parasitology. Founded in 1924, ASP members have contributed not only to the development of parasitology as a discipline, but also to primary research in systematics, medicine, molecular biology, immunology, physiology, ecology, biochemistry, behavior, and more.

Scientific Program Officers

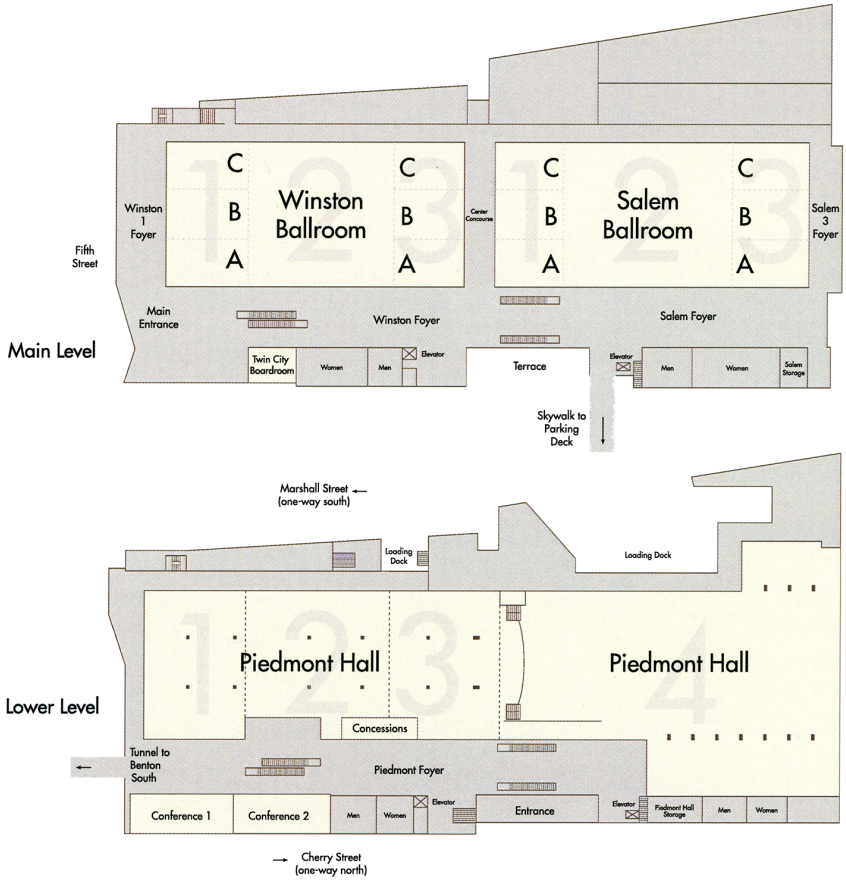
Susan Perkins & Kirsten Jensen (amsocparasit.meetings@gmail.com)

Map of Meeting Rooms

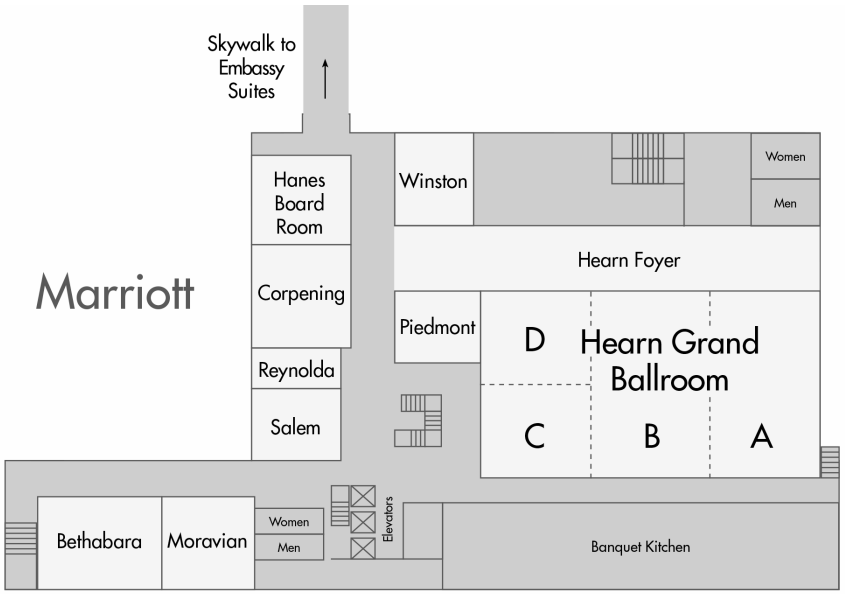
The BENTON CONVENTION CENTER
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General Schedule

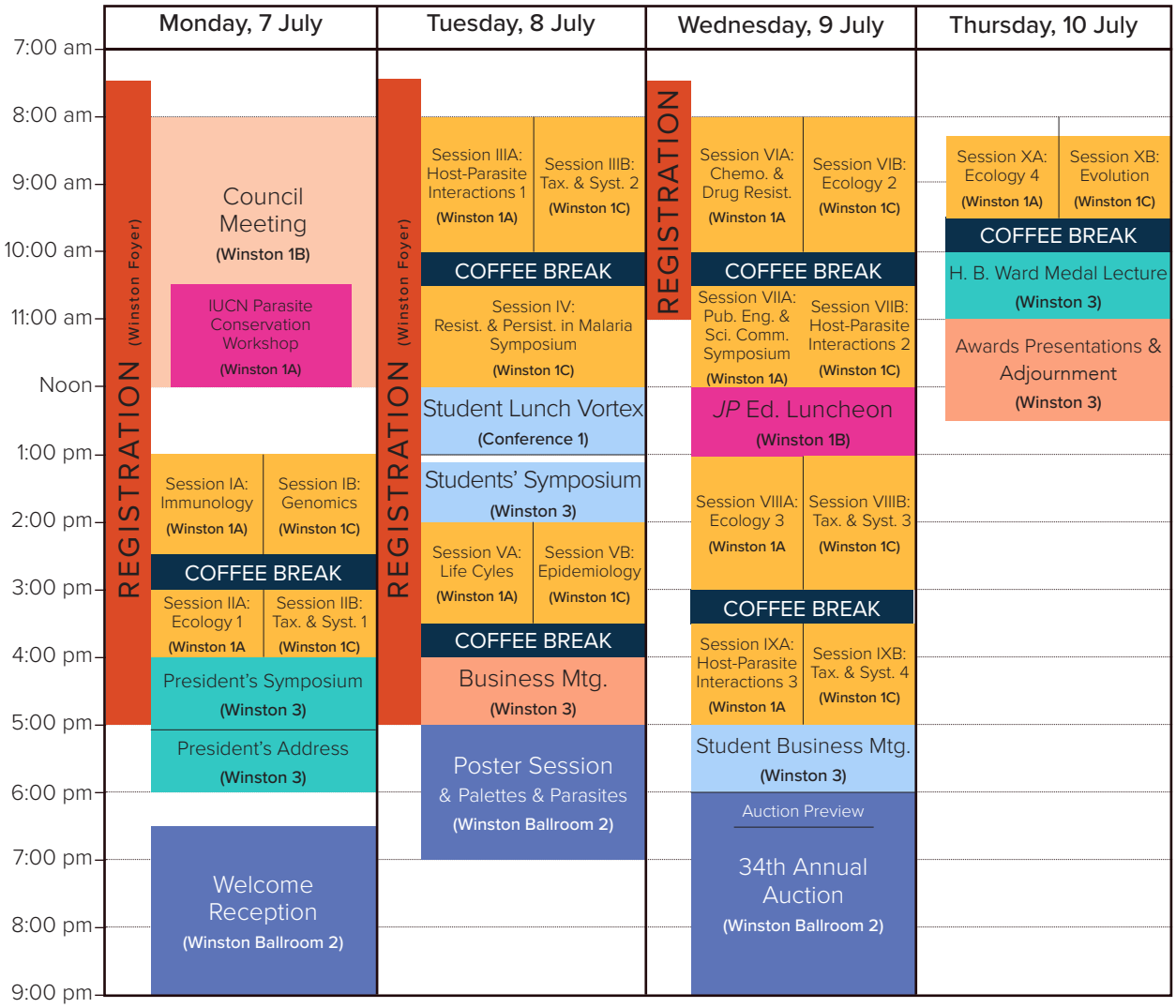
Day/Times	Activity/Function	Room/Space
Monday, 7 July		
7:30 am–5:00 pm	Registration	Winston Foyer
8:00 am–Noon	Council Meeting	Winston 1B
10:30 am–Noon	IUCN Parasite Conservation Workshop	Winston 1A
1:00–2:30 pm	Session IA: Immunology	Winston 1A
1:00–2:30 pm	Session IB: Genomics	Winston 1C
2:30–3:00 pm	Coffee Break	Winston Foyer
3:00–4:00 pm	Session IIA: Ecology 1	Winston 1A
3:00–4:00 pm	Session IIB: Taxonomy & Systematics 1	Winston 1C
4:00–5:10 pm	President's Symposium	Winston 3
5:10–6:00 pm	President's Address	Winston 3
6:30–9:00 pm	Welcome Reception	Winston Ballroom 2
Tuesday, 8 July		
7:30 am–5:00 pm	Registration	Winston Foyer
8:00–10:00 am	Session IIIA: Host-Parasite Interactions 1	Winston 1A
8:00–10:00 am	Session IIIB: Taxonomy & Systematics 2	Winston 1C
10:00–10:30 am	Coffee Break	Winston Foyer
10:30–Noon	Session IV: Resist. & Persist. in Malaria Symposium	Winston 1C
Noon–1:00 pm	Student Lunch Vortex	Conference 1
1:10–2:00 pm	Students' Symposium	Winston 3
2:00–3:30 pm	Session VA: Life Cycles	Winston 1A
2:00–3:30 pm	Session VB: Epidemiology	Winston 1C
3:30–4:00 pm	Coffee Break	Winston Foyer
4:00–5:00 pm	Business Meeting	Winston 3
5:00–7:00 pm	Poster Session & Palettes & Parasites	Winston Ballroom 2
Wednesday, 9 July		
7:30–11:00 am	Registration	Winston Foyer
8:00–10:00 am	Session VIA: Chemotherapy & Drug Resistance	Winston 1A
8:00–10:00 am	Session VIB: Ecology 2	Winston 1C
10:00–10:30 am	Coffee Break	Winston Foyer
10:30–Noon	Session VIIA: Pub. Eng. & Sci. Comm. Symposium	Winston 1A
10:30–Noon	Session VIIB: Host-Parasite Interactions 2	Winston 1C
Noon–1:00 pm	*Journal of Parasitology* Editorial Luncheon	Winston 1B
1:00–3:00 pm	Session VIIIA: Ecology 3	Winston 1A
1:00–3:00 pm	Session VIIIB: Taxonomy & Systematics 3	Winston 1C
3:00–3:30 pm	Coffee Break	Winston Foyer
3:30–5:00 pm	Session IXA: Host-Parasite Interactions 3	Winston 1A
3:30–5:00 pm	Session IXB: Taxonomy & Systematics 4	Winston 1C
5:00–6:00 pm	Student Business Meeting	Winston 3
6:00–9:00 pm	Auction Preview & Auction	Winston Ballroom 2

Thursday, 10 July

8:15–9:30 am	Session XA: Ecology 4	Winston 1A
8:15–9:30 am	Session XB: Evolution	Winston 1C
9:30–10:00 am	Coffee Break	Winston Foyer
10:00–11:00 am	H. B. Ward Medal Lecture	Winston 3
11:00 am–12:30 pm	Awards Presentations* & Adjournment	Winston 3

*Awards being presented include the Distinguished Service Award, the Ashton Cuckler New Investigator Award, the Best Student Presentation Awards, and the Marc Dresden Student Travel Grant Awards.

Schedule Overview



NOTE TO PRESENTERS

Please upload your presentation as early as possible—preferably the day before your session. If presenting in the morning, upload by 7:45 am; for afternoon talks, upload by 12:45 pm at the latest.

Detailed Schedule

Monday, 7 July 2025

● student presentation in the Best Student Presentation Competition

7:30 am–5:00 pm	Registration	Winston Foyer
8:00 am–Noon	Council Meeting	Winston 1B
10:30 am–Noon	IUCN Parasite Conservation Workshop	Winston 1A

Organizer: Skylar Hopkins (North Carolina State University)

Introduction to the process used to conduct assessments for the IUCN Red List, including examples of parasites that have been accessed by the IUCN SSC Parasite Specialist Group (PSG). (Preregistation required.)

1:00–2:30 pm — Sessions IA & IB

	Session IA: Immunology — Winston 1A Presiding: Reginal Blaylock (University of Southern Mississippi); Philip Loverde (University of Texas Health)	Sesson IB: Genomics — Winston 1C Presiding: James Bernot (University of Connecticut); Margaret Doolin (University of Massachusetts Boston)
1:00 pm	**(1) Dorien Mabille, Kayhan Ilbeigi, Kevin Lamote, Guy Caljon** The journey of tsetse transmitted trypanosomes: from the skin invasion to systemic infection	● **(7) Elizabeth Zeldenrust, Ricardo Camarinho, John Barta** Mitochondrial mayhem: Mitochondrial genome rearrangements in the genus *Klossiella*
1:15 pm	● **(2) Isabel Roddy, Ben Hanelt** Immunity under pressure: lysozyme-mediated immune response to parasitic infection in the house cricket, *Acheta domesticus*	**(8) Jan Janecka, Matthew Jevit, Martin Nielsen, Brian Davis, Terje Raudsepp** Horizontal gene transfer between *Parascaris* spp. and equids of equine testis-specific transcripts massively amplified on horse X and Y chromosomes
1:30 pm	● **(3) Daniel Gordillo, Anna George, Bernard Kuhajda, Steven Ksepka, Haley Dutton, Kamila Mora, John Brule, Stephen Bullard** Histopathology and molecular detection of a pathogenic infection of *Mycobacterium gordonae* among captive-held, federally-endangered laurel dace, *Chrosomus saylori* (Leuciscidae: Laviniinae) from a closed recirculating aquaculture system	**(9) Kaylee Herzog, Savanna Randi, Dickson Osabutey, Jeffrey Sumboh, Christina Paraggio, Martina Wade, Richard Bungiro, Irene Owusu Donkor, et al.** This worm is just right: using "Goldilocks" sample types for population genomics in the human hookworm (*Necator americanus*)
1:45 pm	● **(4) Philip Yeboah, Demilade Ibiwoye, Thaciane Lorenzo, Muhammad Hassan, Lisa Bielke** Alterations in ileal microbiota of turkey poults following *Eimeria* vaccination	● **(10) Natasha Slawnych, Larsen Iorgovitz, Alexandre Léveillé, Perryn Kruth, Sara Terier, Winter Kraemer, John Barta** Reeling in the genomes: molecular characterization of fish-infecting *Goussia* species
2:00 pm	● **(5) Ania Bialic** Interrogation of *Entamoeba histolytica* in a human intestinal tissue microphysiological system	● **(11) Zach Pella, Kaylee Herzog, Joseph Fauver** From sample to expression: extracting, annotating, and analyzing *Necator americanus*
2:15 pm	**(6) Gul Ahmad** Diagnosis of *Toxoplasma gondii* in cat (*Felis catus*) populations in Southeast Nebraska	**(12) Scott Cain** BRC Analytics: a new Bioinformatics Resource Center

2:30–3:00 pm — Coffee Break — Winston Foyer

3:00–4:00 pm Sessions IIA & IIB

	Session IIA: Ecology 1 — Winston 1A **Presiding:** Derek Zelmer (University of South Carolina Aiken) Kelly Weinersmith (Rice University)	Session IIB: Taxonomy & Systematics 1 — Winston 1C **Presiding:** F Agustín Jiménez (Southern Illinois University) Chris Whipps (SUNY College of Environmental Science and Forestry)
3:00 pm	● (13) Kevin Lievano-Romero, Miguel Rodriguez-Posada, Scott Gardner Exploring hyperparasitism: the virome of ectoparasites of Colombian bats	● (17) Kamila Cajiao-Mora, John Brule, Haley Dutton, José Caicedo-Portilla, Stephen Bullard Description of a new species of *Acanthostomum* Looss, 1899 (Digenea: Cryptogonimidae) infecting the aquatic coral snake, *Micrurus surinamensis* (Cuvier, 1817) (Serpentes: Elapidae) from the flooded rainforest habitat of the Yahuarcaca Lake System (Amazon River, Colombia)
3:15 pm	(14) Roman Kuchta, Rachel Paterson, Oddgeir Andersen, Juan Balbuena, Isabel Blasco-Costa, Cyril Hammoud, Kamil Hupało, Florian Leese, et al. IMPACT – Integrated monitoring of parasites in changing environments	(18) John Hnida Local fauna as a key resource for advancing coccidian taxonomy (and one's career)
3:30 pm	● (15) Santiago Escobar-Alfonso, Haley Dutton, Frank Williams, Jim Hedrick, Stephen Bullard A state-wide survey for Infectious Pancreatic Necrosis Virus (IPNV) in kidney and spleen of young-of-the-year, wild-caught rainbow trout, *Oncorhynchus mykiss* and brook trout, *Salvelinus fontinalis* in West Virginia Appalachian streams	● (19) Timothy Picozzi, Florian Reyda, Morgan Fleming, Jessica Ozner When best laid plans of worms and men: an investigation of the description and type series of *Neoechinorhynchus strigosus*
3:45 pm	(16) Valerie McKenzie, Rowan Martin, Kim Labuschagne Gut microbes as a novel forensics tool in wildlife trafficking	(20) Vasyl Tkach, Tyler Achatz Current state of knowledge and re-evaluation of the system of the Diplostomoidea

4:00–5:10 pm President's Symposium — Winston 3

Legacy in the making: museums as future gifts through investment
Presiding:
Sara Brant (University of New Mexico)

4:00 pm	Opening remarks
4:05 pm	(21) Anna Phillips Putting the parasite first: the extended specimen concept in parasitology
4:25 pm	(22) Alejandro Oceguera-Figueroa, Luis García-Prieto The Mexican National Helminth Collection as a promoter of scientific research
4:45 pm	(23) James Bernot Exploring parasitic copepod evolution with phylogenomic methods and advanced imaging
5:05 pm	Closing remarks

Monday, 7 July 2025

5:10–6:00 pm | President's Address | Winston 3A–C

Presiding:
Erika Ebbs (Purchase College, State University of New York)

5:10 pm **Erika Ebbs (Purchase College, State University of New York)**
Introduction of President Sara Brant

5:20 pm **Sara Brant, President**
Exploring a century of parasitological stewardship



6:30–9:00 pm | Welcome Reception | Winston Ballroom 2

Tuesday, 8 July 2025

● student presentation in the Best Student Presentation Competition

7:30 am–5:00 pm Registration Winston Foyer

8:00–10:00 am Sessions IIIA & IIIB

	Session IIIA: Host-Parasite Interactions 1 Winston 1A Presiding: Joanna Cielocha (Rockhurst University) Nicholas Negovetich (Angelo State University)	Session IIIB: Taxonomy & Systematics 2 Winston 1C Presiding: Vasyl Tkach (University of North Dakota) Timoth Ruhnke (West Virginia State University)
8:00 am	● **(24) Allison Bryant, Matthew Bolek** A sticky situation: the distinct morphology of coccidian oocysts from pet store squamate reptiles	**(32) Liam Landry, Natasha Slawnych, Elizabeth Zeldenrust, John Barta** Mitochondrial data deficiency in Adeleorina and related Coccidia: bridging gaps in apicomplexan phylogenomics
8:15 am	● **(25) Alyssa Bolger, John Shea, Jansen Julian, Joseph Poggi, Madison Ustohal, Rylie Leffingwell, Cole Salgado, Amy Worthington** Understanding the behavior of *Gryllus firmus* and *Acheta domesticus* infected with *Paragordius varius* in the presence of shelter and water	● **(33) Haley Dutton, Stephen Bullard, Louis Du Preez, Anita Kelly** Redescription of *Polystoma nearcticum* Paul, 1935 (Monogenoidea: Polystomatidae) infecting urinary bladder of Cope's gray treefrog, *Dryophytes chrysoscelis*, from an Alabama beaver pond
8:30 am	**(26) Marliese Truter, Takudzwa Madzivanzira, Josie South, Nico Smit, Aline Acosta** Co-introduction of temnocephalans with the red clawed crayfish into the Barotseland floodplain, Zambia	● **(34) Morgan Fleming, Florian Reyda, Kaylee Herzog** A deeper look at hooks: inter-relationships among neoechinorhynchid acanthocephalans
8:45 am	● **(27) Matthew Moser, Michelle Castelletto, Ruhi Patel, Elissa Hallem** Elucidating the function of astacin metalloproteinases during skin penetration in the soil-transmitted nematode *Strongyloides stercoralis*	● **(35) John Brule, Micah Warren, Stephen Bullard** Redescription of *Benedeniella posterocolpa* (Hargis, 1955) Yamaguti, 1963 (Capsalidae Baird, 1853: Entobdellinae Bychowsky, 1957) with novel sequences and specimens infecting cownose rays (Rhinopteridae spp.) and a giant manta, *Mobula birostris* (Walbaum, 1792) (Mobulidae) and a phylogenetic analysis of Capsalidae
9:00 am	● **(28) Rhianna Metcalf, Scott Gardner, Allison Hearty** *Mathevotaenia* (Cestoda: Anoplocephalidae) from *Galenomys garleppi* (Rodentia: Cricetidae) on the Altiplano of Bolivia	● **(36) Netanya Williams, James Bernot, Geoffrey Boxshall** Rethinking *Pseudotaeniacanthus* diversity: the elongated body form and its unusual attachment site
9:15 am	**(29) Daniel Metz, David Chang van Oordt, Andrea Graham, Clay Cressler** Initial immune conditions predict nematode within-host dynamics	**(37) Veronica Bueno, Janine Caira, Kirsten Jensen, Elizabeth Jockusch, Jill Wegrzyn** Overcoming challenges in taxon-dense tapeworm phylogenomics
9:30 am	● **(30) Rokeya Ahmed, Bryan McLean, Joseph Cook, Kurt Galbreath, Timothy Odom, Stephen Greiman** Cestode diversity of *Sorex* shrews (Eulipotyphla: Soricidae) from Mongolia	**(38) Micah Warren, Steven Ksepka, Stephen Bullard** Hatching fish blood fluke eggs, miracidial morphology, and pathology of an innominate chimaerohemecid (Digenea: Chimaerohemecidae) infecting gills of smooth butterfly rays, *Gymnura micrura* from Mobile Bay, Gulf of America
9:45 am	● **(31) Sara Terier, Natasha Slawnych, Alexandra Pratt, John Barta** Genetic insights into *Lankesterella* blood parasites: evidence of multiple genotypes in Eastern European songbirds	● **(39) Laila Richards, Dmitry Apanaskevich, Stephen Greiman** Improving tick systematics of the subgenus *Scaphixodes* of the genus *Ixodes* (Acari: Ixodidae)

Tuesday, 8 July 2025

10:00–10:30 am	Coffee Break	Winston Foyer
10:30–Noon	Sessions IV	Winston 1C

Session IV: Resistance & Persistence in Malaria Symposium

Organizer & presiding:
Regina Cordy (Wake Forest University)
Cameron Sherlock (Wake Forest University)

10:30 am	Opening remarks
10:35 am	**(45) Akhil Vaidya** New antimalarials targeting ion and lipid homeostasis in parasites
11:00 am	**(46) Dennis Kyle** Persisters and K13-independent artemisinin resistance in *Plasmodium*
11:25 am	**(47) Regina Cordy** Variation in host microenvironment physiology and its impact on *Plasmodium* replication
11:50 am	Closing remarks

Noon–1:00 pm	Student Lunch Vortex	Conference 1
1:10–2:00 pm	Students' Symposium	Winston 3

Parasite Conservation

Organizer & presiding:
Allison Bryant (Oklahoma State University), ASP Student Representative

1:10 pm	Opening remarks
1:15 pm	**(48) Skylar Hopkins** The IUCN SSC Parasite Specialist Group and next steps for international parasite conservation
1:30 pm	**(49) Ben Hanelt, Matthew Bolek** Seedbanks for symbionts: preserving parasitic diversity in a changing world
1:55 pm	Closing remarks

2:00–3:30 pm Sessions VA & VB

	Session VA: Life Cycles — Winston 1A Presiding: Florida Reyda (SUNY Oneonta) Ashleigh Smythe (Virginia Military Institute)	Session VB: Epidemiology — Winston 1C Presiding: John Hawdon (The George Washington University) Julia Buck (University of North Carolina Willmington))
2:00 pm	(50) Luis Cervantes, Kate Sheehan Sunfish parasites in western Maryland, USA.	● (56) Ashley McDonald, Jennifer Schultze, Clayton Nielsen, F Agustín Jiménez Prevalence and distribution of zoonotic pathogens in raccoons (*Procyon lotor*) of northern Illinois
2:15 pm	● (51) Jessica Rotolo, John Barta The life cycles of *Eimeria* species: simple or sophisticated biological strategies?	(57) Charles Faulkner, Vina Faulkner, Autumn Brehm-Goldberg Estimated incidence of canine heartworm infection, *Dirofilaria immitis*, in Claiborne County, Tennessee USA
2:30 pm	(52) Kelly Weinersmith A history of reports of self-experimentation in the *Journal of Parasitology* from 1914–1924	● (58) Beth Cohen, Perryn Kruth, Taylor Lane, John Barta Development of a probe-based RT-qPCR assay to determine *Eimeria tenella* oocyst viability
2:45 pm	● (53) Molly Kennedy, Melanie Langford, Allison Durland-Donahou, Gabriel Langford Hidden in plain sight: combining morphological and molecular tools to study cestode diversity in young-of-the-year bull sharks *Carcharhinus leucas*, with notes on some of their life cycles	● (59) Luke Niemann, Christina Anaya A comparison of parasites in native and invasive snakes in South Florida
3:00 pm	● (54) Taylor Lane, Beth Cohen, Perryn Kruth, Liam Landry, Daniel Lindo, Jessica Rotolo, Natasha Slawnych, Sara Terier, et al. Variation of extrachromosal genome copy numbers of *Eimeria tenella* throughout its life cycle	(60) Reginald Blaylock, Robert Gonzales, Eric Saillant Detection of the dinoflagellate *Amyloodinium ocellatum* in simulated field conditions
3:15 pm	(55) Matthew Bolek, Ben Hanelt, Sara Brant The vegetarian and the blood feeder: evolution of trematode herbivores	

3:30–4:00 pm Coffee Break — Winston Foyer

4:00–5:00 pm Business Meeting — Winston 3

Presiding:
Sara Brant (University of New Mexico)

● student presentation in the Best Student Presentation Competition

5:00–7:00 pm | Poster Session | Winston Ballroom 2

Poster I: Taxonomy & Systematics

● **(130)** René Monzalvo, **F Agustín Jiménez**

A checklist in the diversity, distribution, and host interactions of *Trichuris* spp. (Nematoda: Trichuridae), with a meta-analyses in the intraspecific morphological similarities and variation in diagnostic traits in the genus

● **(131)** Maggie Young, **Tyler Achatz, Jeffrey Bell, Zoe Von Holten, Stephen Greiman, Eric Pulis, Simona Georgieva, Vasyl Tkach**

Diversity and interrelationships of diplostomids (Digenea: Diplostomoidea) parasitic in kingfisher

(132) Christopher Whipps, **Lamjed Mansour, Violetta Yurakhno**

Diversity and host specificity of *Kudoa* species (Myxosporea: Multivalvulida) in fishes of the world

● **(133)** Jafet Hernadez, **Tim Ruhnke**

Mitochondrial genome sequencing of rhinebothriidean and phyllobothriidean tapeworms

● **(134)** Katherine Hanselman, **Kirsten Jensen**

Steppingstones to resolving "*Polypocephalus*"

● **(135)** Sydnie McMahan, **Noraida Martinez-Rivera, Kirsten Jensen**

An investigation into cercarial morphology and anatomy using scanning electron and confocal microscopy

● **(136)** Denise Garcia Salas, **Christina Anaya**

From morphology to molecular: establishing a DNA barcoding framework for hairworm (phylum Nematomorph) identification

Poster II: Host-Parasite Interactions & Epidemiology

(137) Jamshaid Iqbal

Cysticercosis/*T. solium* taeniasis, a potential public health concern in non-endemic country, Kuwait: a new diagnostic method to screen *T. solium* taeniasis carriers among the expatriate population

(138) Sophie Willett, **Sonja Olson, Chase Nelson, Rachel Horejsi, Nicolas Wheeler**

Transcriptomic, behavioral, and morphometric differences between *Schistosoma mansoni* miracidia recovered from different host tissues

(139) Saige Maasz-Seawright, **Sophie Willett, Nicolas Wheeler**

Developing *Girardia dorotocephala* as a model organism for flatworm sensory biology

Poster III: Chemotherapy & Drug Resistance

● **(140)** Chase Nelson, **Rachel Horejsi, Saige Maasz-Seawright, Nicolas Wheeler**

A novel device for high-throughput phenotypic screening of schistosome miracidia enables identification of transient receptor potential (TRP) channels modulators that impact miracidia behavior

● **(141)** Fernanda Fumuso, **Nicolas Villarino, Roberta O'Connor**

Tartrolon E: a new drug candidate against apicomplexan parasitic diseases

(142) Ozge Yilmazli, Murat Hokelek

In vitro anti-leishmanial activity of *Nigella sativa* and *Zingiber officinale* against *Leishmania infantum*

Poster IV: Hosts, Parasites, and Microbiomes

● **(143)** Keri Mitchell, **Sara Weinstein**

The nematode microbiome

● (144) Tryphena Adams, Chester Joyner, MaHPIC Consortium, Rabindra Tirouvanziam, Alberto Moreno, Mary Galinski, Regina Cordy

Clinical phase-specific gut microbiota remodeling in *Plasmodium knowlesi*-infected macaques

Poster V: Education

(145) Ana Garcia Vedrenne

Specifications, bundles, and tokens—Oh my! My journey into alternative grading

Poster VI: Vector Biology

(146) Avery De Ruyter, Helen Gensch, Nicolas Wheeler

Integrated sensory behaviors of larval *Aedes triseriatus* and *Aedes aegypti*

● (147) Piper Zellner, Lisa Brown

Temporal dynamics of midgut pH and serine protease activity in *Ctenocephalides felis*

Poster VII: Ecology

(148) Elizabeth Field, Leticia Giron, Roberto Gomez III, Karen Stopani, Mary Janecka

Habitat degradation muddles sexual signals: disentangling infection, pollution, and sexual selection in *Lepomis* spp. in the Rio Grande Basin

● (149) Mackenzie Grover, Marlon Cobos, Kurt Galbreath, Jocelyn Colella

The importance of no data: Presence and absence data better informs ecological niche models of parasites

(150) Calli Wise, Emma Palmer, Leone Yisrael, Karson Burton-Reeder, Katrina Pagenkopp Lohan

River otters (*Lontra canadensis*) consume many parasites, highlighting the role of directly transmitted parasites in the trophic transfer of energy

● (151) Briana Zaffiro, Eloy Martinez, David Kerstetter, Christopher Blanar

The effect of endoparasites on the thermal tolerance of small fishes

(152) Matthew Bolek, Aryanna Carr, Allison Bryant, Stacey Herriage, Jason Belden, Matteo Minghetti

Impact of mining-derived metal contamination on fish parasites at Tar Creek Superfund Site, Oklahoma

(153) Ephigénie Dione, Cheikh Seck, Jeanne Diouf, Malick Diouf

Ecological parameters of nematode parasites of freshwater fish in the Senegal and Gambia rivers

(154) Julia Davis, Ellie Olsen, Kate Sheehan

From infection to connection: parasites in food webs

● (155) Ellie Olsen, Caleb Amacker, Brian Dorr, Mark Smith, Luke Roy, Kate Sheehan

Endoparasite communities of aquaculture-foraging waterbirds

Poster VIII: Parasite Distributions

● (156) Elizabeth Kays, Kate Sheehan

Observing parasitic diversity in Canadian coastal birds

● (157) Zak Davidson, Kate Sheehan

Comparative parasitology of marine and freshwater loons: what bycatch reveals about loon parasite diversity

(158) Ace Kevin Amarga, Zih-Ting Chang, Yen-Han Chen, Ming-Chung Chiu

First record of the subcutaneous avian mite *Hypodectes propus* (Nitzsch, 1861) (Acari: Hypoderatidae) in Taiwan

● (159) Cameron Gonzalez, Jasmine Sevilla-Mcchargue, Alexis Hernandez, Tamara Cook

Seasonality of gregarine infections in *Enallagma civilie*

● (160) Victor Shr, Alexandria Nelson, Jeff Beane, Skylar Hopkins

Helminth parasites of native North Carolina pit vipers: diversity and host associations

● **(161)** Allison Johnston, **Jacquelyn Salguero, Wilson Freshwater, Julia Buck**

Snake eels (family Ophichthidae) as pseudoparasites of predatory fish

● **(162)** Connor McCowan, **Christina Anaya**

Comparing the parasite fauna of cane toads (*Rhinella horribilis*) originating from three regions of Florida

(163) Kaitlin Gallagher

Survey of water mites parasitizing mosquitoes in central Florida

● **(164)** Caley Chun, **Tyler Achatz, Maggie Young, Jim Page, Matthew Rowe, Caroline Cooper, Laura Wenk, Vasyl Tkach**

Initial detection of rat lungworm, a human pathogen, in invasive snails in Georgia

● **(165)** Marisa Manning, **Christina Anaya**

Prevalence and distribution of parasites infecting canines and felines in Southwest Florida

● **(166)** Delaney Long, **Florian Reyda**

A survey of the parasites of *Morone saxatilis* (striped bass) in the Hudson River, New York

● **(167)** Nina Haag, **Tyler Brock, Christina Anaya**

First report of horsehair worms (phylum Nematomorpha) from plethodontid salamanders in North America

● **(168)** Zoe Von Holten, **Joshua Anderson, Bryan McLean, Stephen Greiman**

Collaborative field collections of *Sorex* shrews in North Carolina uncover novel cestode diversity

● **(169)** Alexia Hilber, **Christopher Blanar, David Kerstetter**

Endoparasite community of the invasive grey-headed swamphen (*Porphyrio poliocephalus*)

(170) Mary Hawkins, Cameron Searfoss, Allison Bryant, **Kristen Baum, Matthew Bolek**

Development and distribution of a pathogenic neogregarine (*Ophryocystis elektroscirrha*) in monarch butterflies

(171) Martin Wolf, Anindo Choudhury

The summer and winter parasite fauna of an apex predatory fish, *Esox lucius* (Northern Pike), from two lakes in Wisconsin, USA.

(172) Megan Studer, Mofolusho Falade

Cryptosporidium in grey squirrels on Transylvania University campus, Lexington, KY

(173) Gabriel Langford, **Katie Brittan, Spencer Asperilla, Bridgette Ward**

A parasite survey of lizards on Andros Island, Bahamas: Do *Anolis* ecomorphs host different assemblages of parasites?

Wednesday, 9 July 2025

● student presentation in the Best Student Presentation Competition

7:30–11:00 am — Registration — Winston Foyer

8:00–10:00 am — Sessions VIA & VIB

	Session VIA: Chemotherapy & Drug Resistance — Winston 1A Presiding: Charles Faulkner (Lincoln Memorial University) Sam Loker (University of New Mexico)	Session VIB: Ecology 2 — Winston 1C Presiding: Kate Sheehan (Frostburg State University) Brandon Ruehle (Peru State College)
8:00 am	● (62) Elise McKean, Damien O'Halloran, John Hawdon Evidence of linked macrocyclic lactone and benzimidazole resistance in the dog hookworm *Ancylostoma caninum*	● (70) Allison Hearty, Gabor Racz, Nyamsuren Batsikhan, Scott Gardner Helminth parasites of Mongolian swifts
8:15 am	(63) Rachel Wheeler, Chase Nelson, Saige Maasz-Seawright, Nicolas Wheeler Quantitative ethology of schistosome miracidia characterizes a conserved snail peptide that inhibits infection	● (71) Garrett Maggio, April Blakeslee, Krista McCoy, James Byers, Jason Williams, Iris Segura-Garcia, Sarah Goodnight, Michael McCoy Evidence of host ecology within the population genetic structure of a unique parasitic trematode
8:30 am	● (64) Kayhan Ilbeigi, Dorien Mabille, An Matheeussen, Rik Hendrickx, Nick Van Reet, Roel Anthonissen, Fabian Hulpia, Cai Lin, et al. Combating animal trypanosomiasis: a dual focus on antiparasitic activity and (eco)toxicity of novel nucleoside leads	● (72) Grace Kokasko, Julia Buck Quantifying the direct and indirect effects of the bopyrid isopod, *Probopyrus pandalicola*
8:45 am	● (65) Mary Piaskowski, Rachel Bone Relat, Priscilla Winder, Amy Wright, Roberta O'Connor Investigating a novel, deep-sea derived natural product as a potential treatment for apicomplexan parasite infections	(73) Hannah Brunelle, Matthew Ogburn, Andrew Davinack, Emma Palmer, Ruth DiMaria, Patricia Santos-Ciminera, Robert Aguilar, Katrina Pagenkopp Lohan Richness and abundance of parasites infecting and consumed by striped bass (*Morone saxatilis*) varies spatially and ontogenically in the Chesapeake Bay
9:00 am	(66) Sevan Alwan, Ramiz Shaheed, Alexander Taylor, Stanton McHardy, Michael Cameron, Philip LoVerde Preclinical impact of a novel compound for *Schistosoma* therapy	● (74) Irvin Arroyo-Torres, Thomas Turner, Lisa Barrow, Ariadna Torres, Takuma Shiina, Layla Denee, Grace Carmona-Yong, Sara Brant The investigation of riparian parasite spillover and spillback in the Southwestern United States
9:15 am	● (67) Miranda Gough, Robert Charvat Mechanistic insights into ip-BPZ as an antiparasitic against *Toxoplasma gondii*	● (75) Alexandria Nelson, Abigail Finch, Victor Shr, Jeff Beane, Michael Cove, Kenzie Pereira, Skylar Hopkins Non-invasive methods for describing internal parasite communities: a metabarcoding case study
9:35 am	(68) Elise McKean, John Hawdon, Damien O'Halloran Drug repurposing to combat naturally emerging resistance in hookworm	● (76) Alaina Young, Alora Hooper, Amelia Haymond, Tara Stewart Merrill, Thomas Miller, R Dean Grubbs Marine tapeworm communities in blacktip sharks: patterns, prevalence, and parasite diversity
9:45 am	(69) Catherine Jackson, Elise McKean, John Hawdon Differential emodepside efficacy and drug-resistant and drug-susceptible *Ancylostoma caninum* highlights variability in potassium channel activity	(77) Ryan Koch, Axel Hoarau, Tryssa de Ruyter, Caitlin Duffy, Lucie Pascarosa, Mary Jo Casalena, Erica Miller, Jay Armstrong, et al. Wild turkey infectious disease prevalence across Pennsylvania landscapes

10:00–10:30 am | Coffee Break | Winston Foyer

10:30 am–Noon | Sessions VIIA & VIIB

	Session VIIA: Public Engagement & Science Communication Symposium Winston 1A **Presiding:** Ania Bialic (University of Wisconsin) Kelly Weinersmith (Rice University) Sara Weinstein (Utah State University)	**Session VIIB: Host-Parasite Interactions 2** Winston 1C **Presiding:** Nicolas Wheeler (University of Wisconsin-Eau Claire) Matthew Bolek (Oklahoma State University)
10:30 am	(78) Ania Bialic Food, health & livelihood in Northeast Thailand	● (84) Alexander Bell, Nicholas Negovetich Assessing the role of chemoreception in parasite avoidance in the acute bladder snail *Physa acuta* from Sunset Pond in San Angelo, Texas
10:45 am	(79) Skylar Hopkins Using social media for public engagement with parasites	(85) Joanna Cielocha, Debra Clopton, Richard Clopton Gregarines parasitizing redshanked and redwinged grasshoppers in Colorado and New Mexico
11:00 am	(80) Janine Caira Shining a positive light on parasites	● (86) Daniel Lindo, Ryan Snyder, Perryn Kruth, Taylor Lane, Julia Whale, John Barta Diagnosing coccidiosis: coupling species identification and enumeration of mixed *Eimeria* species infections via probe-based qPCR
11:15 am	(81) Jayne Raper, Floor Grootenhuis The power of the residency: creating new pathways that foster collaboration and community between art and science	● (87) Jacquelyn Salguero, Sebrina Brooks, Tiffany Keenan, D Wilson Freshwater, Julia Buck Molecular characterization and co-evolutionary relationships of *Crassicauda* spp. (Nematoda: Spirurida) infecting cetaceans of the Northwest Atlantic
11:30 am	(82) Kelly Weinersmith, John Janovy, Jr. Navigating the world of book publishing	● (88) Marisa Manning, Christina Anaya Body development in *Acheta domesticus* (Orthoptera: Gryllidae) infected with the hairworm, *Paragordius varius* (Phylum: Nematomorpha)
11:45 am	(83) Kelli Sapp Increasing community accessibility to the natural sciences using High Point University's Mobile Lab	(89) Ace Kevin Amarga, Richard Robbins, Takafumi Nakano, Ming-Chung Chiu An overview and recent updates on the ectoparasites associated with the herpetofaunas of Taiwan and the Philippines

Noon–1:00 pm | *Journal of Parasitology* Editorial Luncheon | Winston 1B

1:00–3:00 pm Sessions VIIIA & VIIIB

	Session VIIIA: Ecology 3 — Winston 1A Presiding: Sara Weinstein (Utah State University) Roman Kuchta (Czech Academy of Sciences)	Session VIIIB: Taxonomy & Systematics 3 — Winston 1C Presiding: Veronica Bueno (University of Connecticut) Tyler Achatz (Middle Georgia State University)
1:00 pm	**(90) Jeffrey Bell, Timothy Driscoll, Tyler Achatz, Jakson Martens, Jefferson Vaughan** Molecular survey of haemosporidian parasites in hawks, falcons, and owls from Minnesota and North Dakota, with remarks on the phylogenetic relationships of haemosporidians in North American raptors	● **(98) Felix Berrios Ortega, Geoffrey Boxshall, James Bernot** Towards clarity in caligids: imaging and an interactive identification key for *Lepeophtheirus*
1:15 pm	**(91) Emma Palmer, Calli Wise, Kristina Colacicco, Gregory Ruiz, Katrina Pagenkopp Lohan** Trematode and bopyrid isopod prevalences in the grass shrimp, *Palaemon pugio*, from the Rhode River, Maryland, USA	● **(99) Nicholas Lee, Scott Gardner** *Litomosoides westi* (Filarioidea: Onchocercidae) and its intracellular *Wolbachia pipientis*: A new phylogeny shows evidence of additional horizontal transmissions of the *Wolbachia* endosymbiont
1:30 pm	**(92) Brandon Ruehle, Maddy Meador** New sequences of *Posthodiplostomum* spp. in Nebraska and Texas	● **(100) René Monzalvo, F Agustín Jiménez** Phylogenetic relationships of *Trichuris* (Nematoda: Trichocephalida: Trichuridae) inferred with mitochondrial genomes and evolution of host infection and morphological traits in representatives of Trichocephalida a clade of poikilothermic and endothermic hosts
1:45 pm	**(93) John Shea, Caroline Deeter, Colin Fague, Ethan Flores, Abram Harvey, Cadence Johnson, Amy Tran** Behavioral comparisons between an unknown *Gordius* (Nematomorpha) collected from a terrestrial environment and an aquatic hairworm, *Paragordius varius*	**(101) Chrissy Smith, Treit Truong, Stephen Curran, Stephen Bullard** Resurrection and supplemental description of *Crepidostomum transmarinum* (Nicoll, 1909) Hunninen and Hunter, 1933 (Digenea: Allocreadiidae) infecting brook trout, *Salvelinus fontinalis* (Mitchill, 1814) (Salmoniformes: Salmonidae) from Gragg Prong, Johns River, North Carolina
2:00 pm	● **(94) Timothy Brown** Lousy idea or ticking all the boxes? Building an understanding of conservationists' views on parasite conservation to improve outcomes for parasite biodiversity	**(102) Katerina Sawickij, Florian Reyda** Ghosts of parasites past: rediscovery of a species of *Neoechinorhynchus* (Acanthocephala) and its newest congener
2:15 pm	**(95) Sara Weinstein, Simon Groen** Do toxic cardenolides reduce parasitism in monarch-munching mice?	**(103) Roman Kuchta, Tomáš Scholz, Anindo Choudhury, Florian Reyda, Mikuláš Oros, Chris McAllister** Tapeworms of freshwater fish in North America: update and prospects
2:30 pm	**(96) Olabanji Surakat, Azeez Dauda, Damilola Adepoju, Zarah Iwalewa, Monsuru Adeleke, Daniel Boakye** Revisiting onchocerciasis elimination in urban areas: *Simulium damnosum* sl. dynamics and emerging concerns in Osogbo, Nigeria	**(104) Stephen Bullard, Haley Dutton** First record of a polystome (Monogenoidea: Polystomatidae) from a crocodilian: a new genus and species of polystome infecting the eye of an American alligator, *Alligator mississippienesis* Daudin, 1802 (Crocodilia: Alligatoridae) in a north-central Gulf of Mexico saltmarsh (Rockefeller Wildlife Refuge)
2:45 pm	**(97) Akinlabi Rufai, Adenike Fabiyi** Species distribution, molecular characterization and virulence of entomopathogenic nematodes in the Southwest Agro-Ecology of Nigeria: towards agricultural insect pest biocontrol	**(105) Richard Clopton, Debra Clopton** Integrating molecular and morphological methods for delimiting gregarine species

3:00–3:30 pm | Coffee Break | Winston Foyer

3:30–5:00 pm | Sessions IXA & IXB

	Session IXA: Host-Parasite Interactions 3 Winston 1A **Presiding:** Kaitlin Gallagher (Florida Southern College) Ben Hanelt (University of New Mexico)	**Session IXB: Taxonomy & Systematics 4** Winston 1C **Presiding:** Stephen Bullard (Auburn University) Janine Caira (University of Connecticut)
3:30 pm	**(106) Ace Kevin Amarga, Richard Robbins, Michael Hastriter, Ming-Chung Chiu** New host and distribution records of ectoparasitic insects and acarines associated with bats (Mammalia: Chiroptera) from the Philippines	**(112) Aline Acosta, Anastasiia Duchenko, Denis Machado** AI-driven predictions of phylogenetic trees from zoogeographical data in dactylogyrids (Platyhelminthes: Monogenea): a novel strategy for external phylogenetic support
3:45 pm	**(107) Julia Buck, Hailea Boggess, Connor Brainard, Robin Varney, D Wilson Freshwater, Tal Ben-Horin, Ami Wilbur** A newly discovered trematode parasite infecting the bay scallop, *Argopecten irradians*, in North Carolina	**(113) Christina Anaya, Peyton Smith, Jada Bunton** Mining biodiversity data from the largest online citizen scientist platform—but does it work for parasites?
4:00 pm	**(108) Kevin Coffey, Aly Embee, Glen Marrs, Amy Bei, Regina Cordy** Labeling hydrogen peroxide accumulation in the mitochondria of *Plasmodium falciparum* parasites cultured in different oxygen environments	**(114) Christopher Whipps, Emma Kester, Corinne Conlon, Eric Bauer, William Helenbrook** Genetic analysis of myxozoans through Sanger sequencing and metabarcoding reveals cryptic diversity of *Myxobilatus* species from basses in New York State
4:15 pm	**(109) Margaret Doolin, UMass Boston Students BIOL 358, Douglas Woodhams** Testing the impact of probiotic intervention on chytrid fungus loads during amphibian hibernation	**(115) F Agustín Jiménez, Guinevere Drabik, Jorge Falcón-Ordaz, John Kinsella, Vasyl Tkach, Scott Gardner** Phylogenetic relationships of the Nippostrongylinae from the Americas reveals homoplasy in *Carolinensis*, *Hassalstrongylus* and *Vexillata*
4:30 pm	**(110) Sumiti Alam, Maria Nava, Tauqeer Alam** Role of a *Cryptosporidium parvum* signaling kinase in male gametogenesis and virulence	**(116) René Monzalvo, Annika Desai, Kurt Galbreath, F Agustín Jiménez** Characterization of intestinal pinworms (Nematoda: Heteroxynematidae) isolated from endangered Hoffman's (*Ochotona hoffmanii*) and the Daurian pika (*Ochotona dauurica*) from Delgerkhaan and Hantay Mountains, Mongolia
4:45 pm		**(117) Triet Truong, Stephen Bullard** Description of *Baccigeroides currani* n. sp. (Digenea: Gymnophalloidea) infecting intestinal mucosa of gulf menhaden, *Brevoortia patronus* Goode, 1878 (Clupeiformes: Alosidae) from the northern Gulf of America

5:00–6:00 pm | Student Business Meeting | Winston 3

Presiding:
Allison Bryant (Oklahoma State University), ASP Student Representative

6:00–6:30 pm | Auction Preview | Winston Ballroom 2

6:30–9:00 pm | 34th Annual Auction | Winston Ballroom 2

Thursday, 10 July 2025

8:15–9:30 am — Sessions XA & XB

	Session XA: Ecology 4 — Winston 1A Presiding: John Shea (Creighton University) Gabriel Langford (Florida Southern College)	Session XB: Evolution — Winston 1C Presiding: Kaylee Herzog (University of Nebraska Medical Center) Charles Criscione (Texas A&M University)
8:15 am	**(118) Derek Zelmer** Effects of cercaria dose and timing on the infrapopulation structure of *Posthodiplostomum minimum* in bluegill sunfish (*Lepomis macrochirus*)	**(124) Alejandro Oceguera-Figueroa, Víctor Sosa-Jiménez, Natalie Kennedy, Donald Stacey, Danielle de Carle, Anna Phillips, Sebastian Kvist** On the re-discovery of the North American medicinal leech, *Macrobdella decora* (Say, 1824) in northern Mexico
8:30 am	**(119) Donald Behringer** Parasite avoidance behavior is remarkably adaptive for the Caribbean spiny lobster but has indirect consequences and a questionable future in our changing ocean	**(125) Eric Loker** The origin of digenetic trematodes: Did the journey begin with the blood flukes?
8:45 am	**(120) Elizabeth Warburton, Andrew Park, Alexander Strauss** Role of ecosystem characteristics in the evolution of complex helminth lifecycles	**(126) John Barta, Perryn Kruth, Sara Terier, Natasha Slawnych, Alexandra Pratt, Liam Landry, Jessica Rotolo, Elizabeth Zeldenrust, Alexandre Léveillé** Decoding coccidia: mitogenome diversity informs species identifications and evolutionary histories
9:00 am	**(121) Eric Atkinson** Multipathogen interactions and the fecal microbiome of passerines in the Greater Yellowstone Ecosystem: Phase I	**(127) Mary Janecka, Rachael Kramp, David Clark, Renata Ramoutar, Shirley-Ann Ramphal, Samantha Ramnarine, Ryan Mohammed, Mateusz Konczal, Jessica Stephenson** Host community diversity and river structure shape parasite evolutionary potential in a complex river system
9:15 am	**(122) Ephigénie Dione, Cheikh Seck, Jeanne Diouf, Malick Diouf** Current knowledge of parasitic nematodes of fish in Senegal	**(128) Nehemiah Rindoria, José Dumbo, George Morara, Iva Přikrylová, Wilmien Luus-Powell** Morphological and molecular description of a new species of *Heterorchis* (Digenea: *incertae sedis*) parasite of marbled lungfish, *Protopterus aethiopicus* from Lake Kanyaboli, Kenya

9:30–10:00 am — Coffee Break — Winston Foyer

10:00–11:00 am — H. B. Ward Medal Lecture — Winston 3

Presiding:
Tyler Achatz (Middle Georgia State University)

10:00 am Vasyl Tkach (University of North Dakota)
Introduction

10:10 am **Sarah Orlofske** (University of Wisconsin – Stevens Point)
Recipient of the H. B. Ward Medal

From tadpoles to trematodes: Childhood wetland experiences lead to a parasite passion



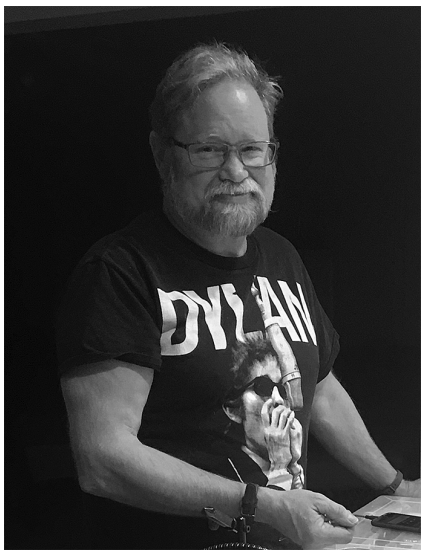
11:00 am–12:15 pm — Awards Presentations — Winston 3

Distinguished Service Award

Presiding:
Tyler Achatz (Middle Georgia State University)

11:05 am Vasyl Tkach (University of North Dakota)
Introduction

11:10 am **Richard Clopton** (Peru State College)
Recipient of the Distinguished Service Award



Aston Cuckler New Investigator Award

Presiding:
Tyler Achatz (Middle Georgia State University)

11:15 am Stephen Bullard (Auburn University)
Introduction

11:20 am **Brett Micah Warren** (Auburn University)
Recipient of the Ashton Cucker New Investigator Award



Best Student Presentation and Mark Dresden Travel Grant Awards

Presiding:
Christina Anaya (Florida Gulf Coast University)

11:25 am Best Student Presentation Awards

11:40 am Mark Dresden Travel Grant Awards

12:15–12:30 pm (Resolutions &) Adjournment Winston 3

See you all next year, July 26–29, 2026, in Orlando, Florida!

Abstracts

Disclaimer: The authors of the abstracts appearing in this program are solely responsible for the content. These abstracts are for informational purposes only and do not constitute formal publication. They should not be cited as published literature.

(1) The journey of tsetse transmitted trypanosomes: from the skin invasion to systemic infection

Dorien Mabille[1], Kayhan Ilbeigi[1], Kevin Lamote[2], Guy Caljon[1]

[1]Laboratory of Microbiology, Parasitology and Hygiene, Infla-Med Center of Excellence, Wilrijk, Belgium. [2]Laboratory of Experimental Medicine and Pediatrics, Infla-Med Center of Excellence, University of Antwerp, Wilrijk, Belgium

The African trypanosome species responsible for human sleeping sickness (*Trypanosoma brucei rhodesiense* and *T. b. gambiense*) are transmitted by tsetse flies (*Glossina* sp.). Due to major control efforts, the annual number of reported human cases has declined to about 800, with a roadmap to reach elimination of the *gambiense* form by 2030. However, the major challenges that remain are the lack of protective vaccines and the occurrence of asymptomatic individuals that sustain the transmission cycle. Moreover, knowledge on the exact immunological basis for the highly efficient trypanosome transmission and asymptomatic infection remains scarce. Following an infectious bite, inoculated metacyclic parasites rapidly adapt to the skin environment to establish a local infection and to continue a journey to systemic colonization. Making use of the tsetse fly vector, parasite reporter lines for fluorescent detection and *in vivo* bioluminescent imaging, immune-deficient mouse models and immunological profiling of parasite/saliva-exposed cells, we explored the role of innate immune responses in infection establishment and systemic colonization. Despite the armory of recruited anti-pathogen effector functions, parasites escape immune elimination and prominently distribute to tissues such as adipose, spleen and lungs. Within the lungs, *T. brucei* inhabit extracellular spaces surrounding the blood vessels of the alveoli and bronchi. This triggers a pronounced local immune response, characterized by elevated levels of monocytes, macrophages, dendritic cells, γδ T cells, and activated αβ T cells, followed by a delayed influx of neutrophils. Notably, a concurrent depletion of other immune cell populations such as B cells, eosinophils and natural killer cells may increase host susceptibility to secondary infections, as shown in co-infection experiments with respiratory syncytial virus (RSV). The discovery of asymptomatic lung colonization as a persistent tissue reservoir not only presents new challenges for disease control but also opens avenues for the development of novel non-invasive diagnostic strategies. To this end, we are currently investigating organic volatiles in exhaled air as infection biomarkers in a “breathomics” diagnostic approach, using *in vitro* models, naturally infected mice, and clinical samples from patients with trypanosome infections in Guinea.

(2) Immunity under pressure: lysozyme-mediated immune response to parasitic infection in the house cricket, *Acheta domesticus*

Isabel A. Roddy, Ben Hanelt

University of New Mexico, Albuquerque, New Mexico, USA

Parasitic infections induce acute physiological stress responses in their hosts, potentially leading to immunosuppression and increased susceptibility to secondary infections. This eco-immunological trade-off has been studied in some arthropods, including crickets. The hairworm *Paragordius varius* is an obligate parasite that relies entirely on its host—the house cricket *Acheta domesticus*—to grow from microscopic larvae into adults reaching up to 25cm in length, often matching the host’s body mass. At the culmination of the host-parasite relationship, *P. varius* depends on a physiologically functional host for transport and release into aquatic environments, where reproduction occurs. This presents a paradox: while the parasite requires a robust, functional host for successful transmission, the physiological stress of infection may impose significant energetic costs and immune trade-offs that compromise host survival. This study investigated the immune capacity of crickets with and without a hairworm infection, specifically analyzing the production of cricket lysozyme. Lysozymes are antimicrobial enzymes that cleave peptidoglycan bonds, which provides structural integrity and protection to bacterial cell walls. Lysozyme levels can serve as indicators of altered immune function, which may be influenced by parasitic infection. To stimulate lysozyme production, both parasite-exposed and uninfected

(control) crickets were injected with dead fragments of the gram-negative bacterium *Serratia marcescens*. Crickets experimentally exposed to the parasite were dissected 21 days post-injection to confirm successful infection. Following dissection, cricket hemolymph was extracted and tested for lysozyme levels using a fluorescence-based assay. The results of this test will be discussed, including the significance of this immune molecule in insect immunology.

(3) Histopathology and molecular detection of a pathogenic infection of *Mycobacterium gordonae* among captive-held, federally endangered laurel dace, *Chrosomus saylori* (Leuciscidae: Laviniinae) from a closed recirculating aquaculture system

Daniel F Gordillo[1], Anna George[2], Bernard Kuhajda[2], Steven Ksepka[1], Haley Dutton[1], Kamila Mora[1], John Brule[1], Stephen Bullard[1]

[1]Auburn University, Auburn, Alabama, USA. [2]Tennessee Aquarium Conservation Institute, Chattanooga, Tennessee, USA

A captive-bred cohort of laurel dace, *Chrosomus saylori* (Leuciscidae: Laviniinae) (a federally endangered fish restricted to 2 streams in eastern Tennessee's Cumberland Plateau) part of the conservation program at Tennessee Aquarium Conservation Institute became moribund and experienced trickling mortalities. Herein, those fish were processed for histopathology and molecular diagnostics. Ziehl-Neelsen (ZN) stained sections revealed an acid-fast microbe within lesions (necrotic areas and intracellularly) in the swim bladder, ovary, spleen, kidney, eye, and body cavity wall. The swim bladder had an acellular, eosinophilic exudate encasing the acid-fast microbe; its serosa was thickened with abundant connective tissue, lymphocytic infiltrates, and severe infiltration of macrophages and multinucleated giant cells (MGCs) plus mixed lymphocytes around some blood vessels. The ovary (60% of sections changed) had variously sized granulomatous nodules containing caseous necrosis and extensive, severe areas of macrophages, epithelioid cells, and eosinophilic granular cells (EGCs). The spleen (30%) had myriad macrophages and associated melanin-like residue (MLR). The kidney (20%) had clusters of macrophages and epithelioid cells that displaced hematopoietic components and was haloed by MLR. The body cavity wall (40%) had clusters of macrophages, epithelioid cells, and MGCs (Langhan's type) that adhered to the hepatic and intestinal serosa and invaded the adipose tissue near some exocrine pancreatic acini. The eye chambers had an eosinophilic exudate and extensive hemorrhages, and 90% of sections showed a choroid plexus infiltrated by macrophages, epithelioid cells, and MGCs plus perivascular lymphocytes and EGCs. We amplified the *hsp65* gene (439 bp) from formalin-fixed, lesioned tissues, and it was identical to that of the type culture of *Mycobacterium gordinae*. This report is the first report of *M. gordonae* from laurel dace.

(4) Alterations in ileal microbiota of turkey poults following *Eimeria* vaccination

Philip Yeboah, Demilade Israel Ibiwoye, Thaciane Amaral Lorenzo, Muhammad Wajeeh ul Hassan, Lisa Bielke

North Carolina State University, Raleigh, North Carolina, USA

This research focused on analyzing the impact of turkey *Eimeria* vaccine (*E. adenoeides*, *E. meleagrimitis*, and *E. gallopavonis*) on the ileal microbiota of turkey poults. The experiment included two treatments: Control (CON) and Vaccinated (VAC), each consisting of 20 poults. Poults in the VAC group were administered 1x dose of commercial vaccine on the day of hatch, with ileal samples collected at 4, 9, and 14 days of age. DNA extraction was conducted utilizing Qiagen standard kits, followed by 16S rRNA amplicon sequencing using the Illumina NextSeq 2000 PE250 platform. Data processing was conducted using QIIME 2, employing DADA2 for the purposes of quality filtering and chimera detection. Alpha diversity indices, including Shannon and Chao1, along with beta diversity metrics such as Bray-Curtis, Jaccard, and Weighted UniFrac, were evaluated through Mann-Whitney and Kruskal-Wallis statistical methods, utilizing Microbiome Analyst Software, with a significance threshold set at $p < 0.05$. Notable variations in alpha diversity were detected in the Shannon index ($p = 0.012$) and Chao1 ($p = 0.082$), suggesting changes in diversity and richness over time. On d4, a decrease in the Shannon index was noted in the VAC group, 0.5 vs 0.9 in the CON group. This trend persisted on d9, with the VAC group showing an index of 0.5 vs 0.75 in the CON group, suggesting indications of microbiome disruptions with lower diversity in VAC. In relation to Chao1, the VAC group exhibited higher indexes on d4, 7 vs 15 in the CON group, on d9, 7.5 vs 16 in the CON group. Beta diversity indexes, such as Bray-Curtis distance ($p = 0.001$), Jaccard ($p = 0.002$), and Unweighted UniFrac distance ($p = 0.001$), indicated a significant change

in microbial community composition in the d14 VAC group compared to the CON. A higher abundance of potentially pathogenic bacteria, specifically Streptococcaceae and Clostridiaceae, was observed in the VAC group on d14. Furthermore, the VAC group exhibited a reduction in Ruminococcaceae and Butyricicoccaceae on d14, suggesting a delayed recovery of beneficial bacteria. Future strategies must prioritize the reduction of transient dysbiosis to enhance the effectiveness of vaccination in commercial poultry production.

(5) Interrogation of *Entamoeba histolytica* in a human intestinal tissue microphysiological system

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The infectious burden of protozoan parasites is extremely significant worldwide and some parasitic species, such as *Entamoeba histolytica* (*E. histolytica*), are vastly understudied. Despite its high worldwide burden, little is known about the dynamics of E. histolytica pathogenesis in the gut. This gap in research knowledge is largely due to the difficulties associated with analyzing host-pathogen interactions and parasite dissemination in applicable models for human disease. In recent years, great strides have been made in the field of microfluidics, allowing for the integration of human organ systems, which can facilitate tissue-tissue crosstalk and effectively model these complex microenvironments. We have developed a human microphysiological system of intestinal tissue and a vascular compartment to investigate *E. histolytica* pathogenesis. This system not only models human architecture but also integrates the microbiotic environment necessary to accurately represent the microbial interactions that underlie *E. histolytica* non-pathogenic and pathogenic infection.

(6) Diagnosis of *Toxoplasma gondii* in cat (*Felis catus*) populations in Southeast Nebraska

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Toxoplasma gondii (*T. gondii*) is an Apicomplexan parasite that causes pathogenic effects in infected immunocompromised individuals and pregnant women. The resulting zoonotic disease, known as Toxoplasmosis, may elicit severe physiological impairment, including chorioretinitis, encephalomyelitis, and miscarriage of a fetus. Currently some 16% of the United States population is seropositive for toxoplasmosis while up to 2% of the mentally retarded children are reportedly born to mothers who were infected with *Toxoplasma gondii* during the pregnancy. The domestic feline is a reservoir host for *T. gondii*. The parasite is transmitted to domestic cats via a fecal-oral route, often through the ingestion of infected animals, such as birds and mice. Humans get the infection by ingesting contaminated foods, such as garden fruits or vegetables, or due to improper hygiene after handling feline fecal matter. Domestic felines are common in households and farmlands and across the United States, which may be a cause for concern of feline-human *T. gondii* transmission. Fecal samples from 100 domestic cats in southeastern Nebraska were collected and analyzed via Zinc floatation and coproantigens techniques. Statistical analysis of the data indicated that 68% samples were positively diagnosed with *Toxoplasma gondii* using coproantigen test. Only 53% of the samples were positive using optical microscopy after concentration of the samples with ZnSO4 technique. The results showed that *T. gondii* is considerably prevalent amongst the population of domestic felines in this study. The details of the investigation will be discussed at the conference.

(7) Mitochondrial mayhem: mitochondrial genome rearrangements in the genus *Klossiella*

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The suborder Adeleorina (Apicomplexa; Eucoccidiorida) contains parasites united by the biological process of syzygy; the association of haploid micro- and macrogamonts prior to their maturation into gametes. Members of the genus *Klossiella* (family Klossiellidae) are an anomaly in the Adeleorina because its members are monoxenous in vertebrates. This is unlike the rest of the genera in the suborder that require an invertebrate definitive host during their life cycle. The type species, *Klossiella* muris Smith and Johnson, 1902, was described from the kidneys of the house mouse *Mus musculus* and causes macroscopic lesions in heavy infections. There is a paucity of complete mitochondrial genome sequences available from members of the Adeleorina and only one of those few is from the Klossiellidae, *Klossiella equi* (Léveillé et al, 2019). Like most other coccidia, it contains 3 coding sequences (COI, COIII and CytB) and numerous fragments from the

large and small subunit ribosomal DNAs (rDNA). From *Klossiella muris*, there are only 2 nuclear 18S rDNA sequences available and no mitochondrial data. Kidneys from *Mus musculus* specimens were collected on São Miguel Island in the Azores from areas that were known to have mice infected with *Klossiella muris* from previous observations (Camarinho et al., 2021). One kidney was formalin fixed for histopathology and the second kidney was macerated in DNAzol for later DNA extraction according to the manufacturer's instructions. PCR using Apicomplexa-specific primers generated fragments of the *Klossiella muris* nuclear 18S rDNA and mitochondrial genome while avoiding amplification of contaminant host and bacterial DNA. Resulting products were Sanger sequenced, and resulting chromatograms were assessed for quality and assembled using Geneious. Surprisingly, there was little apparent synteny between the mitochondrial genomes of *Klossiella muris* and *Klossiella equi*, an observation shared with some *Hepatozoon* species that share diverse rDNA fragment arrangements. Despite these mitochondrial rearrangements, these 2 *Klossiella* species still form a well-supported clade among the adeleorinid coccidia. It would not be surprising if the mitochondrial genomes of *Klossiella* species infecting marsupials were also vastly different in their arrangements when compared to *Klossiella equi* and *Klossiella muris* considering the distinctive differences between placental mammals and marsupials.

(8) Horizontal gene transfer between *Parascaris* spp. and equids of equine testis-specific transcripts massively amplified on horse X and Y chromosomes

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Horizontal gene transfer (HGT) has been recognized as a frequent and important process shaping the genomes of prokaryotes. This has also been documented among eukaryotes, with increasing evidence that it plays an underappreciated role in their evolution. The mechanisms for HGT in eukaryotes remain enigmatic and there are still relatively few definitive cases involving mammals. We previously assembled the equine male specific region of the Y (eMSY) and functionally annotated Y genes including the ampliconic Equine Testis-Specific Transcript on the Y 7 (ETSTY7). Using BLAST we found ETSTY7-like sequences also on horse chromosomes X, ECA2, ECA26, and ECA31, as well as on genome scaffolds of donkey, Przewalski's horse, and the equine intestinal parasite *Parascaris* spp. To ensure the presence of ETSTY7 in the parasite scaffolds was not a result of contamination or ingestion of horse DNA by the roundworm, we designed horse-specific and *Parascaris*-specific primers. PCR assays on DNA from dissected nematode body structures verified the ETSTY7-like sequences were indeed present in *Parascaris*. We PCR amplified and sequenced ETSTY7-like haplotypes from *Parascaris* in DNA extracted from different adult tissues and eggs. Using FISH, we verified that ETSTY7 is present on Donkey X, plains zebra, and mountain zebra X, Y, and autosomes. We aligned and reconstructed a phylogeny of ETSTY-7 like sequences from the *Parascaris*, horse Y, horse X, Przewalski's horse and donkey scaffolds. The *Parascaris* sequences were primarily nested in a clade with horse Y copies, towards the terminal end of the tree. However, the topology was quite complex with some horse and *Parascaris* copies being identical. Taken together, our work indicates that *Parascaris* and horse have exchanged ETSTY7-like sequences that are expressed in equine testes. Horizontal transfer of these sequences potentially influenced their host-parasite interactions. The equine-nematode exchange of ETSTY7 serves as an important model for understanding eukaryotic HGT mechanisms, as well as functional and evolutionary consequences.

(9) This worm is just right: using "Goldilocks" sample types for population genomics in the human hookworm (*Necator americanus*)

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Mitogenome data suggest the current reference strain for the human hookworm (*Necator americanus*) is not genetically representative of strains circulating in other hookworm-endemic regions. Our research team recently established a novel laboratory strain of *N. americanus* using third-stage (L3) larvae collected from human subjects in Beposo, Ghana in 2019. To measure how diversity has been lost or maintained in this model through time, we used whole genome amplification (WGA) of L3 larvae to generate genome-wide single nucleotide polymorphism (SNP) datasets from individual specimens. L3s are the ideal sample type as they are more accessible from natural populations than adults and easier to manipulate than eggs. To validate our approach, we extracted gDNA from an adult of *Ancylostoma ceylanicum* (1ng/µL), then generated serial dilutions to represent the range of gDNA concentrations observed from L3s. Dilutions were amplified using a GenomiPhi V3 Ready-To-Go DNA Amplification Kit. Unamplified and amplified gDNA was sequenced on an Illumina NovaSeq 6000 targeting 50× depth of coverage. Sequence data were aligned to a reference genome and SNPs were called and filtered using bcftools mpileup. PicardTools was used to measure sensitivity, specificity, false discovery rate, and genotype concordance between the unamplified "truth" gDNA and the amplified dilutions. We found that the total amount of gDNA obtained from a single L3 (~0.1ng) produces a SNP dataset with nearly 97% genotype concordance to the unamplified truth dataset, and a false discovery rate of only 2.31%. Following validation, gDNA was extracted from L3s of *N. americanus* each from the F0 (2019) and F14 (2024) animal model passages, and from field-collected Beposo samples (2024). Successful extractions as confirmed by qPCR were used as input for WGA, sequencing, and SNP calling as described above. Principal component analysis (PCA) in Plink2 was used to visualize genomic similarity, and Arlequin was used to estimate population-level summary statistics.

(10) Reeling in the genomes: molecular characterization of fish-infecting *Goussia* species

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Coccidia infecting ectothermic vertebrates like fish are largely understudied. This includes members of one of the most speciose genera of fish-infecting coccidia, *Goussia* Labbé, 1896. Historically, differences in the morphology of specific life stages have been used to infer evolutionary relationships among coccidia; however, genomic data from fish-infecting coccidia supporting these inferences are lacking. Currently, molecular data from *Goussia* species are largely limited to partial nuclear 18S and 28S rRNA genes; no complete genomes or apicoplast data have been published from these species. Due to the lack of molecular data from *Goussia* species, phylogenetic relationships among coccidia parasitizing fish remain unclear. PCR and Sanger sequencing were utilized to generate the first mitochondrial (mt) genomes from two fish-infecting Goussia species from southern Ontario, *G. degiustii* and *G. leucisci*. A novel method to deplete host DNA from coccidial oocysts infecting extraintestinal fish tissue was developed and evaluated. This method was utilized to obtain parasite (*G. degiustii*) DNA samples depleted of host DNA for sequencing on short- and long-read next-generation sequencing (NGS) platforms. Despite being congeneric, the mt genomes from *G. degiustii* and *G. leucisci* were highly divergent in terms of both content and organization. Evaluation of our host DNA depletion method showed that NGS reads from treated samples achieved ~182- and ~204-fold increases in coverage of parasite mt and nuclear DNA targets, respectively, compared to those from a non-treated sample. Paired Illumina reads from treated samples were assembled to achieve over 7,000× coverage of the *G. degiustii* mt genome and generate the first nuclear ribosomal array and apicoplast sequences (34,216 bp total encoding 29 CDS, 4 rRNAs, and 33 tRNAs) from any *Goussia* species. Additionally, both short- and long-reads generated from treated samples helped show that the predominant form of the *G. degiustii* mt genome is a circular monomer, while that of the apicoplast genome is a linear monomer. The novel molecular data and methods presented will enable the future generation of complete genomes from additional fish-infecting coccidia and improve understanding of the evolution of these understudied parasites.

(11) From sample to expression: extracting, annotating, and analyzing *Necator americanus*

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The human hookworm (*Necator americanus*) represents a significant health burden, affecting about 500 million people worldwide causing anemia and stunted development in vulnerable populations. The hookworm life cycle progresses from L1 and L2 soil-feeding larvae to non-feeding L3 infective larvae, and finally to adult worms in the small intestine. L3 larvae represent a paradoxical stage - anatomically incapable of feeding yet as the infective stage they are very metabolically active. We aimed to assess differential gene expression between L3 larvae and adult male and female hookworms, hypothesizing that L3 larvae transcriptomes would reveal pathways that explain their metabolic activities and energy sources despite their non-feeding status. Using our improved *N. americanus* reference genome (contiguity improved from 11,864 to 987 contigs), we identified 1705 genes significantly upregulated in L3 larvae compared to adults. Gene Ontology analysis revealed upregulation in protein binding (160 genes), cytoplasm (130 genes), and membrane pathways (124 genes). Reactome pathway analysis identified enrichment in neutrophil degranulation (137 genes), clathrin-mediated endocytosis (42 genes), carnitine shuttle (34 genes), and organic anion transporters (27 genes). Interestingly, the phytanate metabolism pathway (alpha-oxidation of phytanate, Reactome ID: R-CEL-389599) was uniquely enriched in L3 larvae only. This pathway could enable the non-feeding L3 larvae to metabolize microbially derived phytanic acid from chlorophyll breakdown as an alternative energy source - a mechanism absent in adult stages. This specialized metabolic adaptation could allow L3 larvae to maintain energy for extended periods in soil while seeking hosts, despite lacking conventional nutrient intake capability. The upregulation of carnitine shuttle genes further supports enhanced fatty acid metabolism, facilitating transport of fatty acids into mitochondria for energy production. These findings shed light on how non-feeding L3 larvae maintain their metabolic activity through unique biochemical pathways, providing crucial insights into the parasite's energy metabolism during this critical life stage.

(12) BRC Analytics: a new Bioinformatics Resource Center

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Infectious disease research requires advanced computational resources to analyze complex datasets and uncover insights critical to public health. BRC Analytics (https://brc-analytics.org) is a new NIAID-funded Bioinformatics Resource Center (BRC) built on the open-source Galaxy and UCSC Genome Browser platforms and provided with compute resources by the Texas Advanced Computing Center. BRC Analytics provides a comprehensive, user-friendly environment for researchers in microbiology and infectious disease. The platform offers free access to robust computational infrastructure, enabling researchers to process and analyze high-throughput sequencing data without the burden of technical barriers. Curated workflows tailored for infectious disease research are readily available, streamlining analysis pipelines and ensuring reproducibility of results. By leveraging community-driven tools and offering seamless integration with Galaxy's versatile workflow engine and UCSC Genome Browser's visualization capabilities, BRC Analytics fosters collaborative and efficient research, enabling both novice and experienced researchers to unlock new discoveries in vector and parasite genomics and disease surveillance. This platform democratizes access to critical computational tools and resources, helping to advance global efforts in infectious disease research and public health.

(13) Exploring hyperparasitism: the virome of ectoparasites of Colombian bats

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Colombia is a megadiverse country with one of the highest numbers of bat species worldwide; however, the diversity and ecology of their parasites remain poorly understood. In particular, no large-scale faunal surveys have been conducted on bat parasites in Colombia, and knowledge about these organisms and the viruses that may infect them is limited. As in most regions, hyperparasitic relationships involving viruses remain largely unexplored, despite their potential influence on parasite pathogenicity and host fitness. Bat ectoparasites

have been shown to harbor medically relevant viruses, suggesting a possible role in the maintenance of these pathogens within bat populations. Here, we report the discovery of previously undescribed hyperparasitic viruses found in bat ectoparasites collected during fieldwork in one of the world's hotspots of bat diversity. Bats were collected using mist nets in the Apure–Villavicencio Dry Forests ecoregion of eastern Colombia. Ectoparasites were removed from captured bats, and RNA was extracted from four species of blood-feeding bat flies (Diptera: Streblidae). Through next-generation sequencing and *de novo* viral genome assembly, we identified novel viral sequences and examined their phylogenetic relationships with known viruses. We also standardized an effective RNA extraction protocol for parasitic arthropods. These findings represent a foundational dataset for understanding how viruses may shape the evolution of both parasites and their hosts in representative ecosystems, including those under anthropogenic pressure. As human–wildlife interactions increase due to colonization, deforestation, and pervasive agricultural incursions, we highlight the need of evolutionary approaches such as the Document–Assess–Monitor–Act (DAMA) protocol to help predict and mitigate emerging infectious diseases. The discovery and study of hyperparasites in bats and their parasites form a key component of this documentation effort.

(14) IMPACT—integrated monitoring of parasites in changing environments

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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; a risk that is exacerbated when host coextinctions are considered. However, parasites are portrayed as biological villains, even though most species pose no threat to human health or wildlife conservation. Unsurprisingly, parasites are the most neglected components of biodiversity management strategies, and unlike their more charismatic free-living hosts, are completely absent from conservation discussions. Furthermore, the decline and disappearance of parasites is rarely the focus of long-term or distribution monitoring programs due to the lack of cost-effective monitoring tools to detect broad-scale biodiversity changes. Here we present the EU Biodiversa+ project—IMPACT—which aims to integrate parasites into aquatic biodiversity monitoring guidelines and environmental decision making. Specifically, IMPACT will determine the spatio-temporal status and long-term trends of European freshwater fish parasite biodiversity, establish a reference library of specimen and molecular barcodes to future-proof the identification of freshwater fish parasites, evaluate eDNA as an integrative tool to assess fish parasite diversity in aquatic biodiversity monitoring, and gain insights into stakeholder perceptions of parasites and their role in environmental policy. As a result, IMPACT will address key barriers to the inclusion of parasites in transboundary biodiversity and ecosystem change monitoring by working with stakeholders to develop a framework that facilitates the inclusion of parasites in national and international biodiversity management and conservation strategies.

(15) A state-wide survey for Infectious Pancreatic Necrosis Virus (IPNV) in kidney and spleen of young-of-the-year, wild-caught rainbow trout, *Oncorhynchus mykiss* and brook trout, *Salvelinus fontinalis*, in West Virginia Appalachian streams

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Infectious Pancreatic Necrosis Virus (IPNV) is a double-stranded RNA (dsRNA) (genus *Aquabirnavirus*; family *Birnaviridae*) that can cause disease and kill cultured salmonids in some cases whereas in other cases the infected fish is an asymptomatic carrier. The effects of this virus on wild fish populations are indeterminate because viral surveys of wild fish are seldom conducted. The purpose of this study is to surveil for IPNV among

wild rainbow trout (*Oncorhynchus mykiss*) and brook trout (*Salvelinus fontinalis*) from streams in West Virginia. A total of 164 young-of-the-year susceptible individuals were captured from 10 freshwater streams in WV. Kidney and spleen were pooled individually from each fish and a reverse transcription polymerase chain reaction (RT-PCR) protocol targeting the VP2 gene of IPNV was applied to the samples. In parallel, the homogenized kidney+spleen from each fish was plated onto Chinook Salmon Embryo (CHSE) and Epithelioma Papulosum Cyprini (EPC) cell lines. A total of 43 (25.6% overall prevalence) fish were positive (25 brook trout [14.9%]; 18 rainbow trout [10.7%]). No cytopathic effect was observed in cell culture. The phylogenetic relationships of our strains, with one clustering with the first Chinese isolate and another with Spanish strains, along with observed inter-clade variability, suggest multiple independent introductions of IPNV into these streams. The study contributes to understanding the epidemiology of IPNV in West Virginia and offers insights into enhancing management practices to mitigate the impact of this pathogen on trout populations.

(16) Gut microbes as a novel forensics tool in wildlife trafficking

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In recent years the trade in wildlife produced in captivity has expanded rapidly and now accounts for the majority of global trade in CITES-listed birds. While legal supply-chains have the potential to offset demand for wild-sourced animals, contribute to livelihoods and conservation through revenue generation, they also pose potential risks to wild populations through laundering of wild-sourced animals used as breeding stock and for commercial sale. The challenges of distinguishing captive-bred from wild-sourced animals is a major source of vulnerability in legal supply-chains which are exploited by wildlife traffickers to launder animals illegally sourced in the wild. Parrots are among the taxa most heavily impacted by this trade - a situation exemplified by the IUCN Endangered Grey parrot (*Psittacus erithacus*) which have been among the most traded of all CITES listed birds. In a collaborative project between the University of Colorado Boulder (USA), World Parrot Trust (UK), and the South African National Institute of Biodiversity, we collected a dataset to test whether the gut microbiome is a robust indicator of African Grey Parrot rearing history. We collected 166 fecal samples from captive parrots across 22 different captive breeding facilities in South Africa, 122 fecal samples from wild parrots in Nigeria, and 59 fecal samples from recently trafficked birds intercepted in Nigeria and being held in a rehabilitation facility. We obtained all relevant export and import permits; samples were shipped to the University of Colorado to extract DNA and run bar-coded metagenomic sequencing to profile microbial communities. Results demonstrated that both bacteria and eukaryotes were significantly different in captive versus wild parrots. Results showed that trafficked birds that did not receive probiotics aligned with the wild samples, as expected, and trafficked birds that did receive probiotics were similar to wild samples and still distinct from captive samples, indicating the sensitivity of the method to detect treatment status. Overall, results indicated that gut microbes, including bacteria and eukaryotes, provide a robust signal of parrot rearing history and demonstrate strong potential for application as a forensics tool for use in investigations of suspected illegal wildlife trafficking in animal trade routes.

(17) Description of a new species of *Acanthostomum* Looss, 1899 (Digenea: Cryptogonimidae) infecting the aquatic coral snake, *Micrurus surinamensis* (Cuvier, 1817) (Serpentes: Elapidae) from the flooded rainforest habitat of the Yahuarcaca Lake system (Amazon River, Colombia)

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We described *Acanthostomum yahuarcaquense* Cajiao-Mora and Bullard, 2025 (Digenea: Cryptogonimidae) based on specimens we collected from the intestine of an aquatic coral snake, *Micrurus surinamensis* (Cuvier, 1817) (Serpentes: Elapidae) from the flooded rainforest habitat of the Yahuarcaca Lake System (Amazon River) Leticia, Amazonas, Colombia. We assign the new species to *Acanthostomum* Looss, 1899 because it lacks a gonotyl and has an elongate body, spinose tegument, funnel-shaped oral sucker with circumoral spines, ceca each having a posterolateral and nearly terminalpore, and excretory vesicle arms reaching anteriad to the pharynx. The new species differs from its 19 congeners by having 24–30 circumoral spines (vs. fewer than 20 or aspinose), vitellarium extension (from ovary to posterior half of body vs. from testis or ovary to anterior half

of body), and symmetrical ceca each having an anal pore (vs. asymmetrical ceca, a single cecum, or lacking anal pores). Our 28S phylogenetic analysis recovered a paraphyletic *Acanthostomum* within a clade sister to other cryptogonimids. Regarding advancing the systematics of the family, we discuss oral sucker shape and position, circumoral spine distribution, tegumental spine distribution, ceca symmetry, anal pore presence/absence and position, and gonotyl presence/absence as useful genus-level features. Many of these features remain indeterminate for several species. This is the first published study of a parasite infecting a tetrapod in the Yahuarcaca Lake System, first to record a parasite infecting a coral snake (*Micrurus* spp.) in Colombia, and only the second trematode species reported from the aquatic coral snake.

(18) Local fauna as a key resource for advancing coccidian taxonomy (and one's career)

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Since joining Midwestern University (Glendale, AZ) in 2014, I have conducted surveys of the coccidia of round-tailed ground squirrels on the university grounds, Arizona cotton rats and Harris's antelope squirrels in nearby Mesa, AZ, gray-collared chipmunks and golden-mantled ground squirrels in northern AZ, and captive Sonoran Desert tortoises housed by the Phoenix Herpetological Sanctuary. Focusing on local host taxa that had never, or rarely, been surveyed for coccidia resulted in the discovery and description of three new species of eimeriid coccidia and five reports that have expanded the host, and geographic, ranges of four species of *Eimeria*.

(19) When best laid plans of worms and men: an investigation of the description and type series of *Neoechinorhynchus strigosus*

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Neoechinorhynchus Stiles and Hassall, 1905 is a highly diverse genus of acanthocephalans consisting of 130+ species worldwide. Most species parasitize fish. In this genus, there are 3 species that were described by Van Cleave and reported from Buffalo fish (*Ictiobus* spp.; Rafinesque, 1820) as the type host: *N. australis*, *N. distractus*, and *N. strigosus*. During recent surveys our efforts to collect these species from the type localities listed by Van Cleave in his initial descriptions were unsuccessful despite repeated attempts. Instead, during subsequent fieldwork at the Illinois River in Illinois we obtained specimens of a currently unidentified species of *Neoechinorhynchus* in a Smallmouth Buffalo (*Ictiobus bubalus*). Of the three species of *Neoechinorhynchus* reported from *Ictiobus*, our specimens most closely resemble *N. strigosus*. However, there are numerous morphological discrepancies within the type series, and between the type series and our own collection. The museum specimens deposited by Van Cleave are damaged and appear to represent a species complex, calling the current collection into question. Unfortunately, this damage has made comparison of the proboscis and hooks more difficult or even impossible due to complete degradation. Large variation in the size of eggs, asymmetry of lemnisci, and overall trunk size can be observed among other morphological features. We posit that these differences justify differentiation between the two collections into different species. Specifically, we believe that the worms from the type series collected from Redhorse (*Moxostoma*) and Buffalo are conspecific with our samples from Illinois and New York, while the type specimen and others from White Sucker (*Catostomus commersonii*) are the true *N. strigosus*.

(20) Current state of knowledge and re-evaluation of the system of the Diplostomoidea

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The superfamily Diplostomoidea is a large, globally distributed group of digeneans characterized by the presence of a unique holdfast organ and parasitic in most major groups of vertebrates as definitive hosts. A number of diplostomoideans are associated with diseases in their intermediate and, more rarely, definitive hosts. Prior to this work and upon the recent synonymization of the Brauninidae, the Diplostomoidea included 5 families: Bolbocephalodidae, Cyathocotylidae, Diplostomidae, Proterodiplostomidae and Strigeidae. The separation of these families was based primarily on the structure and shape of prosoma and holdfast organ as well as the presence/absence of cirrus sac and paraprostate; more rarely, distinguishing among families was based on life

cycles and types of larval stages, excretory system or even host specificity. However, due to the inconsistent nature of most of morphological and biological characters across the Diplostomoidea and nearly universal lack of agreement on their relative value, the systematic history of the group has been extremely tumultuous and none of many systems proposed over the last 140 years has become broadly accepted or supported. Extensive molecular phylogenetic studies of the Diplostomoidea in the last 15 years helped to partly improve the system and resolve multiple taxonomic questions. Notably, practically all molecular phylogenies have clearly demonstrated non-monophyly of the two largest families, the Diplostomidae and the Strigeidae and indicated it as a systematic problem. We provide a brief overview of the history and current state of knowledge of diplostomoidean systematics and re-evaluate the system of the Diplostomoidea based on morphological and molecular evidence.

(21) Putting the parasite first: the extended specimen concept in parasitology

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The extended specimen concept conveys that a physical specimen offers a wealth of informativeness in the form of additional physical preparations, digital resources, and derivative samples and data. Parasites add an additional layer of complexity by not only being a derivative of a primary (host) specimen, but also can be considered a primary specimen with its own derivatives. This is not a new concept to parasitologists, although these connections are especially challenging to implement in database and digital record management. Integrated data within collections and between institutions allows investigating broad questions about parasite diversity and distribution with more power. For example, we have used occurrence and geographic distribution data to assess parasite, particularly helminth, species vulnerability to changing climate scenarios on a global scale and to reveal large-scale patterns of how parasitology knowledge accumulates. Collections of parasitic organisms have the potential to transform and add depth to biological investigations, yet have the additional challenge that they can be difficult to query and are poorly represented relative to other taxa. Having parasite and host specimens at the same institution, or at least connected through specimen records, fosters more comprehensive studies. Extending and integrating the knowledge gained from a physical parasite specimen begins with vouchering host, parasite, and associated tissue samples in permanent, scientific collections.

(22) The Mexican National Helminth Collection as a promoter of scientific research

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For nearly a century, the National Collection of Helminths (CNHE) of the Institute of Biology (IB), National Autonomous University of Mexico, has documented parasite diversity in Mexico and its neighboring regions. Although originally conceived as a scientific resource for taxonomists focused on the description of species, the CNHE has become a major source of high-quality data on host–parasite association through space and time. Each voucher specimen is accompanied not only by its currently accepted name and classification but also by the collection date, collector's name, locality, host species, parasitized organ, and, in many cases, prevalence and abundance data can be derived from the metadata. In the face of environmental change worldwide, the CNHE offers a unique and irreplaceable source of information for reconstructing ecosystems that have since been profoundly altered or destroyed. One striking example is Mexico City, now home to over 20 million people, but once a complex system of lakes inhabited by numerous endemic species, many of which are now severely threatened or extinct. The CNHE houses biological samples from Xochimilco, a remnant of the ancient lakes and a UNESCO World Heritage Site since 1987. The collection includes specimens and metadata for nearly 120 records of 49 species of helminths. Comparing historical records and specimen characteristics with newly collected samples offers a unique opportunity to investigate and quantify changes in parasitic fauna over the past century. Beyond the CNHE, nine other scientific collections are based in the IB, each of them housing specimens that potentially can be studied as hosts. The parasitological examination of these specimens provides a relatively simple and cost-effective way to generate high-impact data, in particular for extinct species and for animals that are difficult to collect or are protected by local and international laws. Finally, we emphasize the importance of incorporating voucher specimens into scientific collections as a long

term-strategy for maintaining biological samples and metadata for future generations. We urge parasitologists from all subdisciplines to engage with regional or national collections, to promote their use and to routinely incorporate specimens to ensure the continued growth and utility of these invaluable resources.

(23) Exploring parasitic copepod evolution with phylogenomic methods and advanced imaging

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Copepoda is a class of small crustaceans comprising about 14,500 described species. They are found in all aquatic environments and are the dominant members of marine plankton communities. More than 6,000 species of copepods live in association with aquatic animals, mostly as parasites, including several species that are economically important pathogens in aquaculture, especially of salmon and other farmed fish. Despite their abundance and importance, phylogenetic relationships among copepods are poorly resolved, even at the ordinal level. Until now, molecular analyses of copepods have generally been limited to a narrow suite of taxa and a sparse assortment of molecular markers, with single gene phylogenies predominating. This study was undertaken to examine copepod phylogeny with genome-scale data. Two methods for copepod phylogenomics were tested: phylotranscriptomics and target enrichment. Results from these methods are compared and recommendations are made for when to use the different approaches. I find that phylotranscriptomic and a custom target enrichment probe set produce congruent phylogenies for copepods. While phylotranscriptomics generates substantially more data (900,000 amino acid positions vs 200,000 base pairs here), it requires special preservation, destructive sampling, and is more expensive, while the target enrichment approach utilized here can be used on any material preserved in high concentrations of ethanol, can retain exoskeletons as voucher specimens, and is cheaper. My research group is now using a custom target enrichment probe set to substantially increase our taxon sampling in order to examine parasitic copepod evolution. Results on copepod phylogeny and the evolution of parasitic clades are discussed. This work is complimented with new data from microCT, confocal laser scanning microscopy, and z-stacked macrophotography of museum specimens.

(24) A sticky situation: the distinct morphology of coccidian oocysts from pet store squamate reptiles

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Coccidia are a group of obligatory intracellular parasites that infect all classes of vertebrates. However, coccidia of reptiles are understudied. For example, there are approximately 6,300 species of lizards in 40 families, but only a few hundred species from 15 lizard families have been evaluated for coccidia infections (Duszynski, 2021). However, it is estimated that the coccidian diversity in lizards is species rich, with estimates suggesting as many as 12,600 species. Surprisingly many of the coccidian species descriptions from lizard hosts came from lizard species that are now maintained in zoos or breeding facilities for the pet industry. For example, of the 19 common lizard species available for purchase from two large pet store chains in the US, 13 species of lizards have had 29 species of coccidia described from them. In this study, we sampled feces from squamate reptiles from pet stores in Oklahoma and evaluated them for coccidia and related protozoan infections. We found that of the 5 species of squamate reptiles sampled, 2 species were infected with 2 species of coccidia. These included *Isospora jaracimrmani* from the Yemen chameleon, *Chamaeleo calyptratus* and *Isospora amphiboluri* from the Bearded Dragon, *Pogona vitticeps*. These *Isospora* infections have only been reported in reptiles in captivity except for one instance. The oocyst morphology of these *Isospora* species show oocyst wall features, such as wrinkles and being covered in particles as well as always being observed stuck together, that suggest the ability to maintain populations in enclosures through standard cleaning procedures. To examine the oocysts wall morphology in more detail, the coccidia oocysts were isolated and SEM was performed. The oocysts wall showed numerous particles and debris on the surface of the oocysts wall as well as oocysts that were adhered together by the oocyst wall surface. The commonness of infections with these two *Isospora* species in captive bread lizards and their unique oocyst wall morphology suggests that maybe they are difficult to eliminate in typical cage cleaning practices in pet stores and zoos and this should be investigated in the future.

(25) Understanding the behavior of *Gryllus firmus* and *Acheta domesticus* infected with *Paragordius varius* in the presence of shelter and water

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Many species of parasites can change the behavior of their hosts during infection such as crickets infected with *Paragordius varius* that have been observed entering water where the parasite exits the host and lays eggs. However, these observations do not show cause and effect, which require experimentally infected hosts. We experimentally infected and sham-infected crickets (*Gryllus firmus* and *Acheta domesticus*) with cysts of *P. varius* and observed their behavior in the presence of either water or shelter over the course of their infection. We hypothesized that there will be no difference in behavior during week one between the infected and sham-infected crickets. However, infected crickets during week four will spend more time in or near the water, with less overall visits to the shelter, and less time spent in the shelter. To test this hypothesis, we conducted ten-minute trials under red-light conditions in two separate arenas (59.7 cm x 42.9 cm x14.9 cm) each containing one cricket per trial. The water arena contained two petri dishes (145 mm x 20 mm) level with the sand bottom and placed on opposite sides, one filled with water, and one filled with sand. The shelter arena contained a shelter, and a petri dish filled with sand. The trials were recorded using EthoVision to track the movement and behavior of each cricket. After excluding infected crickets that contained over five mature worms, the sample size of infected *G. firmus* was 3 while the number of sham-infected crickets was 17. The sample size for *A. domesticus* included 9 infected and 21 sham-infected crickets. Statistical analysis will be conducted to determine if infection with *P. varius* alters cricket behavior.

(26) Co-introduction of temnocephalans with the red clawed crayfish into the Barotseland floodplain, Zambia

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Freshwater crayfish do not occur naturally in African freshwater bodies. However, nine crayfish species have been reported as being introduced in the continent. Amongst them, *Cherax quadricarinatus* occurs in southern Africa with already established populations. The Temnocephalidae comprises symbiotic turbellarians that use different freshwater animal groups as their hosts (e.g. mollusks, crustaceans, insects and turtles). Three taxa of temnocephalan ecto-symbionts, *Craspedella pedum*, *Diceratocephala boschmai* and *Didymorchis* sp. have been co-introduced in continental African waters. These organisms have the potential to infest invertebrate hosts outside of their natural host, the invasive *C. quadricarinatus*. This can impose a threat to endemic decapods, which did not evolve naturally with these turbellarians, therefore a potential of having their immune system impaired may exist. During a collaborative field survey in the Barotseland floodplain in Zambia, several specimens of *C. quadricarinatus* were infested with two temnocephalans morphotypes and eggs capsules. The large morphotype and egg capsules were found on the abdomen, cephalothorax and feeding appendages. The small morphotype occurred on the cephalothorax, often hiding at the point of attachment with the walking legs. The temnocephalan species were morphologically identified as *Diceratocephala* sp. and *Craspedella* sp. Molecular analyses of the partial 28S rDNA and COI genes revealed that the large morphotype and egg capsules corresponded to *D. boschmai*, while the small morphotype corresponded to *Craspedella* sp. Morphometrics and scanning electron microscopy were also conducted to confirm species identity. This study furthers the still limited knowledge of temnocephalans co-introduced in African freshwater environments. Surveying the extent of the unnatural occurrence of these ecto-symbionts in Africa will shed light on their potential to colonize endemic invertebrates, as well as contributing to enhance monitoring programs in relation to the introduction of *C. quadricarinatus*.

(27) Elucidating the function of astacin metalloproteinases during skin penetration in the soil-transmitted nematode *Strongyloides stercoralis*

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Strongyloides stercoralis is a skin-penetrating nematode that infects over 610 million individuals worldwide and is responsible for chronic, debilitating conditions. Infection occurs when infective third-stage larvae (iL3s) locate and burrow into host skin. The molecular mechanisms by which the iL3s penetrate through host skin are not well understood. Astacins, a large family of zinc metalloproteinases, are abundant in *S. stercoralis* iL3 excretory-secretory product (ESP) and have been suggested to be involved in skin penetration. However, a direct functional role for *S. stercoralis* astacin genes has yet to be elucidated. We conducted a bioinformatic search for astacin genes that are highly upregulated in the iL3 stage based on publicly available RNA-seq data. We then generated reporter constructs for several of these astacin genes to analyze their spatiotemporal expression patterns. Astacin gene expression was localized to the pharyngeal cells, while secreted protein was found throughout the pharynx and at the back of the buccal cavity (mouth). To elucidate the function of astacin genes during skin penetration, we generated stable lines of homozygous knockout *S. stercoralis* using CRISPR/Cas9-mediated mutagenesis. We focused on a cluster of eight astacin genes (comprising a ~15 kb genomic region), designated the 42E cluster, because their consecutive positioning in the genome allowed us to simultaneously disrupt all eight genes. Successful deletion of the 42E cluster was confirmed by PCR genotyping. *Ex vivo* skin-penetration assays revealed that mutant iL3s had an impaired ability to penetrate skin. Many of the mutant iL3s failed to complete skin penetration, and those that did showed a significant delay in the time of penetration. Our results identify a set of astacin genes that are involved in skin penetration. We are now using a similar approach to characterize additional astacin genes. Elucidating the role of astacins during helminth infections can provide novel avenues for the development of targeted prophylactics.

(28) *Mathevotaenia* (Cestoda: Anoplocephalidae) from *Galenomys garleppi* (Rodentia: Cricetidae) on the Altiplano of Bolivia

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In 1986, a single individual of an unidentified mouse was collected during field-work on the Altiplano of western Bolivia. The mouse was first identified as a common species of *Auliscomys* and was later identified at the Museum of Southwestern Biology as the elusive *Galenomys garleppi* Thomas, 1898 (Rodentia: Cricetidae). At necropsy, cestodes and nematodes were found in the small intestine. The nematodes were identified to be trichostrongolids, and the cestodes were of the genus *Mathevotaenia* Akhumyan, 1946 (Cestoda: Anoplocephalidae). In our work in Bolivia that extended from 1984 - 2000, thousands of mice were collected from throughout the country, but no additional specimens of *Galenomys* were obtained. Further work on the systematics of the mice of Bolivia by one of the authors created great enthusiasm for determining what parasites were present in this mouse collected four decades ago. No gravid cestodes were collected from the specimen, highlighting a need for additional collections from this area to progress understanding of this specimen's lifecycle and impact on its ecosystem. These helminths appear to be undescribed.

(29) Initial immune conditions predict nematode within-host dynamics

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Duration of infection is often difficult to predict from a purely genotype-by-genotype basis. Even when host and parasite genetic backgrounds are genetically controlled, infection outcomes diverge: some infections are rapidly cleared, while others become chronic. We recently published theory predicting that positive feedback in mammalian immune systems, combined with immune state at time of infection, generate conditions either permitting or preventing infection chronicity. Here, we tested this theory by experimentally infecting both "susceptible" and "resistant" mouse genotypes with whipworms (*Trichuris muris*) under two environmental re-

gimes. “Lab-housed” mice were held in standard lab conditions in which their immune profiles are well-studied and predictable. “Rewilded” mice were housed in outdoor exclosures that mimicked natural conditions and, importantly, permitted the gut microbiome to rapidly transition to a “wild-type” community. Rapid changes in intestinal flora are known to provoke a Th1 immune response, which permitted us to manipulate the initial immune bias of both susceptible and resistant mice at the time of infection. At a number of time points following infection with *T. muris*, we recorded worm burden, developmental stage, volume, sex, and (if adult female) number of eggs. We also recorded host immune markers, such as leucocyte fraction, neutrophil density, and T-bet and GATA3 expression (markers of Th1 and Th2 differentiation, respectively). Combining our existing immunological model with a novel within-host dynamics model, we used these experimental data to estimate nematode vital rates (e.g., egg production, molt interval, death rates), the effect of nematodes on host immune state, and host immunological constants relating to parasite clearance efficiency and Th1/Th2 regulation. By treating the host-parasite system holistically, we show that immunological history (lab-housed versus rewilded) interacts with host genotype (susceptible versus resistant) and parasite-mediated immune stimulation/modulation to explain how and why infection duration varies, both within and across host genotypes.

(30) Cestode diversity of *Sorex* shrews (Eulipotyphla: Soricidae) from Mongolia

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Shrews (Eulipotyphla: Soricidae), insectivorous small mammals, serve as definitive hosts for a diversity of cestode species, yet soricid parasites remain understudied. Mongolia is currently facing extensive anthropogenic change, which threatens its distinctive ecosystems. To establish foundational data regarding shrew parasite diversity, we collected a total of 157 shrews (56 *Sorex roboratus*, 68 *Sorex tundrensis*, and 33 *Sorex caecutiens*) in the summers of 2015, 2016, and 2022 from 7 major sites distributed across Mongolia and identified 19 unique cestode species within 12 genera, from 2 major families (11 from Hymenolepididae and 1 from Dilepididae). Phylogenies based on complete mitochondrial genomes provide new insights into their evolutionary histories. Elements of metacommunity structure (EMS) revealed coherent, dynamic cestode metacommunities with parasite species replacement occurring between localities as well as host species. Boosted regression trees indicate that locality and host (shrew) weight have the greatest relative influence on parasite community structure, likely attributable to differences in host species occupancy and average body size of infected shrews.

(31) Genetic insights into *Lankesterella* blood parasites: evidence of multiple genotypes in Eastern European songbirds

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Members of the Lankesterellidae are heteroxenous coccidia that have endogenous development in their vertebrate hosts with the production of sporozoites that are transmitted among hosts via the bite of haematophagous invertebrates. *Lankesterella* species are observed commonly in the blood of a variety of wild birds. However, despite being first documented over a century ago, many species descriptions lack the morphological and life cycle data necessary for differentiating and classifying these parasites. Additionally, the taxonomy of *Lankesterella* species is complicated by limited information regarding their host specificity, both for their vertebrate and invertebrate hosts. Understanding host specificity is crucial for predicting how these parasites interact with different hosts and their environments, given that minimal morphological differences exist among species of *Lankesterella*. One way to overcome this is to obtain molecular data to accurately differentiate and classify these parasites. Coding sequences within the mitochondrial genome are particularly useful for identifying and differentiating organisms at the species level because they have high enough interspecific variation to allow for species-level differentiation and low enough intraspecific variation to provide consistent results within a species. To differentiate *Lankesterella* species infecting 3 species of avian hosts, we generated and compared mitochondrial cytochrome c oxidase subunit III sequences from these parasites. DNA was obtained from blood samples belonging to 9 passerine birds from 3 Eastern European host species. PCR reactions were

conducted using primers specific to *Lankesterella* species and related parasites. PCR products were Sanger sequenced and then assembled and annotated within Geneious Prime. Our analysis revealed 4 genetically distinct yet morphologically identical Lankesterella genotypes in the 9 blood samples; notably, 1 bird was found to have all 4 genotypes in its blood. Pairwise alignment of the 4 genotypes revealed sufficient genetic diversity (1.9-6.4% single nucleotides differences over 756 bp) to support species-level differentiation. Future research can focus on similar sampling of *Lankesterella* species from invasive birds in Ontario to generate additional molecular data, and perhaps reveal more hidden species diversity, among these poorly studied parasites.

(32) Mitochondrial data deficiency in Adeleorina and related coccidia: bridging gaps in apicomplexan phylogenomics

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Research into the mitochondrial genomes of some coccidian parasites, like the Adeleorina, has been limited. Many species have been described based solely on limited morphological data which has led to some classifications being called into question in recent years. For example, a recent study by Na et al. (2024) generated molecular data indicating that adeleorinid parasites may be genetically distinct from coccidia. However, further verifying the position of these lesser known coccidia is difficult due to their limited representation within molecular databases. The only mitochondrial genomes currently available for Adeleorina are *Klossiella equi*, *Hepatozoon catesbianae*, *Hepatozoon canis*, *Hepatozoon griseisciuri*, *Hepatozoon muris*, *Klossia helicina*, *Klossia razorbacki* and *Legerella nova*, which is insufficient to represent the likely genetic variation among the 7 families and 19 genera within this suborder. As such, much work needs to be done to isolate and assemble these genomes to verify and correct, where necessary, the currently established taxonomy. To accomplish this, parasites of interest need to be identified based on their current morphological descriptions and samples obtained for molecular characterization. Our work with a wide range of coccidia has produced multiple primers designed to target conserved regions of the mitochondrial genomes, particularly a number of well-conserved, fragmented small and large subunit ribosomal DNAs that can be exploited in initial PCR reactions. Using the sequences derived from those reactions, taxon-specific primers are designed for further amplify and assemble full mitochondrial genomes. With these genetic data, we can then move forward with establishing a more stable and evolutionarily consistent taxonomic framework for these understudied, but cosmopolitan and abundant, parasites.

(33) Redescription of *Polystoma nearcticum* Paul, 1935 (Monogenoidea: Polystomatidae) infecting the urinary bladder of Cope's gray treefrog, *Dryophytes chrysoscelis*, from an Alabama beaver pond

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We redescribe *Polystoma nearcticum* Paul, 1935 (Monogenoidea: Polystomatidae) based on its holotype, vouchers, and newly collected specimens from *Dryophytes chrysoscelis* (Anura: Hylidae) we collected from a beaver pond in Walnut Hill, Alabama. The only other *Polystoma* Zeder, 1800 species infecting a North American frog is *P. cinereum*. We provisionally assigned our specimens to *Polystoma* (type species *Polystoma integerrimum* [Fröhlich, 1791] Rudolphi, 1808), a polyphyletic taxon needing revision, because they have a diverticulate intestine, cyclocoel (intestine confluent posteriorly), 3 pairs of haptoral suckers, a single pair of hamuli, a single diffuse testis, a tubiform uterus with <20 eggs, and a pre-equatorial ovary. We identified our specimens as conspecific with *P. nearcticum* because our specimens matched Paul's 1935 original description and were indistinguishable from the holotype and existing vouchers of *P. nearcticum*. The new 28S sequences were nearly identical to *P. nearcticum* and *P. cinereum*. Phylogenetic analyses recovered North American *Polystoma* as a distinct lineage, sister the central and South American frog infecting polystomatids. This is the first record of a frog polystomatid from Alabama and only the second record of a species of *Polystoma* (or any frog polystomatid) from the Southeastern United States. Our taxonomic and phylogenetic results highlight the need to diagnose morphological differences between the "*P. integerrimum* clade" (which must be regarded as *Polystoma* because it contains the type species) and the "North American treefrog polystomatid clade" recovered in the nucleotide-based analyses (the latter comprising the anticipated new genus).

(34) A deeper look at hooks: inter-relationships among neoechinorhynchid acanthocephalans

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Acanthocephalans are integral parts of ecosystems and can damage host populations. There is, however, an existing knowledge gap about most species of acanthocephalans and many of them have yet to be studied using modern approaches, including 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 consist of 18 genera worldwide. Our approach is to compare species of the nine genera that occur in the United States using morphological data, with a focus on hook morphology, and using DNA sequence data. The first phase of this project is survey work to obtain representatives of species of each of these 9 genera from at or near their type localities. As a result of various surveys, we now have study sets of specimens of 8 of the 9 genera, with yet-unsuccessful attempts to collect a representative of the 9th genus. The samples acquired include *Tanaorhamphus longirostris* (Van Cleave, 1913) Van Cleave 1919 and *Gracilisentis gracilisentis* (Van Cleave, 1913) Van Cleave 1919 from Gizzard shad (*Dorosoma cepedianum*) from the Illinois River near Havana, Illinois; *Octospiniferoides chandleri* Bullock, 1957 from Eastern mosquitofish (*Gambusia holbrooki*) from the Florida Everglades; *Floridosentis elongatus* Ward, 1953 from White mullet (*Mugil curema*) from coastal Florida; *Atactorhynchus verecundus* Chandler, 1935 from Bolivar Peninsula, Texas; *Paulisentis fractus* Van Cleave & Bangham, 1949 from Wayne County, Ohio; *Octospinifer macilentus* Van Cleave, 1919 from localities in New York; and additional species of *Neoechinorhynchus* Stiles and Hassall, 1905 from various localities. We are utilizing a preliminary phylogenetic analysis as a framework to identify patterns in the morphology of the species and genera. Notably, in our tree *Paratenuisentis ambiguous* (family Tenuisentidae) nests within a clade of members of the family Neoechinorhynchidae, while another clade illustrates the potential for hook roots as a morphological synapomorphy.

(35) Redescription of *Benedeniella posterocolpa* (Hargis, 1955) Yamaguti, 1963 (Capsalidae Baird, 1853: Entobdellinae Bychowsky, 1957) with novel sequences and specimens infecting cownose rays (Rhinopteridae spp.) and a giant manta, *Mobula birostris* (Walbaum, 1792) (Mobulidae) and a phylogenetic analysis of Capsalidae

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We collected capsalids from cownose rays, *Rhinoptera bonasus* (Mitchill, 1815) (Myliobatiformes: Rhinopteridae) and Brazilian cownose rays, *Rhinoptera brasiliensis* Müller, 1836 from the Gulf of America and from a giant manta, *Mobula birostris* (Walbaum, 1792) (Myliobatiformes: Mobulidae) from a public aquarium. Capsalids were fixed in 10% n.b.f. for morphology or preserved in 95% EtOH for sequencing of the *28S*, *ITS1*, and *CO1*. All specimens matched the holotype of *B. posterocolpa* (anterior attachment organs with anterior grooves and one pair of dorsal papillae; a haptoral peduncle with one pair of papillae; and a long and narrow vaginal duct that opens laterally at the level of or posterior to the testes). Fifteen novel sequences were generated in this study (cownose ray and giant manta: 2 capsalids each for *ITS1*, *28S*, *CO1*; Brazilian cownose ray: 1 capsalid for the same genes). No *ITS1* or *CO1* sequence existed for *B. posterocolpa* previously. The only extant GenBank 28S sequence previously ascribed to *B. posterocolpa* was identical to our *28S* sequences, and the new *ITS1* sequences were identical. Two morphologically identical specimens (2 “hologenophores”) of *B. posterocolpa* from the same patch of skin on the same cownose ray had distinct *CO1* sequences (2 bp; 0.2% difference). The *CO1* sequences from 2 specimens of *B. posterocolpa* from giant manta were identical to each other and differed from the previous sequences by 4 bp (0.5%). The *CO1* sequence from the specimen of *B. posterocolpa* from the Brazilian cownose ray differed from the previous sequences by 5 bp (0.6%). The *28S* analysis recovered our sequences of *B. posterocolpa* in a clade comprising other species of Entobdellinae. The *28S* and *CO1* phylogenetic analyses recovered Entobdellinae sister to Capsalinae Baird, 1853; both of which were recovered sister to an unpublished sequence of an innominate species of *Dionchus* Goto, 1899 (Dionchinae Johnston and Tiegs, 1922). This is the first study of *B. posterocolpa* that combines morphology and nucleotide sequences from multiple infections and host species, first record of *B. posterocolpa* infecting the Brazilian cownose ray, and first detailed taxonomic description of specimens of *B. posterocolpa* infecting giant manta.

(36) Rethinking *Pseudotaeniacanthus* diversity: the elongated body form and its unusual attachment site

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The genus *Pseudotaeniacanthus* consists of 11 species of copepods that parasitize the gills of marine eels. This study was prompted by the discovery of 4 new species of *Pseudotaeniacanthus* found in moray eels off Australia, Japan, and Vietnam. While most members of this genus have a body form typical of Taeniacanthidae and related families, one described species is much more elongate, with a narrow body that is about 3x longer than the other members of the genus. Surprisingly, 3 of the 4 new species discovered here exhibit a similarly elongated body form. Unlike the other members of the genus, all 3 elongate new species were found to attach in the throat of their eel hosts rather than on the gill filaments. In addition to traditional descriptive methods like compound microscopy and line drawings, we are also incorporating confocal laser scanning microscopy (CLSM) in our descriptions. CLSM provides high resolution, z-stacked images where features in multiple focal planes are captured in focus in a single flat image. This approach minimizes error in morphological interpretation and maximizes the information obtained from each specimen, providing an objective view of features critical to species identification as well as new observations of appendage orientation. We also present an interactive online key hosted on the World Register of Marine Species for identifying all species of *Pseudotaeniacanthus*. Relative to traditional dichotomous keys, interactive keys are built upon a character matrix and have several advantages: they are easily updated to include new species and characters and allow users to begin the identification process on any character, skip characters, and score characters ambiguously. CLSM images are provided for each character state to make the character scoring more explicit and the key more user-friendly. Together, this study increases the species diversity of *Pseudotaeniacanthus* by >33%, demonstrates that the elongate body form is more common than originally thought and may be related to attachment site, and provides a user-friendly identification key with rich images to lower barriers of entry to the taxonomy of the genus.

(37) Overcoming challenges in taxon-dense tapeworm phylogenomics

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Many phylogenomic datasets consist of a modest number of taxa, mostly due to the high computational burden associated with analyses. However, a taxon-dense approach was necessary to resolve the deeper nodes of the tapeworm phylogeny. Here we show how we overcame three major challenges of our taxon-dense phylogenomic analyses. Our complete dataset consisted of 402 orthogroups (~800+ exons) obtained using targeted gene capture for a total of 1,259 OTUs. The first challenge was finding a suitable pipeline to process the raw read data for phylogenetic inference. We used the pipeline CAPTUS, which runs a series of programs to clean raw reads, assemble contigs and scaffolds, extract the target orthogroups, remove paralogs, and generate trimmed alignments ready for phylogenetic inference. Using a concatenated alignment, we ran a partitioned analysis in which ModelFinder was used to determine the best partitioning scheme and models for the dataset. We also ran an analysis using a mixture model of site heterogeneity. Here is where we encountered our second challenge—how best to ensure the analyses would run to completion in a reasonable amount of time using the computational resources at our disposal. We ultimately settled on the Posterior Mean Site Frequency (PMSF) model, which significantly speeds up the analysis and reduces the amount of RAM required, without compromising accuracy. Identifying a way to effectively evaluate branch support was our third challenge. Computing non-parametric bootstraps (STDBOOT) for such a large dataset with complex models proved to be prohibitively time-consuming. Thus, we explored other measures of evaluating branch support such as ultrafast bootstrap (UFBOOT), implemented in IQ-TREE. We employed the Nearest Neighbor Interchange (-bnni) option to reduce the impact of model violations that can lead to inflated UFBOOT values. We also ran the same two analyses on a reduced version of the dataset that included ~50% of the original OTUs and calculated STDBOOT on those topologies. The analyses of both the complete and the reduced datasets resulted in highly resolved phylogenies that help inform major restructuring of tapeworm classification and a better understanding of the drivers of tapeworm diversification.

(38) Hatching fish blood fluke eggs, miracidial morphology, and pathology of an innominate chimaerohemecid (Digenea: Chimaerohemecidae) infecting gills of smooth butterfly rays, *Gymnura micrura* from Mobile Bay, Gulf of America

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While searching for monocotylids (Monogenoidea) and blood fluke (Digenea: Schistosomatoidea: Chimaerohemecidae Yamaguti, 1971) infections in smooth butterfly rays captured in Mobile Bay (Gulf of America), we observed blood fluke eggs (Chimaerohemecidae sp.) embedded in the gill epithelium that were hatching. Eggs presented as large, nearly grossly visible, opaque white or slightly tan, irregularly shaped, oblong masses ~3 mm in maximum length. Wet-mounting excised live eggs and examining them with a compound microscope showed that each egg had an actively gyrating and ciliated miracidium. Unhatched miracidia began rapidly extending and contracting their body, stretching the pliable eggshell immediately before emerging from the egg, darting away, and swimming rapidly in a seemingly haphazard manner. The resulting 28S sequence (1537 b.p.; OQ709103) of Chimaerohemecidae sp. claded with that of other chimaerohemecids and was most similar (87%) to that of another Gulf of America chimaerohemecid, *Myliobaticola richardheardi* Bullard and Jensen, 2008. The miracidium of Chimaerohemecidae sp. is morphologically unique among fish blood flukes by lacking eyespots and a stylet as well as by having 2 large vacuoles. Our pathology results showed that infection (probably egg hatching) disrupted the overlying gill epithelium and contributed to crater-like lesions but that an inflammatory response and gill epithelial hyperplasia were lacking. This is the first observation of chimaerohemecid eggs hatching while embedded in the gill epithelium and the first elasmobranch gill pathology study involving a blood fluke.

(39) Improving tick systematics of the subgenus *Scaphixodes* of the genus *Ixodes* (Acari: Ixodidae)

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Despite parasites' interactions with virtually all organisms and their role as vectors for disease transmission they are widely understudied. Ticks are ectoparasites of terrestrial vertebrates that mostly live outside their host and have wide geographic ranges. Understanding the phylogeny of this group of organisms is a critical step in bridging the current gap in knowledge about tick systematics. Species of the subgenus *Scaphixodes* in the genus *Ixodes* are primarily found on various birds in the Palearctic and Nearctic Regions. Ticks categorized as *Scaphixodes* are especially unknown given that their ranges are relatively remote and there are very limited studies on the subgenus as a whole. This study aims to find the phylogenetic position of this subgenus and identify synapomorphies that define it. This was achieved through morphological assessments of the features of adult female ticks currently classified as *Scaphixodes*. Morphological assessment was supplemented with genetic sequence data to determine phylogenetic relationships between the tick species. This study found clear morphological synapomorphies that in conjunction with genomic data provide us with the evidence that two species currently categorized as *Scaphixodes* are misplaced and belong outside of the subgenus.

(45) New antimalarials targeting ion and lipid homeostasis in parasites

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The control and elimination of malaria would require continued development of new antimalarial drugs for the foreseeable future to counter the ever-present threat of drug resistance. New antimalarials being sought need to address treatment of acute and severe malaria as well as long-lasting prophylaxis. Among the promising new antimalarial compounds to emerge in recent years are those that disrupt Na+ homeostasis by inhibiting PfATP4, a Na+ efflux pump in *Plasmodium falciparum*. Two of these compounds have undergone clinical trials and shown to be highly potent against *P. falciparum* and *P. vivax* infections with rapid clearance of parasitemia in patients. Our laboratory has been pursuing additional scaffolds targeting PfATP4 to address the threat of high-level resistance. We are investigating mechanisms underlying the parasite demise following PfATP4 inhi-

bition. PfATP4 inhibition resulted in: 1. Rapid alterations in lipid homeostasis within the parasites with reversible accumulation of cholesterol in the parasite plasma membrane (PPM); 2. Morphological changes resembling premature schizogony; and 3. Metabolic slowdown of the parasite. Here, I will describe our studies involving cholesterol dynamics in *P. falciparum* that requires an interaction between PfATP4 and a cholesterol pump, PfNCR1. Based on additional studies, we are proposing a model for the role of cholesterol in fatty acid/lipid acquisition by intraerythrocytic malaria parasites.

(46) Persisters and K13-independent artemisinin resistance in *Plasmodium*

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Artemisinin combination therapy (ACT) is the frontline treatment for *Plasmodium falciparum* infection. Artemisinin has the fastest parasite clearance rate of all anti-malarial drugs; however, it is typically partnered with another drug to compensate for a short half-life and frequent recrudescence when used alone. The emergence and spread of resistance to artemisinin has posed a significant threat in malaria control. Delayed clearance and recrudescence are frequently associated with artemisinin resistance clinically. One of the major difficulties in drug discovery is the ability to identify and kill a latent cell. Drug-induced cell cycle arrest has been widely observed in many human diseases, including malaria, and have posed a significant challenge in searching for improved therapies. Previously we reported that exposure to artemisinin drugs induces a cell cycle arrest at ring stage that is known as artemisinin-induced dormancy. These dormant parasites can persist for many days before they either recover or die. However, the contribution of artemisinin induced dormancy to parasite survival and recrudescence remains poorly understood. In this study, we developed Quantitative Tracking of Recovery After Chemotherapy Exposure (qTRACE), a novel method that reliably quantifies viability at single parasite resolution. This method is based upon the concept that with significant dilution of parasitized erythrocytes, one parasite grows into a colony. qTRACE is a versatile method that simultaneously tracks survival, time-dependent recovery, and drug-induced growth effects *in vitro*. This quantitative high-content imaging assay provides precise estimates of parasite killing as well as viability of persisters that recover and cause recrudescent infections. We discovered that *P. falciparum* clones differ significantly in survival of dormant ring stages and that a novel copy number variant on chromosome 10 of *P. falciparum* corelates with decreased susceptibility to artemisinin drugs.

(47) Variation in host microenvironment physiology and its impact on *Plasmodium* replication

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Malaria is a devastating disease of global health importance, which caused an estimated 263 million infections and 597,000 deaths worldwide in 2023. It is caused by a protozoan parasite of the genus *Plasmodium*, with the species *P. falciparum* causing the highest number of malaria-associated deaths, occurring primarily in children under five in Sub-Saharan Africa. Some children experience more severe outcomes of malaria infection than others, despite having similar levels of exposure and immunity. Variations in the host microenvironment may explain some of the heterogeneity observed in malaria disease outcomes, but there is limited knowledge on this topic. During a malaria infection, the host's blood chemistry undergoes vast fluctuations in the levels of many metabolites, including amino acids, vitamins, and lipids. An observation from our work on the plasma metabolome of acute versus chronic malaria in rhesus macaques is that the metabolite differences that we identified as separating acute from chronic disease overlap somewhat with metabolites that are impacted during hypoxia. We wondered if physiological oxygen levels in the body, which can vary temporally during disease progression and spatially between different body organs, could affect *Plasmodium* replication rate *in vivo*. It is well established that *Plasmodium* parasites grow best *in vitro* in conditions of low oxygen (between 0.5 – 5%) and poorly in ambient oxygen conditions (21%). In a healthy human body, oxygen concentrations range from 0.5% in deep tissues to around 13% in pulmonary capillaries and arterial venules, and oxygen concentration further declines from those levels during acute disease. Our work seeks to understand how fluctuations in oxygen concentration affect the multiplication rate of *Plasmo-*

dium falciparum. Our lab performs longitudinal studies of *P. falciparum* parasites grown in red blood cells inside chambers placed under 1% or 13% oxygen, mimicking the low and high ends of the human body's physiological range. Our current work focuses on studying parasite growth rate variation in microenvironments with differing oxygen concentrations, modeling the theoretical impact of such variation on an *in vivo* infection, and investigating the underlying mechanisms for how *P. falciparum* navigates growing in high and low oxygen microenvironments within a human host.

(48) The IUCN SSC Parasite Specialist Group and next steps for international parasite conservation

Skylar R Hopkins

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After decades of sporadic and uncoordinated interest in parasite declines and extinctions, parasitologists have come together to take actionable steps towards conserving parasite biodiversity. To facilitate these efforts, we formed a volunteer expert specialist group within The International Union for Conservation of Nature (IUCN) in 2023. The IUCN SSC Parasite Specialist Group already has 52 members, including one steering committee member from each continent. The group contains parasitologists, ecologists, conservation practitioners, and social scientists who work for academic institutions, governments, zoos, veterinary organizations, and more. In 2025, we are completing our first Red List assessments for metazoan parasites and training more parasitologists regarding how to conduct Red List assessments. In this talk, I will explain how to get involved in these efforts, if you are interested. I will also provide a brief overview of our other efforts to grow our networks, develop species recovery plans, support parasite conservation actions, and communicate our work to the public.

(49) Seedbanks for symbionts: preserving parasitic diversity in a changing world

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Mounting evidence supports the assertion that Earth is undergoing a 6th mass extinction event, driven exclusively by human activity. Among the many taxa at risk are parasitic organisms, which are often overlooked in biodiversity assessments. Parasites, particularly those with complex life cycles like gordiids (hairworms), are highly susceptible to extinction through mechanisms including host loss, habitat alteration, and climate-induced phenological mismatches. Gordiids, freshwater parasitic worms requiring both aquatic and terrestrial insect hosts, are widely distributed but largely understudied, with over 80% of species diversity yet to be described. In the southwestern USA, a region disproportionately affected by climate change, endemic gordiid species face unprecedented threats. These threats include prolonged droughts, reduced streamflow, insect host declines, and increasingly frequent and severe wildfires. Gordiid life cycles rely on the availability and synchrony of aquatic paratenic and terrestrial definitive hosts, both of which are negatively impacted by these anthropogenic changes. For example, host decline reduces infection success and adult mating opportunities—especially problematic in dioecious species where worm density is naturally low, and mating occurs in aquatic habitats outside of the host. Furthermore, wildfires alter terrestrial and aquatic habitats, disrupt host communities, and increase post-burn erosion, potentially flushing parasite stages downstream and out of suitable habitats. Recent studies have documented apparent extinctions of several gordiid species with restricted ranges in the Sky Islands and Rocky Mountains. These include *Paragordius amicus*, *Gordius* sp., and *Gordionus lokeri*, each known from single localities prior to devastating megafires. Laboratory efforts to maintain gordiid seedbanks face substantial logistical challenges due to the requirement of maintaining multiple synchronized host species. However, cryopreservation offers a potential long-term strategy, as gordiids larva can be easily frozen and reanimated even after more than a decade. This approach introduces the idea of "seed banking" to parasites possibly allowing the reintroduction of extinct species. Our findings underscore the urgent need to integrate parasitic taxa into conservation strategies and biodiversity assessments. Gordiids exemplify the hidden casualties of global change and highlight the fragility of parasitic symbioses in rapidly shifting ecosystems.

(50) Sunfish parasites in western Maryland, USA

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While their ectoparasites have been well cataloged, few assessments have documented the endoparasites of centrarchid fishes in the freshwater systems of the Chesapeake and Ohio drainages that come from the Appalachian region of western Maryland, USA. Here, we document some of the helminths infecting internal organs of sunfish, including bluegill (*Lepomis macrochirus*), pumpkinseed, (*Lepomis gibbosus*), and black crappie (*Pomoxis nigromaculatus*). Although we have yet to distinguish the taxonomies of many parasites to species due to their larval form and the preliminary state of the assessments, it appears that there is a high diversity of digenean trematodes in the region, with a modest number of cestodes and acanthocephalans represented in centrarchid fish. We have successfully excysted several taxa and maintained them in the laboratory in culture media, warming them to encourage maturation under the assumption that they would reproduce within warm-blooded vertebrates. While this was not the case for a few taxa, others were successfully coaxed to maturity. In the case of several trematodes and one cestode, we could keep them in the laboratory for over 40 days. We can preserve and confirm these individuals' identities based on adult morphology. In addition to working with the second intermediate hosts of these helminths, we are also evaluating the molluscs within the region for trematode infections. This system is intended for use in college classroom activities and experiments. Both projects are in their infancy, and we welcome words of wisdom and encouragement from those with similar work experience.

(51) The life cycles of *Eimeria* species: simple or sophisticated biological strategies?

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The phylum Apicomplexa is comprised of a wide array of protists whose development can include complex mechanisms for immune evasion and host modifications. Comparatively, the life cycle of *Eimeria* species (Eucoccidiorida) is basic: sporulated oocysts are ingested by a host from the environment, the parasite undergoes merogony and gametogony in the intestinal tract producing unsporulated oocysts that are shed in the feces and sporulate to infectivity in the environment (sporogony). Even in its simplest form, this apicomplexan life cycle is responsible for significant production losses in commercial poultry barns. Examination of the endogenous development of some coccidia that infect gamebirds and related hosts reveals just how sophisticated these parasites can be. Chukar partridges, Northern bobwhites and turkeys were experimentally infected with single-species isolates of *Eimeria hargisi*, *Eimeria lettyae* and *Eimeria innocua*, respectively. Infected tissues were collected for histology to examine the endogenous development every 6 hours throughout the prepatent period. Invasion of enterocytes by large first generation meronts of *Eimeria hargisi* dramatically altered enterocytes in the upper intestinal tract of chukar partridges; although truly intracellular, these meronts appeared epicellular due to their superficial positioning within cells. Infiltration of second generation meronts was localized within single crypts that attracted numerous eosinophils. Despite the location of *E. hargisi* within enterocytes and the massive recruitment of immune cells, these stages were only observed within epithelial cells. Sporozoites of *E. lettyae* were observed in the lamina propria in addition to enterocytes in Northern bobwhites; however, sporozoite development in the lamina propria was not observed. Unlike either of these, invasion of $CD3^+$ intraepithelial lymphocytes for the development of sporozoites to first generation meronts of *Eimeria innocua* in turkeys was identified using immunohistochemistry, in addition to expected infections of enterocytes. To varying degrees, each of these *Eimeria* spp. interact with the host immune system. Parasite-initiated invasion of immune cells for replication remains understudied and further examination of these infections may reveal a portion of the life cycle that, currently, is poorly understood. The specific location of infections within certain tissues, cells and regions within these cells effectively demonstrate the myriad ways *Eimeria* spp. infect their hosts.

(52) A history of reports of self-experimentation in the *Journal of Parasitology* from 1914–1924

Kelly L Weinersmith

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In the very first paper published in the *Journal of Parasitology* in 1914, Brayton Howard Ransom reports that *Cysticercus bovis* is safe to consume in beef provided it has been frozen at -9.44°C for six days. His method

for determining this included observing cysticerci that had been frozen for a variety of days, and observing the what happened after he consumed this "measly beef" himself. Self-experimentation of this sort was common at the time, and *JP*'s first decade includes reports of consumption of dog tapeworms, descriptions of symptoms following self-inflicted black widow and tarantula bites, volunteers providing blood meals to, consumption of *Ascaris* larvae while studying *Ascaris* development times, and more. Sometimes these experiments provided scientists with important information, including descriptions of parasite life cycles and a better understanding of methods required for removing lice from soldiers' uniforms during World War I. But not all experiments yielded useful results, and in some cases it is not even clear was the scientist was hoping to learn from their experiments in self-infection. In this talk I will discuss the history of self-experimentation as reported in the *Journal of Parasitology* during the journal's first decade (1914-1924).

(53) Hidden in plain sight: combining morphological and molecular tools to study cestode diversity in young-of-the-year bull sharks *Carcharhinus leucas*, with notes on some of their life cycles

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Despite their abundance throughout the world's oceans, the diversity of parasites infecting Bull Sharks *Carcharhinus leucas* is not well understood, nor has there been a significant effort put forward to investigate the parasite diversity and abundance in neonatal bull sharks. Additionally, unraveling parasite life cycles is challenging under almost all conditions, even when many aspects of the host(s) and parasite can be manipulated in the laboratory. The challenge increases in marine ecosystems when studying host-parasite systems that cannot be maintained in controlled conditions. Given this limitation, it is unsurprising that the life cycles of parasites are unknown for most large marine hosts, such as elasmobranchs (sharks, skates, and rays). Recently, studies have shown the usefulness of molecular tools, when combined with morphology, as an alternative method for linking different organisms that likely serve as hosts for marine parasites. This study has utilized these tools to identify five adult cestodes from the spiral valves of young bull sharks in the Alafia River Estuary from Tampa Bay, Florida. These identifications include *Poecilancistrium caryophyllum*, *Paraorgymatobothrium* sp., *Cathetocephalus* sp., *Triloculatum* sp., and *Pseudotobothrium* sp. Further, morphological and molecular results suggest that three of these worms may be new species. Molecular analysis also provided identification for a larval cestode extracted from the gallbladder and cystic duct of the hardhead catfish *Ariopsis felis* as a *Triloculatum* sp. Allowing for the partial completion of the lifecycle of this genus. Additional results from this analysis will be presented.

(54) Variation of extrachromosomal genome copy numbers of *Eimeria tenella* throughout its life cycle

Taylor Lane, Beth Cohen, Perryn Kruth, Liam Landry, Daniel Lindo, Jessica Rotolo, Natasha Slawnych, Sara Terier, Julia Whale, Elizabeth Zeldenrust, John R Barta

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Similar to many apicomplexan parasites, *Eimeria tenella* possesses 3 genomes; a mitochondrial, a nuclear, and an apicoplast genome. *Eimeria* spp. possess a single mitochondrion and apicoplast, but each respective organelle contains variable genome copy numbers. Previous work documented the dynamic proportionality of these genomes during the exogenous oocyst development stage of the parasite's lifecycle (Kruth et al., 2024), including wide variation in the ratio of organellar genome copy numbers to the nuclear genome during sporulation. In this study, chickens were infected with sporulated oocysts of *Eimeria tenella* Guelph strain to initiate the endogenous lifecycle of the parasite. Throughout endogenous development, mucosal scrapes from the ceca of infected birds were collected every 6 hours over the course of the 7 days of *in vivo* parasite development. In addition to the 6-hour lifecycle snapshots of parasite development, isolation and purification of second generation merozoites and macrogametes was carried out in order to minimize noise at these stages due to differential rates of parasite development. A probe-based qPCR assay is under development to assess the relative proportion of genome copies of each of the 3 *Eimeria tenella* genomes. Appropriate probes and primers were designed to target known single copy genes within each genome that possess stability under shared thermocycler parameters. The genome targets will be compared to a synthetic oligonucleotide control containing a single copy of each target gene fragment separated by random spacers. In studying the genome dynamics throughout the lifecycle of *Eimeria tenella*, some useful insights into gene activation and metabolic

changes within the parasite at different life stages may be gleaned. The data provided in this experiment will hopefully highlight potential targets for future inquiry into biological processes of this parasite and may harbor insights into other related pathogens.

(55) The vegetarian and the blood feeder: evolution of trematode herbivores

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Digenetic trematodes are a species-rich group of parasitic flatworms, with estimates suggesting there are more than 24,000 species. Digeneans are known for their complex life cycles, but depending on the species, these cycles can vary in the number of hosts they infect, ranging from one in some species to as many as four in others. Previous studies on the feeding mode and diet of trematodes in their definitive hosts indicate that they are sectorial feeders, and gut-dwelling trematodes feed on epithelial tissues and associated mucoid secretions; whereas trematodes living within the respiratory and circulatory systems feed exclusively on blood. However, recent studies on gut-dwelling trematodes that infect tadpoles (the larval stages of anurans) or marine herbivorous fishes have observed them ingesting algae. Here we review how common this herbivorous feeding strategy is in trematodes, and whether there are any similarities in their life cycles and/or host-parasite interactions. Not surprisingly, our review indicates that all herbivorous trematodes infect herbivorous definitive hosts and have truncated life cycles. However, our review also shows that not all gut-dwelling trematodes infecting herbivorous hosts are themselves herbivores. Among those, herbivorous trematodes have only been documented in tadpoles of anurans and marine fishes that feed on algae. It also appears that two types of host-parasite interactions exist in these species: trematodes that ingest and appear to digest algae within their digestive tracts, and trematode species that contain large amounts of algae that remain bright green and undigested. The latter reside in hosts with transparent tissue around the lower portion of the body cavity and intestines, suggesting these algae may be photosynthesizing within the trematodes. Remarkably, these distantly related trematodes from marine fish and anuran tadpoles both show striking size variation in gravid worms, with large forms that are 3.3 to 4.6 times the size of small ones. We hypothesize that these drastic size differences may be related to the trematodes' unique diets, and we discuss ways to test this hypothesis.

(56) Prevalence and distribution of zoonotic pathogens in raccoons (*Procyon lotor*) of northern Illinois

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Raccoons (*Procyon lotor*) are mesopredators that are distributed across the entire continental United States. The growing abundance of raccoons has led to heightened concern regarding disease transfer between raccoons, other wildlife, and humans. Zoonoses are attributed to approximately 75% of emerging infectious diseases. Contraction of zoonotic infections is linked to urbanization, as land development increases the probability of human interaction with wildlife. Raccoons are known to carry various zoonotic pathogens, but efforts to quantify their prevalence and distribution along a rural-urban gradient are scarce. The goal of this study is to assess the prevalence and distribution of zoonotic pathogens, namely *Rickettsia rickettsii*, *Borrelia burgdorferi*, *Babesia microti*-like, *Anaplasma phagocytophilum*, and *Ehrlichia chaffeensis*, in raccoons at 5 study areas in northern Illinois that represent a rural-urban gradient. Raccoons (n=280) were captured and removed from sites by collaborators during April-June 2022-2024. Upon necropsy, tissue samples of the heart, liver, spleen, and diaphragm were collected. DNA was extracted from tissue samples and analyzed for pathogen presence via qPCR using pathogen-specific primers and probes. Percentage developed land cover was calculated within a 0.8 km buffer around each site using the National Land Cover Database (NLCD). A logistic regression was used to investigate the relationship between urbanization and pathogen prevalence. Due to the abundance of ticks in the region, pathogen prevalence will likely be high, especially at rural sites where ticks are more abundant. The results of this study will allow an assessment of public health risk that raccoons pose to humans and will help inform wildlife management decisions to integrate the health and wellbeing of wildlife and humans.

(57) Estimated incidence of canine heartworm infection, *Dirofilaria immitis*, in Claiborne County, Tennessee USA

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Canine heartworm infection (CHW) is arguably the most significant veterinary health issue in companion animal practice. Cases continue to increase and spread each year despite the availability of effective prophylactic drugs and increasing awareness of the insidious nature of the disease. Although organizations within the veterinary community have done much to increase public awareness of CHW disease, the message is not universally accepted and approximately 40% of pet dog owners do not employ regular prophylactic programs to prevent CHW in their pets. The American Heartworm Society (AHS) and Companion Animal Parasite Council (CAPC) compile CHW incidence and prevalence data at 3- and 1-year intervals, respectively, to monitor the occurrence of infection and inform the public. Our previous pedestrian-based survey in Claiborne Co. TN resulted in an estimated CHW prevalence of 2.3% in pet dogs with 60% household prophylactic compliance to affirm the reliability of CAPC maps as an estimate of local prevalence. To better characterize the dynamic nature of CHW acquisition locally we estimated annual incidence in the population at risk by the mathematical relationship where incidence is calculated from CHW prevalence divided by disease (infection) duration. Using CHW mapped prevalence for Claiborne Co. and household census data (2019-23) we estimated that annual recruitment of 13 new cases of CHW is sufficient to sustain the local 2.1% prevalence mapped by CAPC over the same period. Coincidentally, this number is comparable to the number of cases ($\bar{x}$ = 11) of CHW identified independently and treated in local veterinary practices during 2024. This research is supported by funding from the Richard A. Gillespie College of Veterinary Medicine, Lincoln Memorial University

(58) Development of a probe-based RT-qPCR assay to determine *Eimeria tenella* oocyst viability

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Until recently, understanding the state of viability for *Eimeria tenella* oocysts has required the use of an in vivo host system to permit endogenous development. This is then assessed through examination of fecal material during the patent period. While this process provides an accurate snapshot of viability, it requires upwards of 10 days to produce results as well as high costs, labour and ethical considerations of running animal trials. Previous work has documented that several mRNA transcripts are expressed in oocysts of *E. tenella* when they are incubated at avian body temperature (41°C), even in the absence of excystation medium. One such transcript, encoding a putative partial translationally controlled tumor protein, demonstrated an 84.1-fold increase with heat stimulation compared to steady state in live oocysts but no difference was observed when the heated oocysts were non-viable. Consequently, a set of primers was designed to span at least one exon/exon junction allowing for the amplification of the target region for quantification using RT-qPCR. The present work expands these preliminary observations by optimizing the assay using probe-based RT-qPCR for *E. tenella* with the possibility of expanding the assay to accommodate *E. maxima* and *E. acervulina* as well in a multiplex RT-qPCR assay. These data are expected to represent precent viability of oocysts collected from live animal models and will serve as the first step in developing a molecular method for determining oocyst viability. This finalized assay will provide timely results in a more cost-effective manner that also eliminates the use of live animal trials.

(59) A comparison of parasites in native and invasive snakes in South Florida

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The Burmese python (*Python bivittatus*) is an invasive snake that arrived through the illegal pet trade and subsequent release by pet owners but is now established in South Florida. Due to their booming population and no natural predators, they have become a major environmental concern due to their impact on native wildlife. Not only have they preyed on the native species inhabiting southern Florida, but they could also potentially introduce new parasites into the ecosystem that could impact native snake species. The objective of this

study was to compare the diversity, prevalence, and intensity of parasites between native and invasive snake species. We collected 118 snake specimens for necropsy, of the 65 Burmese pythons dissected, 69.64% were parasitized, only finding nematodes and pentastomes. In native species, 75% of specimens were infected; nematodes, trematodes, cestodes and pentastomes were all present. *Raillietiella orientalis* was collected from both native and non-native snakes. Prevalence of *R. orientalis* in the Non-native Burmese pythons was 7.14%, with a mean intensity of 1.25 (± 0.5, range 1-5). Native snakes had an 11.36% prevalence of *R. orientalis*, with a mean intensity of 7.00 (±7.07, range 1-20). Additional parasite species found, and their intensities will be discussed. Knowing the parasites of invasive species has implications for land management and the potential for invasive species control. It is also vital to understand the potential effects of parasite spillover and spillback since factors contributing to these processes are present in this ecosystem due to the disruption caused by the invasive python species. We are currently completing morphological and DNA analyses, to create a checklist of parasites for each snake species.

(60) Detection of the dinoflagellate *Amyloodinium ocellatum* in simulated field conditions

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Amyloodinium ocellatum is a cosmopolitan dinoflagellate ectoparasite with a wide temperature, salinity, and host range that causes significant mortality in warmwater marine aquaculture. The life history comprises three stages – the parasitic trophont, the free-living reproductive tomont, and the infectious dinospore. Each tomont can produce up to 256 dinospores resulting in a high reproductive capacity. Thus, early diagnosis is critical for controlling outbreaks. The current diagnostic standard is microscopic examination of gill tissue, but that may miss light infections (false-negatives) and/or misdiagnose other organisms as *A. ocellatum* (false-positives). Moreover, microscopy cannot detect the parasite in water samples. Both a conventional PCR and a LAMP assay are available. The LAMP is technically easier, quicker, highly specific, and more sensitive than PCR in tissue and water samples at the benchtop scale. We compared the sensitivity of light microscopy to that of the LAMP assay for detection of *A. ocellatum* in gill tissue and water in simulated field conditions. Forty-two 10-gallon aquariums filled with 20 L of 25 psu artificial seawater were inoculated with either 0, 1, 10, 100, 1000, 5000, or 10,000 laboratory-grown dinospores (six tanks per dose), resulting in concentrations of 0, 0.05, 0.5, 5, 50, 250, and 500 dinospores/L, respectively. Ten 1-L aliquots from each of 21 tanks (3 tanks per dose) were removed and filtered on a 0.22 µm 47 mm nitrocellulose filter membrane and stored at -80 °C. The other 21 tanks (3 per dosage) received four naïve spotted seatrout (*Cynoscion nebulosus*). After 7 days or upon fish death, 4 gill arches per fish (2 per side) were examined via microscopy then preserved in 95% ethanol for DNA extraction and LAMP analysis. The lowest dinospore concentration detectable by the LAMP assay in water samples was 0.5 dinospores/L. The lowest concentration detectable in tissue samples was 5 dinospores/L or higher when using either LAMP or microscopy. Thus, LAMP of water samples is a superior diagnostic tool. Simulations of replicated assays indicated that a 95% probability of detection was achieved with 10 replicated assays of water samples when the dinospore concentration is as low as 1 dinospore/L.

(62) Evidence of linked macrocyclic lactone and benzimidazole resistance in the dog hookworm *Ancylostoma caninum*

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The development of anthelmintic resistance poses an increasing threat to the treatment and control of parasitic nematode infections. In the dog hookworm *Ancylostoma caninum*, multi-anthelmintic drug-resistant (MADR) isolates have been identified, but the potential for underlying cross-resistance between drug classes remains unclear. In this study, we investigated the relationship between resistance to macrocyclic lactones (MLs) and benzimidazoles (BZs) using two isolates: WMD (drug-susceptible) and BCR (triple-resistant). In an *in vivo* selection experiment, a dog infected with the BCR isolate was treated with a combination of moxidectin (ML) and pyrantel (tetrahydropyrimidine). The genetic causes of resistance to the different classes of drugs are still being investigated, but there are several well-documented mutations in the β-tubulin gene that confer resistance to BZs in this isolate (i.e. Q134H, F167Y). Larvae collected after each of three treatments showed a progressive increase in the β-tubulin F167Y mutation frequency, rising from ~50% to ~77%, despite no BZ exposure.

In a separate observation, passage of the WMD isolate without any drug treatment revealed a spontaneous increase in the F167Y mutant allele frequency over time, from <0.001% to 8.5%, which was associated with increased ivermectin (ML) resistance in larval development assays, but no significant change in susceptibility to thiabendazole (BZ). Together, these results provide strong evidence that resistance to MLs in *A. caninum* may be genetically linked to the β-tubulin F167Y mutation, previously characterized as a BZ resistance marker. Furthermore, the increase in mutant allele frequency in the absence of drug pressure, alongside enhanced egg output and infection duration, suggests there may be little to no fitness cost, and potentially a selective advantage, associated with this mutation. These findings have important implications for resistance monitoring and for optimizing treatment regimens to slow the spread of MADR in hookworm populations.

(63) Quantitative ethology of schistosome miracidia characterizes a conserved snail peptide that inhibits infection

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Schistosomes are parasitic flatworms that cause schistosomiasis, a highly prevalent neglected tropical disease impacting over 250-million people worldwide. The schistosome life cycle progresses through an obligate snail intermediate host, which is infected by miracidia, the first larval stage that hatches from eggs in fresh water. Snail infection is a natural choke point in the schistosome life cycle but approaches to controlling snail infection have been incompletely explored. A better understanding miracidia responses to snail cues may lead to novel approaches to schistosomiasis control. Miracidia behavioral responses to snails have been qualitatively described, but the quantitative features and molecular mechanisms deployed by miracidia use to locate snails are not known. However, a secreted snail peptide known as P12 has been shown to elicit responses from miracidia, suggesting that it may serve as a primary cue in locating the snail hosts. We cloned and sequenced P12 from five snail species, revealing natural variation at 7 key residues. Quantitative methods using high-resolution wide-field imaging of custom arenas and high-throughput screening chips were employed to characterize miracidia behavioral responses to snail cues and P12 variants. We found that gradients are required to elicit behavioral changes in miracidia, as cues are inactive when presented in a homogenous form. Finally, we show that low concentrations of P12 inhibit penetration of snails by miracidia, likely by masking the naturally formed cue gradient formed by snail secretions. Control strategies by dysregulation of snail infection dynamics are an under-researched approach to reducing the prevalence of schistosomiasis, and they could have especially significant impacts in endemic regions of the world.

(64) Combating animal trypanosomiasis: a dual focus on antiparasitic activity and (eco)toxicity of novel nucleoside leads

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Animal trypanosomiasis (AT) is a widespread disease caused by *Trypanosoma* spp. and has a devastating effect on animal husbandry all over the world due to the scarcity of efficient drugs and development of drug resistance, hence emphasizing the need for novel treatment options. Following previous identification of

3'-deoxytubercidin as a highly potent trypanocide with curative activity in mouse models of both stage-1 and stage-2 Human African Trypanosomiasis (HAT), we now present a comprehensive preclinical evaluation of new 6-amino substituted tubercidin analogues with promising activity against a broad range of AT species. Potent hits were identified *in vitro* across all important AT species, i.e. *Trypanosoma brucei brucei*, isometamidium (ISM)-resistant and -susceptible *Trypanosoma congolense*, *Trypanosoma vivax*, *Trypanosoma evansi* (type A and B) and *Trypanosoma equiperdum*. Selected 'hits' were further tested for *in vitro* metabolic stability (using bovine, horse and piglet liver microsomes), *in vivo* mouse models for each AT species, genotoxicity assays and mode-of-action studies (i.e. genome-wide RNA interference library screening, metabolomics). Analogue 3 was highly active in *T. vivax*, *T. congolense*, *T. equiperdum*, *T. evansi* and *T. brucei* curative mouse models. Furthermore, there was no indication of *in vivo* toxicity or *in vitro* genotoxicity in Vitotox®, micronucleus and comet assays. Mode-of-action studies for 3 revealed that the P1 nucleoside transporter and adenosine kinase are involved in drug uptake and activation, respectively. Ecotoxicological assessments on *Daphnia* and green alga *Desmodesmus* revealed that the compound has an acceptable ecotoxicological footprint. Given the preferred target product profile for a broad-spectrum drug against AT, analogue 3 represents an advanced lead candidate for treatment of animal trypanosomiasis, regardless of the causative species.

(65) Investigating a novel, deep-sea derived natural product as a potential treatment for apicomplexan parasite infections

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Cryptosporidium parvum and *Toxoplasma gondii* are parasites with global distributions. Due to their widespread prevalence, transmission, and impacts on individuals with weakened immune systems, combined with their limited treatment and prevention options, they are infectious diseases of substantial importance. *Cryptosporidium* species cause diarrheal disease. The infectious particle is transmitted via the fecal-oral route and is environmentally present in water, soil, and food. Immunocompromised individuals and small children face the highest risk of mortality from cryptosporidiosis. The only FDA-approved drug is ineffective in these populations, leading to a critical medical need for new medicines. *T. gondii* is the causative agent of toxoplasmosis. While most people infected remain asymptomatic, it can cause serious complications in immunocompromised patients, pregnant women, and newborns. Current treatments for toxoplasmosis are targeted toward acute infection; no approved drugs target the chronic, latent stage of infection where *T. gondii* forms tissue cysts. Natural products, which are compounds derived from living organisms, are a promising avenue for potential drugs to treat these parasitic infections. A natural product, euryponolide, was isolated from a deep-sea sponge and has picomolar activity against *C. parvum* and nanomolar activity against *T. gondii*. We aimed to create a phenotypic profile of euryponolide's effects against *C. parvum* and *T. gondii* and determine euryponolide's molecular target. We have established that euryponolide rapidly kills intracellular *C. parvum* and *T. gondii* parasites. Euryponolide does not inhibit *C. parvum* excystation from the oocyst, does not inhibit sporozoite invasion into host cells, and has no effect on extracellular tachyzoites. Euryponolide specifically targets the asexual life stages of the *C. parvum* life cycle, with no significant activity against sexual stages. To identify a potential target gene of euryponolide, we performed forward genetics using *T. gondii*. Chemically mutagenized *T. gondii* were selected for resistance to euryponolide. The resistant population was cloned, and whole genome sequencing was performed on the resistant clones and the susceptible wild-type parental population. We have identified genomic variants shared across clones not seen in wild-type parasites. Identifying the target of euryponolide will provide critical information for future structure-activity studies.

(66) Preclinical impact of a novel compound for *Schistosoma* therapy

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Human schistosomiasis is a disease caused by parasitic species of the genus *Schistosoma* that affects over 250 million people worldwide, accompanied by severe clinical symptoms, socioeconomic problems, and

more than 200,000 deaths per year. About 90% of the schistosomiasis disease burden occurs in sub-Saharan Africa, where the major forms of schistosomiasis are caused by *Schistosoma haematobium* (urogenital disease) and *S. mansoni* (intestinal-hepatic disease). Due to the large overlap of *S. haematobium* and *S. mansoni* endemic regions in Africa, many people are at risk of co-infection, these mixed foci have a potential adverse effect on their association with bladder and liver pathology. Treatment has relied on the anthelmintic drug Praziquantel (PZQ) for more than 20 years. Mass drug administration in sub-Saharan Africa, where most of the cases occur, has led to the appearance of reduced efficacy of PZQ, which portends the selection of fully drug-resistant pathogens. Moreover, PZQ does not prevent reinfection and is not active against juvenile stages resulting in rapid re-activation after 1 to 3 weeks from PZQ treatment. These limitations strongly warrant the need for new therapeutics with better cure rate. Our focus is on Oxamniquine (OXA), a previous treatment of *S. mansoni* that fails to treat *S. haematobium* infections. We have successfully reengineered OXA using structure-function-guided approaches to produce CIDD-0150**303** (aka. **303**) with major advancements over current *Schistosoma* therapies. **303** reduced the worm burden of *S. haematobium* and *S. mansoni* adult worms > 80% in animal models, an advantage over OXA. Similarly, **303** overcame one of the major limitations of PZQ treatment. 303 kills 80% of juvenile stage of *S. haematobium* and *S. mansoni* in an animal model. Importantly, **303** kills >90% of PZQ-resistant parasites in *in vivo* studies. Our goal is to demonstrate the preclinical efficacy of 303 and to prepare for clinical studies. We expect CIDD-0150**303** will have broader spectrum activity and a higher clinical impact compared to PZQ, which only targets adult parasites. By targeting juvenile, PZQ-resistant, and adult parasites CIDD-0150**303** will reduce egg production, prevent re-infection from juvenile worms, reduce morbidity and disease symptoms.

(67) Mechanistic insights into ip-BPZ as an antiparasitic against *Toxoplasma gondii*

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Toxoplasma gondii is an obligate intracellular parasite that affects roughly one-third of the world's population. Toxoplasmosis is the second leading cause of death from food-borne illnesses in the United States, after salmonellosis, which signifies the demand for an effective treatment. As an intracellular parasite, current treatment methods are poorly tolerated by patients, as the drugs tend to destroy healthy cells in the process. Past research from this lab identified novel anti-cancer bisphenol Z (BPZ) derivatives to be effective at targeting and destroying *T. gondii* cells. These drugs inhibit the growth of the parasitic cells by preventing them from replicating. This project aims to explore the mechanism of these novel compounds in order to address the need for new therapeutic strategies against *T. gondii*. To accomplish this, the primary focus was to identify the gene targets that allow the most promising BPZ derivative, isopropyl BPZ, to destroy *T. gondii* cells. This was achieved through the creation of a mutated parasite line that is resistant to the isopropyl BPZ compound. The intracellular replication patterns of this mutated line were tested in varying concentrations of the compound via doubling assays, which demonstrated adequate resistance as compared to that of the parental strain. As a means to assist in understanding the mechanism of action, transcriptional analyses were completed through RNA sequencing between the parental and mutant strain under normal conditions as well as following isopropyl BPZ treatment. The results of this technique identified several genes of interest that reacted differently in the mutated strain versus the parental as a result of treatment with isopropyl BPZ. The genomes of each strain were investigated via DNA sequencing in order to compare the RNA genes of interest to DNA genes of interest. The information gathered from the sequencing results can be used to create custom gene knockout strains using CRISPR-Cas9 technology, which could further uncover the mechanisms of drug activity as well as the normal function of the genes. The outcomes of this project have the potential to identify a novel treatment of toxoplasmosis that is more effective than the current treatment methods.

(68) Drug repurposing to combat naturally emerging resistance in hookworm

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Anthelmintic resistance (AR) is an escalating issue in parasitic nematodes, particularly in livestock, where resistance to benzimidazoles, macrocyclic lactones, imidazothiazoles, and tetrahydropyrimidines has been observed. The widespread implementation of mass drug administration (MDA) programs targeting entire at-risk populations, regardless of individual infection status, has raised concerns that increased selective pressure on human parasites may also promote resistance. Drawing from the experience of AR in livestock, there is a critical need for alternative approaches to combat resistance in human parasitic populations. Naturally resistant nematode isolates can offer valuable insights into the genetic basis of resistance, while also facilitating the development of molecular surveillance tools and new strategies for parasite control. In this study, we focus on a naturally occurring multidrug-resistant isolate of the canine hookworm *Ancylostoma caninum* called BCR. Using machine learning (ML) algorithms, our goal is to identify repurposed drug candidates for treating drug-resistant hookworm infections. We have developed a cheminformatics pipeline that incorporates ML-based models to predict potential anthelmintic activity. Subsequently, we trained ML classification algorithms on datasets containing active anthelmintics and decoy compounds to differentiate effective candidates. We then prioritized compounds from the DrugBank database using the top-performing algorithms, and high-priority compounds are now being tested against the BCR A. caninum isolate in egg-hatch and larval development assays to assess their efficacy. Our ML-driven approach has facilitated the identification of a broad range of potential repurposed anthelmintics. Moreover, testing these repurposed drugs against a resistant *A. caninum* strain holds promise as a viable strategy for combating emerging resistance in hookworm populations.

(69) Differential emodepside efficacy and drug-resistant and drug-susceptible *Ancylostoma caninum* highlights variability in potassium channel activity

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Multi-anthelmintic resistance in hookworms poses a significant challenge to both human and veterinary health, underscoring the need for novel treatment strategies. In this study, we evaluated the *in vitro* efficacy of three anthelmintics—pyrantel, ivermectin, and emodepside—against drug-susceptible (WMD) and triple-resistant (BCR) isolates of *Ancylostoma caninum* L3 larvae. While pyrantel was largely ineffective and ivermectin induced high mortality in both isolates, emodepside displayed a surprising trend: the drug-resistant BCR isolate was more susceptible than the drug-susceptible WMD isolate. To explore the underlying mechanism, we performed survival assays in the presence of penitrem A, a BK channel (SLO-1) inhibitor. The addition of penitrem A reversed the enhanced emodepside sensitivity in BCR, implicating elevated basal expression of SLO-1 channels as a potential factor. These findings suggest that emodepside, via its action on SLO-1, may offer a promising therapeutic avenue to combat multidrug-resistant hookworm infections.

(70) Helminth parasites of Mongolian swifts

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Three species of swifts (Aves: Apodidae) are found in Mongolia during the breeding season, including: the common swift, Apus apus Linnaeus, 1758, the Pacific swift, *Apus pacificus* Latham, 1801, and the white-throated needletail, *Hirundapus caudacutus* (Latham, 1801). Thirty-six species of helminths have been reported from these species from widespread localities; however, no records have come from Mongolia. Even though these swifts overwinter in separate geographical areas, they occur in syntopy during the summertime in Mongolia. As part of the NSF-funded Mongolian Vertebrate Parasite Project, from 2009 through 2012, ten individuals of *A. apus* and a single individual of *A. pacificus* were collected from seven localities in the Gobi of Southern Mongolia. Parasites were recovered from seven of the eleven swifts examined and four helminth species were identified, including: *Pseudangularia europaea* Georgiev and Murai, 1993 (Cestoda: Dilepididae), *Notopentorchis vesiculigera* (Krabbe, 1882) (Cestoda: Paruterinidae), *Brachydistomum olssoni* (Railliet, 1900) (Trematoda: Dicrocoelidae), and *Plagiorchis maculosus* (Rudolphi, 1802) (Trematoda: Plagiorchiidae). This is the first report of *P. europaea* from *A. pacificus*; the species was previously only known from *A. apus*. In addition, this is the first record of *P. europaea*, *N. vesiculigera*, and *B. olssoni* in Mongolia. Coinfection of helminths was observed in four swifts. Three individuals of *A. apus* were infected with *P. europaea* and *N. vesiculigera*, one of which

was also infected with *B. olssoni*. An additional individual of *A. apus* was infected with *P. europaea*, *P. maculosus*, and an unidentifiable cestode. The presence of *P. europaea* in both *A. apus* and *A. pacificus* provides indirect evidence that the intermediate host for this parasite is found in the swifts' breeding range. Examining swifts upon first arrival from their wintering grounds would enable a firm test of whether the cestodes found in the swifts in Mongolia are brought in from their wintering ranges or whether the birds pick up their parasites each year after arriving back in the breeding range.

(71) Evidence of host ecology within the population genetic structure of a unique parasitic trematode

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Parasites are increasingly being utilized as tools for investigating the ecology of their hosts. Digenean trematodes ("flukes") are parasites with multi-host life cycles, typically relying on gastropod intermediate hosts before infecting vertebrate definitive hosts. These life cycles allow flukes to be relatively abundant within intermediate hosts, yet their reliance on vertebrates for dispersal results in congruent patterns of population genetic structure between flukes and vertebrate hosts. Flukes could therefore serve as proxies for apex predator hosts that may be difficult to sample. This was investigated using the fluke *Pleurogonius malaclemys* (the "terrapin fluke") and its two hosts, *Ilyanassa obsoleta* (eastern mudsnails) and *Malaclemys terrapin* (diamondback terrapins) as a model system. We hypothesized that the population genetic structure of the terrapin fluke would reflect diamondback terrapin dispersal and population connectivity despite being relatively abundant in mudsnail populations. This could have great significance in the fight to protect terrapins and support their conservation by managing populations effectively. The fluke was collected within mudsnail hosts at sites from Massachusetts to Florida where host ranges overlap. Fluke mtDNA was sequenced at the COI marker, providing a 620bp fragment. Analysis revealed high levels of structure and diversity that correspond with terrapin ecology. This is a promising step towards using the fluke to support terrapin conservation and also represents a valuable contribution to our understanding of the life history of the fluke itself. Future work will explicitly examine all three species to establish an explicit proof-of-concept.

(72) Quantifying the direct and indirect effects of the bopyrid isopod, *Probopyrus pandalicola*

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Predators can have both direct consumptive and nonconsumptive effects on their prey that trigger density mediated (DMIEs) and trait mediated (TMIEs) indirect effects respectively on species with which their prey interact. Parasites can mirror these relationships, however when we apply the model for predator/prey to parasite/host interactions, parasites are able to consume (i.e., infect) the host nonlethally. Partial consumption can lead to TMIEs that are triggered by consumptive effects, an indirect effect unique to parasite/host systems. This implies that parasites cause three different types of indirect effects: density and trait mediated indirect effects triggered by consumptive effects and trait mediated indirect effects triggered by nonconsumptive effects. Acknowledgement of the level of influence that parasites have on their community has only appeared in recent years, leading to a noticeable gap in the literature regarding the indirect effects of parasitism. Using the model system of the parasitic isopod, *Probopyrus pandalicola*, its intermediate copepod host, *Acartia tonsa*, and its definitive shrimp host, *Palaemonetes pugio*, we intend to quantify both the direct and indirect effects of the parasite by examining effects on host survival, fecundity, and resource consumption. Bopyrid larvae are easily detected by the copepod host and impose a significant burden, suggesting that infection avoidance behaviors should be observable. In our preliminary work, we have found that copepods in the presence of the infectious larvae will quickly increase speed and travel greater distances in order to avoid infection - a risk-induced trait response. Comparing this to the behavior of infected and control copepods, we found that the risk-induced trait response is greater in magnitude than and in the opposite direction as the infection-induced trait response. Currently, we are in the process of quantifying survival, fecundity, and resource consumption

of parasite cue-exposed, infected, and control copepods. By quantifying the direct and indirect effects of this parasite on its hosts and their resources, we can better understand the role of parasites in ecosystems.

(73) Richness and abundance of parasites infecting and consumed by striped bass (*Morone saxatilis*) varies spatially and ontogenically in the Chesapeake Bay

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Striped Bass (*Morone saxatilis*) are anadromous, piscivorous fish whose diets shift as they grow and migrate between freshwater to saltwater habitats. This migratory behavior, coupled with their generalist diet, makes them an ideal species for assessing the role of parasites in diet across ontogeny. Our previous work using genetic methods to examine the diets of Striped Bass revealed a high occurrence of parasites in fish stomach contents. In this study, we integrate parasite data generated from the amplicon-based high-throughput sequencing of stomach contents with morphological assessments of parasite infections in various fish tissues. Based on dissection data, 73% of the fish examined were infected with at least one parasite, with the highest prevalences occurring in members of Acanthocephala, Nematoda and Ergasilidae. None of these parasites appeared to significantly impact fish health. Analysis of diet detected parasites in 28% of the stomachs examined and included eight parasitic phyla. Among these, Acanthacephala had the highest relative abundance (67%; based on number of sequences), followed by Gregarinomorphea (15%) and Myxozoa (13%). Parasites that have parasite induced trophic transmission (PITT) comprised 73% of those recovered genetically from the stomach contents and 45% of those found during dissection. By combining traditional examinations of tissues with highly sensitive genetic methods for detecting parasites in diet, our results provide an unparalleled examination of the role of parasites in the trophic transfer of energy.

(74) The investigation of riparian parasite spillover and spillback in the Southwestern United States

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Parasites are often overlooked and poorly understood and yet have potential to impact survival and reproduction of their hosts. Introduced species may bring novel parasites to an ecosystem (parasite spillover) or amplify the abundance of native parasites (parasite spillback), both of which may negatively affect native hosts. Here we investigate the influence of non-native fishes and frogs on the riparian parasite communities of the federally threatened Narrow-Headed Garter Snake (*Thamnophis rufipunctatus*), the Black-Necked Garter Snake (*Thamnophis cyrtopsis*), and the Western Terrestrial Garter Snake (*Thamnophis elegans*) in the Mogollon Rim. We aim to (1) establish historical baselines of parasite communities prior to the introduction of non-native hosts, (2) model parasite infection intensity and prevalence from native and non-native host abundance, and (3) identify the most mobile host for the parasites we find. To approximate the historical composition of riparian parasite communities, we examined 193 museum specimens of garter snakes and their prey (frogs and fishes) for parasites, with 400 total host specimens expected to be dissected. We found 37% of *T. rufipunctatus* to be infected with helminths (larval Spiruridae, adult Spirocercidae, Acanthocephala, and adult *Ophiotaenia* sp.), 11% of *T. elegans* (adult *Parapharyngodon* sp., larval Cosmoceridae, and adult *Ophiotaenia* sp.), and 35% of *T. cyrtopsis* (larval *Abbreviata* sp., *Alaria* sp. metacercaria, *Telorchis* sp. metacercaria, and larval *Mesocetoides* sp). We additionally found 30% of *R. catesbeiana* to be infected with helminths (adult *Haematoloechus* sp. and adult *Gyrinicola* sp.) and 4% of *A. microscaphus* infected (larval *Abbreviata* sp.). Although sympatric, the hosts dissected thus far display different parasite communities from each other. Future directions include the dissections of *Rana chiricahuensis*, *Rana pipiens*, and fish specimens; stable isotope analysis of host tissues to track dietary change over time; time-series analyses; field surveys to model contemporary parasite infection intensity and prevalence; and cophylogeny tests to identify the most mobile host species for the parasites. The results from this study will be used to identify any threats from parasitism to endangered herptofauna and ichtyfauna, inform management actions for the conservation of riparian herptofauna and ichthyofauna, and further describe the parasite diversity of the Mogollon Rim.

(75) Non-invasive methods for describing internal parasite communities: a metabarcoding case study

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Internal parasite communities can provide insights into host ecology, including habitat, diet, and overall health. However, these insights are often logistically impossible using classical parasitological methods. Methods that require necropsies are not feasible for rare or threatened hosts or for study designs that cannot accommodate destructive sampling (e.g., longitudinal studies). Methods that require fecal samples are not feasible for hosts whose feces are difficult to collect, and even when feces can be collected, parasite eggs are difficult to identify beyond the family level. Therefore, we developed and tested a metabarcoding pipeline that can use non-invasive swabs of captured animals to provide high resolution snapshots of internal parasite communities. We developed the pipeline using four snake host species: Timber Rattlesnakes (*Crotalus horridus*, species of special concern in North Carolina), Northern Pine Snakes (*Pituophis melanoleucus*, threatened in North Carolina), and Northern and Banded Water Snakes (*Nerodia* spp., least concern in North Carolina). We first used roadkill snake specimens to compare DNA detected on swabs collected from the stomach, intestine, and cloaca to the internal parasite communities observed using classical parasitological methods. During our necropsies, we documented 14 unique parasites, which we used to build a reference DNA library: 2 Acanthocephala (*Macracanthorhynchus ingens* and an unknown oligacanthorhynchid); 1 Cestoda (*Ophiotaenia* sp.); 6 Nematoda (*Capillaria* sp., *Kalicephalus* sp., *Ophidascaris ashi*, *Physaloptera* sp., *Spirocera* sp., and *Spiroxys* sp.); 1 Pentastomida (*Kiracephalus coarctatus*); and 4 Trematoda (*Strigea* sp. metacercariae, *Renifer ellipticus*, *Renifer kansensis*, and *Styphlodora magna*). We will showcase two case studies for applying the validated pipeline to hosts where full necropsies were not possible: a longitudinal study of live *Nerodia* caught in Wake County, North Carolina (cloacal swabs only) and an invasive Burmese python (*Python bivittatus*) removal program with strict regulations regarding specimen disposition (cloacal swabs or feces only). We will also discuss the benefits, limitations, and challenges of using the metabarcoding pipeline, including necessary steps for adapting it to other host systems.

(76) Marine tapeworm communities in blacktip sharks: patterns, prevalence, and parasite diversity

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An essential goal of community ecology is understanding how species distributions reflect species interactions. Host-parasite distributions provide an excellent model for studying these patterns because we can examine species distributions at two distinct scales: within hosts (where parasite spatial distributions may be affected by shared use of host tissues) and among hosts (where aggregation may be shaped by dispersal ability, co-infection or host traits). For this work, we focus on cestode parasites (class Cestoda, subclass Eucestoda) that localize in the intestinal tracts of shark hosts and exhibit high prevalence within shark populations. Specifically, our study characterizes the distribution of tapeworms within and across intestinal habitats of *Carcharhinus limbatus* (Blacktip Shark) collected from the Gulf of Mexico. To investigate distributional patterns within- and among-hosts, we dissected and collected intestinal tracts from 32 *C. limbatus*. At capture, each shark's size, sex, and maturity were recorded as host traits with the potential to influence the presence and intensity of parasitic infections. Each intestinal tract was divided into equal-length cross-sections (5 cm), from which parasites were extracted, preserved, and cataloged by location within the tract. This allowed for quantifying parasite distributions within individuals as well as across hosts. We asked: (1) How does parasite distribution within the intestine change as a function of parasite density and richness? (2) How do parasite infections vary among hosts based on host attributes (size, sex, age) versus parasite community attributes (e.g., presence, intensity, diversity)? We recovered approximately 4,000 cestodes, representing at least five families, from the 32 *C. limbatus* individuals. Infection intensities strongly increased with body size and were higher in females, highlighting the important role of host traits in shaping parasite communities. Within the host intestine, parasites were more frequently concentrated in the middle portion of the gut, suggesting a structured pattern of habitat use. Our research demonstrates that host traits can influence broad infection patterns, while finer-scale within-host structuring may be driven by competition or resource partitioning among cestodes.

(77) Wild turkey infectious disease prevalence across Pennsylvania landscapes

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Coinfections are extremely common in wildlife yet are often overlooked. Effects of coinfections can have significant impacts on host susceptibility, fitness, and population dynamics, due to complex interactions between different pathogens. Research focusing on a single pathogen may, therefore, lead to a biased perspective of the host populations being managed. Recent work has found that wild turkeys (*Meleagris gallopavo*) are affected by various pathogens. For example, lymphoproliferative disease virus (LPDV) and reticuloendotheliosis virus (REV), two retroviruses, negatively influence reproduction and survival, respectively. Population trends of Pennsylvania turkeys vary across landscapes, but it is unknown how pathogens are structured across landscapes or with each other in hosts. Here, we determined the associations and risk factors of LPDV, REV, and coinfections with intestinal parasites in Pennsylvania wild turkeys. Our results indicate varying infection rates in turkeys with LPDV (70%), REV (1%), and intestinal parasites (63%). LPDV was greater in adults and varied by region, but did not significantly differ with year, sex, or landscape type. Parasite diversity was greater in juveniles and males, varied significantly by year and region, but did not vary by landscape type or LPDV infection. Coinfections with LPDV and parasites were the most common association (40%), compared to infections with only LPDV (27%) and only parasites (23%). Finally, parasites were positively associated with each other, but most parasites were negatively associated with LPDV. These results reveal high rates of coinfections in turkeys, with each pathogen group displaying unique infection dynamics. Ongoing work is in the process of identifying additional pathogens and linking coinfections to turkey movement and reproduction.

(78) Food, health & livelihood in Northeast Thailand

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Transmission of the human-infective and carcinogenic trematode *Opisthorchis viverrini* (OV), a parasite acquired from eating raw or undercooked fish that causes cancer of the bile duct, is ongoing in Southeast Asia. The resulting cancer mainly afflicts individuals aged 40+ and once progressed is rapidly fatal with limited treatment options. Despite decades of control, this cholangiocarcinoma caused by OV remains one of the leading causes of death in Thailand and Laos and incidence rates in Northeast Thailand remain the highest in the world. Determining which interventions will be most effective requires an understanding of fundamental epidemiological processes, many of which are poorly understood. The communities most heavily affected by the parasite are lower-income rural households around the Mekong River and its tributaries where the main sources of employment are fishing, rice farming and fish farming. There is therefore a close connection between people's livelihoods and infection. Persistent public health campaigns have stigmatized the practice of eating raw fish, which has contributed to a disconnect between reported behavior and actual eating habits. To better understand this disconnect and the complex interplay between diet, health and livelihoods from the community perspective, a food festival at a well-established food market was conducted in the highly endemic region of Maha Sarakham. Questionnaires, discussion groups and interactive activities, all conducted in the Thai language by staff and students from Khon Kaen University, formed the basis of the comprehensive qualitative and qualitative data collection from this event. This event engaged with previously overlooked community members – such as fisherman and non-risk-group individuals. Novel evidence and metrics were gathered from this festival that will be used to inform intervention methods, surveillance, treatment, and health policy. This project will also be used as a template for community engagement and epidemiological data collection and has informed research and public health policy for the region.

(79) Using social media for public engagement with parasites

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Parasites have a public relations problem, which is caused by the biased, limited, or incorrect information

available to the public about parasites. How many museums have displays about parasites? How many parasite species can the average person name besides those that infect people or pets? And what can parasitologists do to increase access to parasitological information for children and adults who may never encounter this information in school? In 2025, blogs are not the answer, but there may be some lessons to learn from the Parasite Ecology blog. The blog had regular posts from 2013 to 2017, and the content is still accessed by visitors every day. A small fraction of visits are students following links provided by educators, whereas most visits come from Google when the public seeks out parasitological information. The most searched topics are basic concepts, such as the difference between simple and complex life cycles and the difference between parasites and predators. This suggests that there is still a demand for clear, text-based information about parasites. However, the most popular posts have only been accessed by a few thousand unique visitors each, which is far smaller than the reach of a podcast, YouTube video, or viral social media post in 2025. In this talk, I will argue that podcasters, TikTokkers, and other popular communicators share similar trajectories: they start out with limited reach; they post regularly about topics that they are passionate about; and eventually their content improves, and their reach increases. For example, I published one parasite-themed cartoon per week for several years, and eventually evolved from a terrible artist to a pretty bad artist. I also unexpectedly made important professional connections, including opportunities to write a textbook about infectious diseases and lead the first IUCN SSC specialist group for parasites. I hope this talk will convince parasitologists of all ages and career stages that there are ways to use their passion for parasites to educate and engage the public, especially if they are willing to look silly or fail, and there may be unexpected benefits along the way.

(80) Shining a positive light on parasites

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Associated with the support it provides for research, the National Science Foundation expects all funded projects to have one or more elements of broader impacts aimed at benefiting society in some meaningful way by contributing “to the achievement of specific, desired societal outcomes.” STEM education and public engagement are two of the desired outcomes. By their very nature, parasites are ideal subjects for achieving both! The following examples of the variety of ways we have embraced this “mandate” to share the wonders of parasites with individuals of all ages will be described. (1) The Global Cestode Database—An on-line resource providing access to information and images of all nominal species of tapeworms. (2) An Illustrated Glossary—An on-line resource providing images and definitions of tapeworm terminology. (3) “The ‘Faces’ of parasites”—an exhibit of 6-foot back-lit colourized scanning electron micrographs of tapeworm scoleces at the University of Kansas Biodiversity Institute and Natural History Museum. (4) “Meet the Suckers”—a children’s book about tapeworms. (5) “The Legacy of a Lifetime of Collecting: The Carl and Marian Rettenmeyer Story”—an exhibit at the University of Connecticut highlighting the 50 years the Rettenmeyers spent studying army ants and their associated species, and especially mites, which includes interactive digital media stations. (6) “Be our Guest: The Complex Society of Army Ants and their Guests”—an exhibit at the University of Connecticut that features a 10-foot army ant major and 8 of the species of mites that live only on the bodies of army ants…with giant ants on the outside of the building that houses the exhibit to assist with advertising its location. (7) “Tapeworms Unlocked”—an on-line interactive key to all genera in 15 of the 16 orders of tapeworms that parasitize elasmobranchs. (8) The Connecticut State Parasite Initiative—If successful, Connecticut will be the first state to have a state parasite. This project will focus on parasite specimens deposited in the Lawrence R. Penner Parasitology Collection that were collected from vertebrates in Connecticut.

(81) The power of the residency: creating new pathways that foster collaboration and community between art and science

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This research project investigates how a full-time artist-in-residence position embedded within a scientific research lab can generate new, collaborative pathways between the arts and sciences. Traditional academic structures often maintain rigid disciplinary boundaries, which limit opportunities for interdisciplinary exchange, community engagement, and the co-production of knowledge. By situating a social practice artist within the

Jayne Raper Lab in Hunter College's Department of Biological Sciences, this residency model seeks to re-imagine how scientific research and artistic practice can intersect in meaningful, publicly engaged ways. The residency emphasizes time, autonomy, and the artist's own creative inquiry as essential to its success. This open-ended approach led to collaborations such as *Ask A Parasite?* — an immersive, embodied public experience of parasitology research—and *Our Collective Fabric // The Microbiome*, where artists and scientists invite diverse communities to grow and learn about their microbiomes. These projects exemplify what Pablo Helguera terms "transpedagogy": a blending of education and art-making that challenges both conventional science and traditional art education. Outcomes include the development of an interdisciplinary Social Practice art course for undergraduate and graduate students. This course draws on frameworks such as adrienne maree brown's Emergent Strategy, Mary Overlie's Six Viewpoints, and the scientific method. Students explore the relationships between identity, place, and the collective body through scores, protocols, and mapping exercises, creating a dynamic and embodied learning environment alongside learning and experiencing the science of the human body. This research demonstrates the potential of artist residencies in scientific settings to foster new, community-driven research methodologies. It contributes to a vibrant art education research culture by encouraging transdisciplinary collaboration, experiential learning, and creative engagement with scientific inquiry. Through sustained relationship-building and shared creative processes, the residency model not only bridges disciplines but also reshapes how knowledge is created and shared in both scientific and artistic contexts.

(82) Navigating the world of book publishing

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You've thought of a great idea for a book - but what do you do now? In this session we will talk about the process of publishing a book. We'll each share our experiences with writing pitch packets, finding an agent, finding an editor, supporting the release of the book once it's published, and more.

(83) Increasing community accessibility to the natural sciences using High Point University's Mobile Lab

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The High Point University (HPU) Mobile Lab is part of a science outreach program housed in the Wanek School of Natural Sciences. High Point University's Mobile Lab is a traveling laboratory equipped with state-of-the-art instruments that is staffed by faculty and students dedicated to making science accessible to everyone. As Co-Director of the Natural Sciences Fellows Program, I work closely with undergraduates in the program in the designing and implementing of experimental modules spanning a diversity of areas across the natural sciences including biology, chemistry, biochemistry, physics, environmental science and neurobiology. Bringing hands-on experiments and interactive learning experiences to select HPU campus events, partners in the community (e.g. Greensboro Science Center, Qubein Children's Museum), and K-8 schools throughout the city of High Point and the Piedmont Triad serves to increase accessibility to the experimental sciences in the community. The Mobile Lab not only enhances experiential learning for my students but also fosters a sense of curiosity and engagement among the wider community. Through these outreach efforts, we aim to inspire the next generation of scientists and encourage lifelong learning in the natural sciences. The initiative also provides invaluable hands-on teaching experience for undergraduate students, allowing them to develop their communication skills, deepen their understanding of scientific concepts, and make meaningful contributions to the community.

(84) Assessing the role of chemoreception in parasite avoidance in the acute bladder snail *Physa acuta* from sunset pond in San Angelo, Texas

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Freshwater snails such as *Physa acuta* act as intermediate hosts for a variety of parasitic flatworms in the class Trematoda, incurring high fitness costs due to their exploitation. Due to the long coevolutionary history between parasite and host as well as selective pressure to avoid parasites in their environment, this experiment

sought to examine the ability of *P. acuta* to detect parasites or infected conspecifics using chemoreception, which is a freshwater snail's primary sense to observe their environment. *Physa acuta* has been repeatedly shown to have a higher parasitic load compared to other freshwater snail species existing in similar environments, so it was hypothesized that *P. acuta* would be unable to consistently detect parasites in their environment. To test this hypothesis, uninfected and prepatent-infected *P. acuta* were placed in choice chambers with one chamber containing water taken from wells containing infected conspecifics and the other chamber containing water taken from wells containing uninfected conspecifics. Snails were then observed to determine avoidance of the side containing water from infected conspecifics. Naïve snails raised in captivity as well as wild caught snails were used to identify any innate responses as opposed to responses specific to the environment from which the snails were obtained. Binomial tests and logistic regression models in R were used to identify the significance of any avoidance behaviors as well as what metrics may affect detection rate, such as age, parasite species, or prepatent infection status. Results indicate that there is no significant innate parasite avoidance response in *P. acuta*. However, infected snails still in the prepatent stage of infection showed consistently higher levels of detection amongst all trials. These results indicate the possibility of a learned, adaptive response post-infection in *P. acuta*, which may play a role in reducing risk of multiple infections and the costs incurred with greater parasitic burdens.

(85) Gregarines parasitizing redshanked and redwinged grasshoppers in Colorado and New Mexico

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Gregarines are apicomplexan parasites known to infect many invertebrates, including insects. Gregarine biodiversity is understudied in many insect hosts, including Orthoptera (e.g., grasshoppers and crickets, etc.). About 80 gregarine species have been reported from orthopteran hosts globally, although over 6,500 grasshopper species are recognized. In efforts to better understand gregarine diversity and host-associations, field collections of adult grasshoppers were conducted in the 2024 flight season. The redshanked grasshopper, *Xanthippus corallipes* (Haldeman), was collected from a horse pasture near Elbert, Colorado. The redwinged grasshopper, *Arphia pseudonietana* (Thomas), was collected from a pasture near La Joya, New Mexico. Orthopteran hosts were collected and dissected for observation of gregarine infection. In total 36 of 79 (45.6%) specimens of *X. corallipes* and 20 of 32 (62.5%) specimens of *A. pseudonietana* were infected with gregarines. Gregarines were fixed on glass coverslips, stained, imaged, and measured. Morphometric characters were analyzed for species identity. Preliminary results suggest membership in the genus *Gregarina*, although additional data are needed for complete morphological datasets. Sequence data for two individual gametocysts from each grasshopper species were generated for the *18S* to *28S* multi-gene array. Sequence alignment resulted in 100% similarity for each replicate from the same host and 99.5% similarity between gregarines from different hosts. This study begins to shed light on gregarine diversity and specificity in the grasshopper host system.

(86) Diagnosing coccidiosis: coupling species identification and enumeration of mixed *Eimeria* species infections via probe-based qPCR

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Coccidiosis caused by members of the genus *Eimeria* (Apicomplexa: Eimeriidae) is ubiquitous in poultry production facilities worldwide. The genus *Eimeria* is speciose with thousands of species infecting a wide range of vertebrate hosts. The monoxenous life cycle of this parasite, coupled with high stocking density in commercial flocks, facilitates multiple challenge events, promoting clinical coccidiosis. The resulting over proliferation of asexual stages in the gastrointestinal tract creates severe lesions exacerbated by multi-species infections. This flock-wide disease costs the poultry industry billions of dollars yearly, devastating commercial and small operations alike. The severity of poultry coccidiosis is typically estimated using oocyst per gram (OPG) counts that provide an accurate enumeration of oocysts to inform clinicians as they make decisions regarding treatment. Useful as this method is, species identification and determination of relative numbers of those species is nearly impossible. Previously attempted methods of enumeration and species identification include methods that rely on morphological features to accurately identify species. For example, flow cytometry and image analysis algorithms have been explored, however, both are limited in their ability to distinguish morphologi-

cally similar species. Appropriate molecular methods may be able to provide accurate species identification to complement OPG quantification, allowing for a more specific approach to treatment or prevention. Using the mitochondrial *COIII* gene (mt COIII) as a target, both droplet digital polymerase chain reactions (ddPCR) and next-generation sequencing (NGS) were found to be similarly accurate in determining relative species numbers. These 2 methods, however, have their own advantages and disadvantages. Although ddPCR can provide relative species percentages, it is labor intensive (involving several steps) and needs further validation. Similarly, NGS of genus-specific amplicons can provide similar information to ddPCR but is cost-prohibitive for small numbers of samples. We explored the use of probe-based quantitative PCR, using the same mt *COIII* target, to remedy certain issues faced with ddPCR and NGS. Once validated, molecular differentiation can be performed in conjunction with OPG counts to generate absolute species numbers. This will be a key component of a refined sampling protocol standardizing the often-inefficient diagnostic pipeline for coccidiosis currently available to poultry veterinarians.

(87) Molecular characterization and co-evolutionary relationships of *Crassicauda* spp. (Nematoda: Spirurida) infecting cetaceans of the Northwest Atlantic

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Parasites of the genus *Crassicauda* (Nematoda: Spirurida) are among the most virulent helminth parasites of mysticetes (baleen whales) and odontocetes (toothed whales, including dolphins and porpoises), infecting the cranial sinuses, circulatory, renal, muscular, and reproductive systems. Due to limitations in sampling these giant (>3 meter) worms, morphological descriptions are often based on fragmented specimens. Few studies have analyzed *Crassicauda* molecularly, and none, to our knowledge, have analyzed *Crassicauda* infecting cetaceans of the Northwest Atlantic. In the present study, we 1) molecularly describe and identify *Crassicauda* species infecting five cetacean hosts [*Tursiops truncatus* (bottlenose dolphin), *Grampus griseus* (Risso's dolphin), *Kogia breviceps* (pygmy sperm whale), *Globicephala macrorhynchus* (short-finned pilot whale), *Megaptera novaeangliae* (humpback whale)] using the cytochrome c oxidase subunit 1 (*cox1*) gene marker; 2) evaluate the phylogenetic relationships among our *Crassicauda* spp. samples, augmented with sequences from GenBank, and 3) characterize the co-evolutionary relationships between *Crassicauda* spp. and 14 cetacean hosts using distance-based (PACo, ParaFit) and event-based (Jane 4) analysis methods. Phylogenetic analyses resolved 12 *Crassicauda* clades representing different species. We found instances in which morphologically identical parasites were recorded infecting the same organ tissues of the same host species, but did not group together molecularly, indicating cryptic species, suggesting the number of *Crassicauda* infecting cetaceans is underreported in the literature. Cophylogenetic analyses (PACo and ParaFit) detected significant global and individual-level congruence between parasite and host phylogenies, supporting a highly co-evolutionary relationship. Event-based analysis (Jane 4) detected an event scheme comprising 4 cospeciation, 2 duplication, 5 host-switching, 11 loss, and 7 failure-to-diverge events, resulting in a low overall reconciliation cost (30). Based on the resulting event schemes, we inferred a complex co-evolutionary scenario in which an ancestral *Crassicauda* sp. colonized and cospeciated with mysticetes, host-switched to and diversified in odontocetes, particularly Ziphiidae, and cospeciated with pelagic delphinids. Overall, these results indicate a significant co-evolutionary relationship between *Crassicauda* spp. and their cetacean hosts, reveal underestimated parasite diversity, and provide essential molecular data to support future taxonomic and diagnostic efforts. Furthermore, they enhance understanding of parasite-host co-evolution in the marine realm and have implications for monitoring health and disease in marine mammal populations.

(88) Body development in *Acheta domesticus* (Orthoptera: Gryllidae) infected with the hairworm, *Paragordius varius* (Phylum: Nematomorpha)

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Horsehair worms are parasites of terrestrial arthropods such as crickets and praying mantises. These parasites acquire nutrients from their arthropod hosts for growth and manipulate the host's behavior, often leading to reduction in survival. Unfortunately, few studies have evaluated the impacts on hosts infected with hairworms. In this study, we examined the survivorship and growth of male *Acheta domesticus* crickets infected with the

laboratory cultured hairworm, *Paragordius varius*. First, we exposed snails (*Physella* sp.) to 250 hairworm larvae. Successfully infected snails were then fed to two-day starved crickets. At the onset of the experiment cricket's body length, mass, pronotum, forewing, and hindwing length were recorded and repeated on the date of death. Of 170 male crickets exposed, 150 crickets did not release worms and were not used in the analyses (either because they weren't infected or died before worms could emerge). Twenty male crickets became infected with hairworms and released an average of 3 worms ± 2.6 (range = 1-10). Worms averaged 466 mm ± 270 (range = 110-1087). Infected male crickets survived after releasing worms for 11 days ± 17 (range 0 to 44) while the male control crickets survived 67 days ± 56 (range 8 to 215) after the infected crickets released their worms, suggesting that the worm development inside the infected crickets was detrimental to their survival. On their date of death, there was no difference between the length of control (3.69 ± 0.67; range= 2.25 to 5.40) and infected crickets (3.72 ± 0.29; range= 3.17 to 4.12; n=20 p=0.61). No difference was seen between the wing lengths of control (forewing: 1.27 mm ± 0.79; range= 0.26 to 2.58; hindwing: 1.98 mm ± 1.29; range =0.51 to 4.26) and infected crickets (forewing: 0.84 mm ± 0.57; range=0.51 to 2.19; n=20 p=0.04; hindwing: 1.41 mm ± 0.94; range=0.88 to 3.62; n=20 p=0.09). These results may suggest that infection could impose physiological consequences, such as developmental trade-offs and lifespan reduction. In the future we will measure infected crickets at the time worms emerge in addition to the date of death to remove confounding variables.

(89) An overview and recent updates on the ectoparasites associated with the herpetofaunas of Taiwan and the Philippines

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The Philippines and Taiwan are neighboring archipelagos representing a transitional area from the subtropics to the tropics. The herpetofaunas of these islands have been studied and documented for decades. However, the ectoparasites of Philippine and Taiwan reptiles and amphibians are relatively poorly known, especially with respect to their ecology and life histories. Such ectoparasites often possess interesting morphological and physiological attributes, with host utilization spectra ranging from polyxeny to monoxeny. Using spirit-preserved specimens from museums and field collections, we describe new host associations and geographic records for several herpetofauna ectoparasites known from Taiwan and the Philippine, including species of reptile-associated *Amblyomma* (bont ticks), the invasive reptile mite *Ophionyssus natricis* (Gervais) (Macronyssidae), and mites of the families Pterygosomatidae and Trombiculidae. We also present putative new species of mites belonging to the genera *Geckobia* Mégnin and *Endotrombicula* Ewing. Additionally, we report the first known cases of teratological anomalies of *Amblyomma* ticks in Taiwan and the Philippines. Apart from ectoparasitic acarines, we document new records of parasitism by land leeches (family Haemadipsidae) on the Taiwan/Philippine herpetofaunas, and we provide an overview of the natural history of reptile and amphibian ectoparasites in this region, while highlighting subjects for further research. Our findings augment current knowledge of herpetofaunal ectoparasites in Taiwan and the Philippines and emphasize the role of natural history accounts in the study of wildlife diseases.

(90) Molecular survey of haemosporidian parasites in hawks, falcons, and owls from Minnesota and North Dakota, with remarks on the phylogenetic relationships of haemosporidians in North American raptors

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Avian haemosporidians are a diverse group of apicomplexan parasites that are globally distributed and infect almost all avian orders. Haemosporidian surveys of raptors (birds of prey) are under-represented compared

to those of songbirds, perhaps due to the greater difficulty in capturing and handling raptors. In this study, we captured raptors over a 7-yr period from northeastern North Dakota and northwestern Minnesota. Using standard molecular methods, we successfully screened 595 individuals representing 5 species of hawks (Accipitriformes), 3 species of falcons (Falconiformes), and 7 species of owls (Strigiformes). The overall infection prevalence averaged 41.5%, ranging from 31.6% in falcons (n = 38) to 85.7% in owls (n = 14). Thirty-one (12.6%) of the 247 infected raptors were infected concurrently with two or more haemosporidian genera. *Leucocytozoon* was the most common parasite genus identified. A total of 27 haemosporidian lineages were identified composed of 8 *Leucocytozoon*, 6 *Parahaemoproteus*, and 13 *Plasmodium* lineages. Twelve lineages (44%) were novel lineages identified for the first time. Raptor host order showed a significant phylogenetic signal within the tree topology of haemosporidian lineages from North American raptors. A significant effect of host order was also identified in phylogenetic reconstruction of *Leucocytozoon* and *Parahaemoproteus* lineages, with large clades restricted to mostly Accipitriformes and Strigiformes. Similar host specificity was not evident within the *Plasmodium* phylogeny, with most lineages infecting multiple raptor host orders and some lineages not restricted to raptors. Our results demonstrate that raptors support a unique and diverse community of haemosporidian parasites, many of which are distinct to raptor species. Studying haemosporidians within raptors expands our knowledge of host-parasite evolutionary relationships, species diversity, and cryptic speciation within this ubiquitous group of parasites.

(91) Trematode and bopyrid isopod prevalences in the grass shrimp, *Palaemon pugio*, from the Rhode River, Maryland, USA

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The daggerblade grass shrimp, *Palaemon* (*Palaemonetes*) *pugio*, occurs across the Atlantic and Gulf coasts of North America and plays an important role in food webs as both a food source and host for many parasites. However, the prevalences and coinfections of two known parasitic taxa, trematodes and bopyrid isopods, are poorly understood, particularly in the shrimp's northern range. During the summers of 2018 to 2024, we collected *P. pugio* monthly (June – August) from two sites in the Rhode River (Maryland, USA). Shrimp were measured, sexed, and identified to species. All metacercariae and isopods were numbered and identified to the lowest taxonomic level. We found shrimp infected with metacercariae during every sampling event with prevalences ranging from 42.9% to 89.8% and mean abundance ranging from 1.2 to 8.2 metacercariae. We also encountered bopyrid infections during every sampling event, though prevalence was considerably lower (0.5% - 9.3%). Using GLM models, we found that metacercaria abundance was dependent on location, host sex, host size, and the interaction between location and size, while bopyrid prevalence was related to host sex, host size, and their interaction effect. Next, we are exploring the effects of time, water temperature and salinity on parasite abundance and prevalence. By exploring these host-parasite interactions across multiple years, we aim to assess the role these parasites may play on trophic interactions and how differing environmental conditions impact the strength of this biotic interaction within the Chesapeake Bay.

(92) New sequences of *Posthodiplostomum* spp. in Nebraska and Texas

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Posthodiplostomum is a widely distributed genus of diplostomid trematodes with reports from the Americas, Europe, and Asia. The genus utilizes a standard three host life-cycle, with a physid mollusk 1st intermediate host, a fish 2nd intermediate host, and a piscivorous bird definitive host. Until relatively recently *Posthodiplostomum* specimens were largely relegated to *P. minimum*. However, it is now evident the genus is speciose with numerous cryptic species infecting diverse fish and bird hosts. In North America, *Posthodiplostomum* spp. are commonly found in leuciscids (minnows), however relatively few sequences exist from Nebraska down to Texas. We collected *Posthodiplostomum* spp. metacercariae in southeast Nebraska from red shiner *Cyprinella*

lutrensis (n = 71) and north central Texas from blacktail shiner *Cyprinella venusta* (n = 22). Individual metacercariae were stored in 100% EtOH for DNA extraction or heat fixed in water then transferred to 100% EtOH for either staining or molecular techniques as required. We amplified the mitochondrial CO1 region and analyzed in Geneious Prime the samples with available sequences published on GenBank. Using the Mr. Bayes plug-in a Bayesian inference consensus tree was generated. Our samples from Nebraska and Texas form a clade with *Posthodiplostomum* sp. 4, *Posthodiplostomum* sp. UG1, 2, and 3, and *P. minimum* with 99.0% consensus support. The potential ubiquity of species within this group is likely due to the vagility of bird definitive hosts with sample sites in both Texas and Nebraska sit within major migratory flyways.

(93) Behavioral comparisons between an unknown *Gordius* (Nematomorpha) collected from a terrestrial environment and an aquatic hairworm, *Paragordius varius*

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The life cycle of most hairworms (Nematomorpha) requires an aquatic environment where the adults can lay their eggs. However, two terrestrial hairworm species were described in Oklahoma (2019) and Taiwan (2020). Both species occur seasonally in wet or moist soil. With the assistance of iNaturalist and community scientists, 338 adult hairworms were collected from a large rain puddle in Memphis, TN on January 5, 2025. They were transported to the lab in a sealed Ziplock gallon bag and maintained in the dark. The 331 males (average length = 16.7 cm) were significantly longer than the 7 females (average length = 13.5 cm; two sample t-test, p = 0.0493). Based on adult morphology and cysts recovered from co-occurring *Tubifex* sp., the worms were identified as an unknown *Gordius*. A series of behavioral experiments were performed on these worms as well as the aquatic *Paragordius varius*. If these unknown hairworms are terrestrial, then they should exhibit behavioral adaptations for the terrestrial environment compared to the aquatic *P. varius*. We examined desiccation, burrowing, phototaxis, hydrotaxis, geotaxis, swimming ability and freezing in both worms. When desiccated for three hours, three of five *Gordius* worms survived whereas all *P. varius* died. When placed in a container of soil, four of five *Gordius* females borrowed within 24 hours whereas none of the nine *P. varius* females burrowed. When placed in a half-darkened Petri dish, significantly more *Gordius* males chose the dark side after one hour (n = 19, p = 0.03, binomial test) whereas *P. varius* males showed no preference (n = 20, p = 0.41). When placed in a sealed container, *Gordius* males spent more time elevated and elevated at a higher distance than *P. varius* males. When placed in an artificial stream, *P. varius* males traveled significantly further than *Gordius* males in both flow and no-flow conditions. Neither species survived freezing conditions nor showed a preference towards water. Taken together, these observations suggest that the unknown *Gordius* possesses adaptations for the terrestrial environment. Molecular work and SEM will help determine if this hairworm represents a new species.

(94) Lousy idea or ticking all the boxes? Building an understanding of conservationists' views on parasite conservation to improve outcomes for parasite biodiversity

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Although there has been growing academic interest in parasite conservation over the recent years, practical interventions remain somewhat limited, indicating a significant gap between parasite conservation in theory and in practice. A key barrier to our current understanding of this apparent gap is that there has been little investigation of conservationists' attitudes towards parasite conservation or how these attitudes are related to different sociocultural factors including people's knowledge and perceptions of parasite biodiversity, and their conservation values. Addressing this knowledge gap will support the identification of different barriers to parasite conservation practice, as well as whether such barriers can be navigated in order to improve conservation outcomes for parasites. In order to address this knowledge gap, we conducted a Q-methodological study (a technique from social science for studying in-depth human perspectives) to understand the attitudes of professional conservationists towards parasite conservation. Our global sample includes a wide range of conservation professionals, across different experience levels and institutional roles, including researchers, decision-makers, and hands-on practitioners. Sociocultural factors that are important in informing conservationists' willingness to engage with parasite conservation include perceptions of the risk posed by parasites, cultural factors such as taxonomic bias, different approaches to valuing biodiversity, and access to economic

and technical resources. The results from this study can inform the design of socially acceptable parasite conservation interventions that lead to positive outcomes for parasites, their hosts, and their ecosystems.

(95) Do toxic cardenolides reduce parasitism in monarch-munching mice?

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Animals can reduce parasite loads by modifying their nest environment, avoiding high risk areas, or consuming foods with anti-parasitic properties. We hypothesize that the cardenolide-rich diets naturally consumed by rodents like the Black-eared mouse (*Peromyscus melanotis*) might have anthelminthic effects. Murid rodents (including *Peromyscus* and *Mus*) are highly resistant to cardenolides due to a modified sodium pump (Na^+/K^+-ATPase) structure that reduces binding of these potent sodium pump inhibitors. We used lab mice and *Heligmosomoides polygyrus bakeri* (*Hpb*) to test whether cardenolide consumption could reduce nematode survival. While we hypothesized these nematodes to be susceptible to cardenolides, results from *in vitro* and *ex vivo* experiments suggest that these parasites are relatively resistant to cardenolides. Infected mice fed cardenolide-rich monarch butterflies for five days did not exhibit different parasite loads or egg output compared to mice on control diets. Furthermore, adult worms maintained in 10^{-3} M ouabain exhibited only marginally reduced survival compared to worms maintained in control media. Culturing in 10^{-2} M ouabain reduced parasite survival more; however, 95% of worms survived at least 9 days in these cardenolide concentrations that are well above the lethal dose for rodents. Examination of the sodium pump sequences of *Hpb* and other nematodes revealed that at least two amino acid substitutions associated with reduced pump inhibition by cardenolides are widespread among nematodes. This suggests that cardenolide-rich diets are unlikely to quickly reduce nematode burdens and raises interesting questions about why nematodes are not more sensitive to toxic cardenolides.

(96) Revisiting onchocerciasis elimination in urban areas: *Simulium damnosum* sl. dynamics and emerging concerns in Osogbo, Nigeria

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Onchocerciasis, caused by *Onchocerca volvulus* and transmitted by *Simulium* spp., has historically been targeted for elimination in hyper- and mesoendemic areas. However, recent shifts in global onchocerciasis elimination goals emphasize the need to assess transmission risks in previously hypoendemic urban regions. This study presents a longitudinal analysis of blackfly abundance, seasonal variation, and environmental determinants in Osogbo, Nigeria, between January and December 2024. Blackflies were collected using human landing collection, dissected for parity determination, and analyzed molecularly for *O. volvulus* infections. A total of 493 blackflies were collected, with peak abundance in the dry months of February (268) and March (50), correlating with low rainfall (28.5 mm and 78.5 mm, respectively) and low relative humidity (66% and 78%). The wet season (May–July) saw a sharp decline in catches (2–7 flies/month), correlating with increased rainfall (162.8–232.8 mm) and higher humidity (83–90%). Relative humidity negatively correlated with blackfly abundance (r = -0.923, P = 0.009). Molecular screening for *O. volvulus* DNA in blackflies returned negative results. The persistence of blackflies in Osogbo suggests urban breeding sites, raising concerns about overlooked transmission risks. This study underscores the need for expanded surveillance, breeding site mapping, and targeted interventions in urban settings to eliminate onchocerciasis completely in Nigeria.

(97) Species distribution, molecular characterization and virulence of entomopathogenic nematodes in the southwest agro-ecology Nigeria: towards agricultural insect pest biocontrol

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Insect pests pose a major threat to agricultural productivity in Nigeria, necessitating sustainable control strategies. Entomopathogenic nematodes (EPNs) are promising biocontrol agents due to their natural effectiveness. This study investigated the species distribution, virulence, and molecular characterization of EPNs in the Southwest agro-ecology of Nigeria. The objectives were to isolate indigenous EPNs from Southwest Nigeria soils and assess their potential for insect pest management. A total of 79 soil samples were collect-

ed from agricultural fields across five states in Southwest Nigeria and screened for EPN presence. EPNs were detected in 30 samples (37.97%), with isolates distributed as follows: 7 in Kwara, 4 in Lagos, 5 in Oyo, 5 in Ogun, 8 in Osun, and none in Ekiti. Morphological and molecular analyses identified most isolates as *Heterorhabditis bacteriophora*, but two isolates (CG and MF) exhibited distinct characteristics, suggesting they may be unique variants. Morphological characterization of first-generation males considered spicule length, body shape, infective juvenile (IJ) length, cuticle texture, and anterior/posterior region shape. CG and MF isolates had longer IJs (~500µm), distinct annulations, and more tapered anterior and posterior regions. Molecular analysis of the 28S-D2/D3 region and ITS1 rDNA sequences confirmed CG and MF as distinct from *Heterorhabditis bacteriophora*. Virulence assays showed that CG and MF isolates had high pathogenicity, killing *Galleria mellonella* larvae within 24–36 hours, while other isolates exhibited lower virulence, causing larval death within 60–84 hours. PCR amplification revealed stronger band intensity (500 Bp) in CG and MF isolates compared to others (100–300 Bp). The study concludes that Southwest Nigeria harbors a diverse EPN community, with some isolates showing strong biocontrol potential. Further phylogenetic analysis is needed to confirm the uniqueness of CG and MF isolates. Additionally, research on mass production and field application methods is recommended for integrating EPNs into sustainable insect pest management strategies in Nigeria.

(98) Towards clarity in caligids: imaging and an interactive identification key for *Lepeophtheirus*

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Accurate identification of parasitic copepods is essential for taxonomic research, ecological research, and marine fisheries, particularly in aquaculture where parasitic copepods are significant pests. The genus *Lepeophtheirus* comprises 126 currently recognized species and includes several economically important ectoparasites of marine fishes. However, identification of species of *Lepeophtheirus* is often impeded by the number of species in the genus, outdated keys, scattered taxonomic literature, and subtle morphological distinctions. To address these barriers, we are developing the first interactive identification key for *Lepeophtheirus*. Unlike traditional dichotomous keys, interactive keys offer a more accessible format for users of varying expertise and have several advantages: any character can be used in any order, users can include uncertainty by entering more than one character state, and the key can be continually updated to reflect taxonomic advances—for example, adding new species or additional characters. This tool is built upon an extensive morphological character matrix compiled from original species descriptions, as well as direct examination of specimens through loans and visits to museum collections. We are also incorporating taxonomic data from closely related genera including *Anuretes*, *Pseudanuretes*, *Mappates*, and *Paralebion*, to clarify genus-level distinctions. Morphological traits are being documented using light microscopy, confocal laser scanning microscopy (CLSM), and micro-computed tomography (microCT), generating high-resolution images to accompany the key. These imaging techniques provide clearer views of diagnostic features, aiding in the interpretation of structures that are often difficult to visualize. Once complete, the key will be introduced in an open-access publication and hosted on the World Register of Marine Species (WoRMS), making it freely available to researchers, students, and fisheries professionals. By integrating modern imaging techniques with updated taxonomic data and an interactive interface, this project aims to lower the barrier of entry to copepod taxonomy and enhance the accuracy and accessibility of *Lepeophtheirus* species identification.

(99) *Litomosoides westi* (Filarioidea: Onchocercidae) and its intracellular *Wolbachia pipientis*: a new phylogeny shows evidence of additional horizontal transmissions of the *Wolbachia* endosymbiont

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The family Onchocercidae has over 250 species of nematodes, and at least 60 of those species harbor endosymbiotic *Wolbachia* bacteria in their lateral chords and ovaries. *Wolbachia pipientis*, a parasite of arthropods, has been transmitted to Onchocercid nematodes via hematophagous arthropod vectors, where it now positively influences the nematode's survival and reproductive capacities. The introduction of *Wolbachia* to Onchocercid nematodes has occurred multiple times. The mechanisms of *Wolbachia*'s transition from arthropod parasite to nematode mutualist are not fully understood, and the timeline of its introductions to nematodes

also requires a deeper investigation. *Litomosoides westi*, an Onchocercid whose *Wolbachia* has yet to be analyzed, was sequenced along with its *Wolbachia*. Both *L. westi* and its *Wolbachia* were placed in a phylogeny of Onchocercidae and *Wolbachia* pipientis respectively; the *Litomosoides* genus is monophyletic, but its Wolbachiae are not, suggesting another horizontal transmission of *Wolbachia*.

(100) Phylogenetic relationships of *Trichuris* (Nematoda: Trichocephalida: Trichuridae) inferred with mitochondrial genomes and evolution of host infection and morphological traits in representatives of Trichocephalida a clade of poikilothermic and endothermic hosts

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Members of Trichocephalida typically infect terrestrial tetrapods, with some members infecting aquatic organisms. A prominent member of this taxon includes the monoxenous *Trichuris*, common in terrestrial mammalian hosts. This makes them interesting as a model for studying macroevolutionary transitions in their transmission patterns, site-selection, origin of complex organs, and host-affinity. Based on mitogenomes, we reconstructed the phylogenetic relationships of 33 species of Trichocephalida, included in Capillaridae, Trichinellidae, and Trichuridae. Resulting topologies assisted to reconstruct three ancestral traits: 1. reproductive organs in males, 2. patterns of transmission (monoxenous, heterogenous, autoheteroxenous), and 3. target organ in definitive host. Our results show well supported clades, showcasing 8 independent clades in *Trichuris* (1.- Bovidae, 2.-Suidae, and 3.- Hominids, 4.- Holarctic cricetids, 5.-Nearctic Heteromyids, 6.- Neotropical Cricetids-Hystricognaths, 7.-European-African Murids, and 8.-Asiatic murids). In some cases, the relationships between groups of hosts were the same as in parasites (putative coevolutionary pattern) such as in Cricetid and Murid rodents. Results suggest that the ancestors of Trichuridae and particularly its descendants (*Trichuris*) maintained a monoxenous cycle, conservative and complex reproductive traits, and specificity for the cecum and large intestine (colon). In contrast, ancestors of Capillaridae and Trichinellidae were more adept at presenting heterogeneous and autoheteroxenous life cycles, with the absence of accessory tubular structures as reproductive organs. Their descendants display an array of patterns of transmission (monoxenous, heteroxenous, and autoheteroxenous) and infect different zones of the digestive system, such as esophagus, crop, stomach, small-large intestines. This research provides a more robust understanding of the relationships and evolution of the complexity of reproductive traits and patterns of transmission in a group of parasites of terrestrial and aquatic hosts. However, the reconstruction of these evolutionary transitions in Trichocephalida requires the inclusion of other representatives of Trichuridae, such as *Capillostrongyloides* (parasites of marine and freshwater fish) and *Pearsonema* (parasite of gallbladders in mammals). *Anatrichosoma* as a representative of Trichosomoididae (parasites of buccal-nasal mucosa and ocular organs in mammals) and *Cytopsis* as a representative of Cystoopsidae (parasites of fish and sauropsids).

(101) Resurrection and supplemental description of *Crepidostomum transmarinum* (Nicoll, 1909) Hunninen and Hunter, 1933 (Digenea: Allocreadiidae) infecting brook trout, *Salvelinus fontinalis* (Mitchill, 1814) (Salmoniformes: Salmonidae) from Gragg Prong, Johns River, North Carolina

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Crepidostomum transmarinum (Nicoll, 1909) Hunninen and Hunter, 1933 (Digenea: Allocreadiidae) has been regarded as a junior subjective synonym of *Crepidostomum farionis* (Müller, 1780) Lühe, 1909 since 1918. We herein resurrect *C. transmarinum* and provide a supplemental description for this species based on light microscopy of adult specimens infecting the intestine of brook trout, *Salvelinus fontinalis* (Mitchill, 1814) (Salmoniformes: Salmonidae) from Gragg Prong, Johns River, North Carolina. *Crepidostomum transmarinum* is morphologically distinct from all congeners by the combination of having a ventral sucker that is wider in diameter than the oral sucker, testes that have irregular margins, a genital pore that opens at or immediately posterior to the intestinal bifurcation, a vitellarium that extends anteriad into the forebody, and an excretory bladder that extends anteriad to the posterior margin of the anterior testis. Our new *28S* sequence

of *C. transmarinum* aligned over 1,151 bases was most similar to those of *Crepidostomum nemachilus* Krotov, 1959, (6 base pairs different, representing 0.5%) and *Crepidostomum brinkmanni* Faltýnková, Pantoja, Skírnisson, and Kudlai, 2020 and *Crepidostomum metoecus* (Braun, 1900) Braun, 1900 (type species) (both 7 bp, 0.6%). Our new *ITS2*sequence of *C. transmarinum* spanning the entire *ITS2* region was most similar to that of *C. brinkmanni* (397 bases, differing at 3 bases, representing 0.8%). Phylogenetic analyses of the *28S* and *ITS2* sequences both recovered *Crepidostomum* as polyphyletic within Allocreadiidae Looss, 1902, and *C. transmarinum* was sister to *C. brinkmanni*. This is the first record of *C. transmarinum* from the Johns River or from North Carolina.

(102) Ghosts of parasites past: rediscovery of a species of *Neoechinorhynchus* (Acanthocephala) and its newest congener

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A survey of intestinal parasites of freshwater fish in the Everglades, Florida in 2023 revealed *Neoechinorhynchus doryphorus* in several new hosts as well as the discovery of a new species of *Neoechinorhynchus* in *Micropterus salmoides*, Florida Bass. *Neoechinorhynchus doryphorus* was first described from *Jordanella floridae* in 1949 by Van Cleave and Bangham. This description was based on poor material and has not been observed since its discovery. *Neoechinorhynchus doryphorus* can be easily distinguished from other North American *Neoechinorhynchus* species by its markedly long straight anterior lateral hooks. Based on comparisons of our specimens and the original museum specimens we demonstrate that when properly fixed *N. doryphorus* does not exhibit a “cone”, one of the odd features in Bangham’s original description. Through examination of museum specimens from Bangham’s 1938 South Florida survey it is confirmed *N. doryphorus* was found but not documented from *M. salmoides*. In our survey we observed gravid individuals of *N. doryphorus* infecting *M. salmoides* as well as non-gravid individuals and cystacanths from five other fish species, resulting in six new host records. A new species of *Neoechinorhynchus* was documented from *M. salmoides*. While the species strikingly resembles the well-known and widely reported centrarchid neoechinorhynchid *Neoechinorhynchus cylindratus* it differs in 2 key features. The proboscis of the new species is fleshy and markedly wider than that of *N. cylindratus*. The most distinctive feature of the new species is the egg morphology which differs from all known *Neoechinorhynchus* in North America, whether from fish or turtles, for all species in which egg morphology is known. This new *Neoechinorhynchus* species has been observed in *M. salmoides* from Central and South Florida. Sequence data obtained for the 28S and ITS genes for both *N. doryphorus* and the new species corroborate our morphologically-based findings that these species are distinctive from their North American congeners.

(103) Tapeworms of freshwater fish in North America: update and prospects

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Tapeworms (Cestoda) are an iconic and widespread group of parasites that serve as suitable models for ecological, evolutionary and co-evolutionary studies due to their close association with their hosts – all major vertebrate groups. They are widespread and diverse in North American freshwater fishes. By the end of the 20th century, 125 species of adult tapeworms were reported: 56 species in Canada, 106 species in the USA and only 13 species in Mexico (including 5 in its Neotropical part). However, given the great diversity of North American freshwater fishes, this number seems relatively low. Most of the existing knowledge dates back to the 20th century, but with the notable exception of Mexico, research on fish parasites in this region has declined significantly in recent decades. As a result, the species diversity, host associations and phylogenetic relationships of freshwater fish tapeworms remain poorly understood. Recent taxonomic revisions of several tapeworm groups – particularly within the orders Caryophyllidea, Bothriocephalidea and Onchoproteocepha-

lidea – have incorporated both morphological and molecular data from newly collected specimens and museum collections. This study provides an overview of the current state of knowledge on diversity, systematics and host-parasite relationships of freshwater fish tapeworms in North America. It also critically evaluates host specificity at the definitive host level using molecular data and identifies key areas for future research. These include targeted field sampling and the application of integrative taxonomic approaches to well-preserved specimens. Acknowledgements: This study was supported by the Ministry of Education, Youth and Sports of the Czech Republic (no. LUAUS 23080).

(104) First record of a polystome (Monogenoidea: Polystomatidae) from a crocodilian: a new genus and species of polystome infecting the eye of an American alligator, *Alligator mississippienesis* Daudin, 1802 (Crocodilia: Alligatoridae) in a north-central Gulf of Mexico saltmarsh (Rockefeller Wildlife Refuge)

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During July 2021 through June 2024, we necropsied 35 American alligators from Louisiana, Alabama, and South Carolina (including Gulf of Mexico and Atlantic Ocean river basins). The eye of one wild-caught American alligator measuring 1450 mm in total length and captured from saltmarsh habitat within the Rockefeller Wildlife Refuge (Grand Chenier, Louisiana) on 19 July 2021 was infected by a new genus and species of Polystomatidae. The new species resembles species of Polystomoidinae Yamaguti, 1963 and Oculotrematinae Yamaguti, 1963. It is readily differentiated from species of Polystomoidinae by the combination of having circular haptoral suckers with skeletal elements but that lack hamuli and deep incisions between suckers; ceca having anterior, medial, and lateral diverticula; a compact testis that occupies a small proportion of the intercecal space (vs. a broad testis that spans the intercecal space); a sinistral and intercecal ovary (vs. an ovary that is ventral to the sinistral cecum) having a proximal oviduct extending mediad and then posteriad (vs. proximal oviduct extending anteriad); a uterus that is small (occupying a minute portion of the intercecal space), medial, and located close to the cecal bifurcation; and vaginal pores that open laterally at level of or slightly posterior to the level of the testis. It differs from species of Oculotrematinae by having vaginae and lacking hamuli. No other nominal polystome has this combination of features, and therefore the erection of a new genus for the new species is wholly warranted. We lack a nucleotide sequence for the new species because we used the only specimen we collected as a heat-killed, formalin-fixed, stained wholemount (holotype) for taxonomic study that prioritized morphology. Without a nucleotide sequence (and phylogenetic analysis) we herein refrain from emending an existing subfamily or proposing a new subfamily to accommodate the new genus. This is the first record of a polystome infecting a crocodilian and the first definitive record of an ectoparasitic polystome infecting a host captured in saltwater.

(105) Integrating molecular and morphological methods for delimiting gregarine species

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The difficulty of delimiting species is not unique to gregarines, but clear and uniform methods for alpha-taxonomy are requisite to stable, predictable phylogeny and higher-level classification. We tested an integrated approach combining morphological and molecular methods to examine, revise, and expand the gregarine species comprising known members of Blabericolidae infecting blaberid cockroaches of the subfamilies Blaberinae and Oxyhaloinae. We compare our results to prior integrated studies of gregarine taxonomy and report one new species, three new synonyms and two new combinations recognized in the study. We demonstrate the utility of confidence interval evaluation of morphometric data and demonstrate the value of relative between-species and within-species genetic variance ratios when using molecular data to delimit species. We conclude that morphological and molecular tools contribute disproportionately to Type I and Type II errors respectively, but in combination they provide a reciprocal check on delimitation errors and, that integrated morphological and molecular methods using multiple conspecifics as a reference framework is the preferred approach for delimiting gregarine species.

(106) New host and distribution records of ectoparasitic insects and acarines associated with bats (Mammalia: Chiroptera) from the Philippines

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Bats (Mammalia: Chiroptera) serve as hosts to an interesting assemblage of both micro- and macroparasitic arthropod taxa. Some of the ectoparasitic arthropods are exclusive bat specialists (e.g., Streblidae, Nycteribiidae, Polyctenidae, Ischnopsyllidae, and Spinturnicidae) and display the appealing morphological adaptations through tight coevolutionary relationship. Ectoparasitic arthropods associated with bats have been relatively little studied in the Philippines, and only a handful of reliable taxonomic accounts exist. Here, we present new data concerning the host specificity of Philippine bat parasites and their geographic distribution, based on museum collections and field-collected specimens. Among our findings are several novel host associations and new island records for winged and wingless bat flies in the subfamilies Brachytarsininae, Cyclopodiinae, and Nycteribiinae. Additionally, we provide a review of the Philippine Ischnopsyllidae, a family of fleas known only from bats, together with new host and locality records. We also present new host and island records for soft ticks belonging to the genera *Argas* and *Ornithodoros*, as well as bat mites in the family Spinturnicidae. These results add to our knowledge of the diversity and distribution of ectoparasites associated with bats in the Philippines, underscoring their potential role as disease vectors.

107) A newly discovered trematode parasite infecting the bay scallop, *Argopecten irradians*, in North Carolina

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Starting in 2012, bay scallops (*Argopecten irradians*) in North Carolina were observed to be infected by an unidentified macroparasite, and the same parasite has been observed infecting bay scallops on the west coast of Florida. Phylogenetic analysis of DNA sequence data from a nuclear 28S rDNA fragment indicates that the parasite is a trematode in the superfamily Hemiuroidea, family Didymozoidae, genus *Saccularina*, and that it forms a well-supported clade with another member of the genus from Australia. Dissection and histopathological examination confirm that the trematode is using the scallop as a first intermediate host, infecting and greatly distorting the afferent vessels of the host's gill filaments. Laboratory experiments indicate that infection negatively impacts scallop clearance rates, growth, and fecundity. Population genetic analysis using a fragment of the *cox1* mitochondrial gene indicates a recent population expansion, supporting our hypothesis that the parasite is a recently introduced species. Nevertheless, the parasite is already well-established in North Carolina; our monitoring efforts through space and time found relatively high *Saccularina* sp. infection prevalence in both wild (max 18%) and cultured (max 28%) scallop populations. This newly discovered parasite represents a novel threat to an already-imperiled fishery, and as such, merits further investigation.

(108) Labeling hydrogen peroxide accumulation in the mitochondria of *Plasmodium falciparum* parasites cultured in different oxygen environments

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Malaria is caused by the parasite genus *Plasmodium*, with the deadliest species being *P. falciparum*, which has a global impact of over 600,000 deaths annually. Throughout the human body, oxygen (O_2) concentration varies depending on anatomic location. Within hypoxic sites such as the brain and bone marrow, O_2 concentration can range from 1% to 5%, whereas in sites such as arterial blood, the range is 12% to 13%. *P. falciparum*

is characterized as a microaerophile, and it replicates most efficiently *in vitro* in hypoxic conditions (0.5-5% O_2) during its asexual intraerythrocytic development. *P. falciparum* can replicate in higher oxygen environments *in vitro*, but replication is slower. The mechanism(s) underlying the variability in *P. falciparum* intraerythrocytic replication according to O_2 concentration have not been elucidated. One hypothesis for why higher O_2 may result in slower replication is that higher O_2 environments may induce more oxidative stress within the parasite. We hypothesized that *P. falciparum* parasites grown in 13% O_2 (high end of physiological O_2) would have higher intracellular ROS accumulation levels than those grown in 1% O_2 (low end of physiological O_2). We measured fluorescence intensity within *in vitro* cultures using SYTO 61 as a nucleic acid stain and MitoPY1 as a ROS marker to test this. MitoPY1 is a fluorescence probe that selectively labels H_2O_2 in the mitochondria of live cells, which, to our knowledge, was the first time used in *P. falciparum*. We grew *P. falciparum* parasites *in vitro* and incubated them with either 1% (hypoxic) or 13% (normoxic) O_2, measured fluorescence intensity in 48-hour replication cycle intervals, and quantified fluorescence intensity. We observed higher fluorescence intensity for parasites grown in 13% O_2, indicating higher levels of H_2O_2 accumulation in 13% O_2 compared to 1% O_2. These results suggest that *P. falciparum* parasites grown in normoxia are under higher oxidative stress than those grown in hypoxia, but more work is needed to validate this result.

(109) Testing the impact of probiotic intervention on chytrid fungus loads during amphibian hibernation

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Amphibian immune defenses are reduced in cold temperatures due to low metabolic activity, resulting in potential overgrowth of opportunistic microbes on amphibian skin. The deadly fungal parasite *Batrachochytrium dendrobatidis* (Bd) is an infamous opportunistic grower during cold-weather amphibian hibernation, but it is not known if seasonal depression of the amphibian immune system may also be exploited by beneficial skin microbes that inhibit Bd growth. If so, conservation managers could amplify anti-chytrid defenses more efficiently by applying probiotic skin treatments (i.e., beneficial skin bacteria) to fight Bd during winter months. We tested whether amphibians that received probiotic bacterial treatments during hibernation would retain those bacteria for the remainder of their hibernation and after transitioning back to warm temperatures, and whether they would have less severe chytrid fungal growth than those that did not receive probiotics. To this end, we hibernated eastern newts (*Notophthalmus viridescens*) that were already infected with Bd from their natural environments and treated them with either the anti-Bd skin bacteria *Iodobacter fluviatilis*, *Janthinobacterium lividum*, a combination of both probiotics, or sham treatment with no probiotics. From repeated skin swabbing, we characterized their skin microbiota via *16S rRNA* gene sequencing before treatment and weekly for six weeks after treatment. We also quantified chytrid fungal loads with qPCR targeting the Bd *ITS* gene across all timepoints. Newts in treatment and sham-treated control groups experienced mortality during hibernation that may have been related to Bd or stress of hibernation. Microbiota characterization and qPCR results are forthcoming, and we expect them to reveal whether probiotics established on the skin of their hosts and whether probiotic treatment limited Bd intensity in cold temperatures. The results of this project will inform treatment and management plans for upcoming test applications of the probiotic *I. fluviatilis* to wild eastern newts in Massachusetts. This project was carried out as a CURE course project in Spring 2025, with UMass Boston students planning the final project design and coordinating many steps of this work.

(110) Role of a *Cryptosporidium parvum* signaling kinase in male gametogenesis and virulence

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The protozoan parasite *Cryptosporidium parvum* is a leading cause of diarrheal disease and mortality in young children and neonatal calves. Currently, no drugs or vaccines are available to treat or prevent cryptosporidiosis. Discovering new drug and vaccine targets requires a fundamental understanding of the parasite's lifecycle, which involves a coordinated and timely progression from asexual to sexual stages, ultimately leading to the formation of the oocyst. The molecular signaling mechanisms that control the sexual cycle in *Cryptosporidium* remain poorly understood. To address this knowledge gap, we targeted the *C. parvum* calcium-dependent protein kinase 5 (CDPK5), which is expressed solely during the sexual cycle. We utilized CRISPR/Cas9 genome editing to epitope tag CDPK5 at the endogenous locus. Our cellular biological analysis revealed that this ki-

nase is expressed only during male gamete development and plays an important role in the egress of mature male gametes. Genetic ablation of this kinase resulted in decreased virulence and reduced oocyst shedding in an immunocompromised mouse infection model. Using phosphoproteomics, we identified putative substrates of CDPK5 and the underlying biological processes regulated by this kinase. Our results shed new light on *Cryptosporidium* cell biology by revealing the important role of a signaling kinase in male gametogenesis and identifying an attractive target for blocking disease transmission. Future studies are planned to unravel the role of these identified substrates in male gametogenesis.

(112) AI-driven predictions of phylogenetic trees from zoogeographical data in dactylogyrids (Platyhelminthes: Monogenea): a novel strategy for external phylogenetic support

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In this study, we present a novel application of a modified random forest model to integrate zoogeographical data into phylogenetic analysis, focusing on dactylogyrid monogeneans. These parasites are characterized by high host specificity, limiting their natural distribution to the ranges of their hosts, and have been widely used as models for investigating host-parasite co-speciation. Building on our recently published work in Cladistics, we aim to deepen our understanding of host-parasite coevolution by treating ecological variables—such as host locality and climate—not as independent traits, but as interdependent phylogenetic characters. To evaluate this approach, we apply the model to dactylogyrid groups with published data, including the broadly distributed and highly diverse genus *Dactylogyrus*, as well as Neotropical endemics such as *Anacanthorus*, *Cosmetocleithrum*, *Demidospermus*, and *Urocleidoides*. We hypothesize that phylogenetic trees that can be more accurately predicted from zoogeographical data more closely reflect the parasites' evolutionary history. By incorporating both natural and perturbed datasets, we assess the model's robustness and its capacity to recover consistent topological patterns. This approach offers a novel source of external support for phylogenetic inference and promises to enrich our understanding of host-parasite associations.

(113) Mining biodiversity data from the largest online citizen scientist platform—but does it work for parasites?

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The first horsehair worm reported to iNaturalist from the United States occurred in October 2012. Since then, reports of horsehair worms (Phylum Nematomorpha) by citizen scientists have increased each year, averaging 0.315 reports per day between 2012 and 2023. Today there are more than 2,200 reports from the U.S. with an average of 1.13 reports per day in 2024. But do these reports contribute to our knowledge of the biodiversity of horsehair worms? The purpose of this study was to determine how iNaturalist data can be mined to expand our limited knowledge on nematomorph biodiversity. Reports were downloaded from iNaturalist that were identified as 'Horsehair worms' (Phylum Nematomorpha) with parameters of taxonomic rank, location, data observed, date recorded, coordinates, and iNaturalist assigned identification numbers. The accuracy of taxonomic identifications was evaluated and curated by supporting the observation or revising the taxonomic ranking. We found that of the 2200 reports downloaded from 2012-2024, 26.9% were incorrectly identified or could not be identified. Of the 26.9%, 53.51% were insect parasitizing nematodes in the family Mermithidae (Phylum Nematoda) with superficially similar morphology and often confused with horsehair worms, 15.87% were annelids, 10.70% were indiscernible as an animal, hairworm or otherwise, 5.72% of pictures were too blurry to tell with any accuracy if they were hairworms and the remaining composed several different groups. We then visited two sites in Florida based on coordinates in iNaturalist and searched for worms. Both sites were positive for adult worms and were collected for morphological analysis and may be the first published hairworms described from Florida. While horsehair worms comprise 0.0008% of iNaturalist's 234,625,770+ observations, we will argue they are nonetheless important for parasitologists to expand their biodiversity

studies. Only 360 species of the estimated 2000 species of horsehair worm have been identified. Our results expand the distribution of hairworms by providing the first report from Florida. DNA analysis and morphology will be presented. From a broader perspective, iNaturalist provides species identification and distribution for more recognizable taxa but can be used to assist in biodiversity studies for parasites, at least in some groups.

(114) Genetic analysis of myxozoans through Sanger sequencing and metabarcoding 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 New York 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 using Sanger sequencing in 75% of the 123 specimens (122 LMB, 1 SMB). Mixed infections, as evidenced by overlapping peaks in the sequencing reads, were common with 25% of LMB hosts infected with multiple genotypes. To resolve these mixed sequences, we used the Oxford Nanopore Minion system to generate metabarcoding data. We also developed our own internal index primers to allow for PCR products to be pooled prior to Nanopore indexing, thus reducing metabarcoding cost per sample. From these combined data, we 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. Some *Myxobilatus* genotypes were more common in certain locales than others, but there was no consistent pattern to suggest that these parasites are location 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, evaluates metabarcoding to resolve mixed infections, and provides continuing evidence of cryptic species within this broader group.

(115) Phylogenetic relationships of the Nippostrongylinae from the Americas reveals homoplasy in *Carolinensis*, *Hassalstrongylus* and *Vexillata*

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The Nippostrongylinae is a group that includes cricetid species. In the New World, the taxon is represented by 11 genera and 82 species. Two anatomical regions are used to evaluate the characteristics that allow the identification and classification of the organisms in the taxon: the cuticular ornamentation along the body (synlophe) and the caudal bursa. Diagnostic and classificatory features are derived from details in the orientation of cuticular ridges and bursal papillae and size of the genital cone. However, the analysis of these characteristics requires a partial or total destruction of the specimens, and the variation is observed in a very small subset of organisms per species. To evaluate the phylogenetic signal of these characteristics, we reconstructed the first phylogeny for the taxon using five gene regions and including representatives of the most common and diverse genera. The resulting phylogeny reveals five distinct clades and identifies three non-monophyletyc taxa including *Carolinensis*, *Vexillata* and *Hassalstrongylus*. *Carolinensis* is subdivided into four: *Carolinensis*, *Boreostrongylus*, *Neoboreostrongylus* n. gen. and *Tepalcuanema* n. gen. Adittionally, *Stunkardionema* is resurrected to include *Vexillata noviberiae* while *Hassalstrongylus* is divided into two, erecting *Lovostrongylus* n. gen. to include species that are closely related to *Guerrerostrongylus* and *Trichofreitasia*. These three genera present a caudal arrangement of type 2-2-1. Furthermore, species in *Hassalstrongylus* share a common ancestor with species from *Malvinema* and *Stilestrongylus*. Our results reveal the existence of an additional genus yet unnamed and emphasize the usefulness of framing morphological characters within a testable comparative framework.

(116) Characterization of intestinal pinworms (Nematoda: Heteroxynematidae) isolated from endangered Hoffman´s (*Ochotona hoffmanii*) and the Daurian pika (*Ochotona dauurica*) from Delgerkhaan and Hantay Mountains, Mongolia

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Parasites face disadvantages and a unique conservation challenge for three reasons: Dependence on host survival; Random parasite distribution in host populations; and the conception of parasitic nematodes as unwanted and, therefore, neglected. This problem increases when potential hosts have both a patchy distribution and are protected due to their endangered status, thus preventing endoparasite studies and hindering investigations to document their relevance. Pikas are endemic to montane areas across the Holarctic, with a predominantly Asian presence, yet a few populations are present in America and Europe. Their restricted distribution and specific niches make both pikas and associated microbiota prone to population decline. Herein we document the morphological and genetic diversity of pinworms found in 2 pika species with no previous helminthological studies. Samples were collected from Mongolia's northern and north-central mountainous regions and recovered from catalogued museum specimens. From north-central (Delgerkhaan), *Ochotona hoffmanii*, is an endangered species restricted to Mongolia and Russia; from the northern samples (Hantay), *Ochotona dauurica*, is also present across Russia, Mongolia, and China and it is considered of least concern for protection. Utilizing morphometric analyses and phylogenetic reconstructions employing COI and 28S markers, we assessed their taxonomic diversity based on reciprocal monophyly. Our results suggest 3 putative undescribed *Cephaluris* morphotypes diagnosed by proportions and discrete characters. From *Ochotona hoffmanni*, two putative taxa, including *Cephaluris* sp. 1 and *Cephaluris* sp. 2, that resemble *Cephaluris ochotonae* described from *Ochotona rufescens* in Afghanistan but are different based on the papillae arrangement and shape of the precloacal crests (heterogeneous vs. canine shaped vs canine-ovoid). A third morphotype named *Cephaluris* sp. 3 group was found in *Ochotona dauurica*, which is similar in precloacal crest patterns to *Cephaluris* sp. 1; however, the papillae arrangement differ, and the tail shape in females presents a dentate pattern. We plan to image specimens with SEM to identify additional characters that help characterize species. Our current work underscores the relevance of scientific collections as strongholds for diversity studies. They have become one of our most precious resources, especially for endangered and inaccessible species. Recognizing and utilizing these collections is crucial for advancing our understanding of biodiversity.

(117) Description of *Baccigeroides currani* n. sp. (Digenea: Gymnophalloidea) infecting intestinal mucosa of Gulf menhaden, *Brevoortia patronus* Goode, 1878 (Clupeiformes: Alosidae) from the northern Gulf of America

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We describe a new species of *Baccigeroides* (Digenea: Gymnophalloidea) infecting the intestine of the Gulf menhaden, *Brevoortia patronus* Goode, 1878 (Clupeiformes: Alosidae) from the Gulf of America. The new species differs from its congeners by the combination of having an oral sucker that is narrower than the ventral sucker, ceca that extend posteriad to the middle of the post-testicular space, a cirrus sac that extends posteriad to the middle of or beyond the posterior margin of the ventral sucker, a bipartite seminal vesicle, and a post-testicular ovary. We emend *Baccigeroides* Dutta, 1995 to include features of the new species and its congeners: ceca that extend posteriad to the middle of the post-testicular space, a cirrus sac that extends posteriad to the middle of or beyond the posterior margin of the ventral sucker, a bipartite seminal vesicle, a median genital pore, a post-testicular ovary, and a Laurer's canal pore opening near the posterior body end. The *ITS2* and *28S* sequences of the new species were most similar to those of *Bacciger bacciger* (Rudolphi, 1819) Nicoll, 1914 and *Pseudobacciger cheneyae* Sun, Bray, Yong, Cutmore, and Cribb, 2014. Phylogenetic analyses of the *28S* and *ITS2* each recovered species of *Bacciger* Nicoll, 1914, *Baccigeroides*, and *Pseudobacciger* Nahhas and Cable, 1964 as closely related taxa and sister to gymnophalloids of Tandanicolidae Johnston, 1927. The present study comprises the first phylogenetic analysis that includes a sequence of *Baccigeroides* and the first report of species of *Baccigeroides* infecting an alosid and from the northern Gulf of America.

(118) Effects of cercaria dose and timing on the infrapopulation structure of *Posthodiplostomum minimum* in bluegill sunfish (*Lepomis macrochirus*)

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Cercariae of *Posthodiplostomum minimum* penetrate the integument of freshwater fishes, and rely on the circulatory system (at least in part) for distribution within the fish host. The metacercariae encyst and often develop within multiple organ systems of the same individual host. It has been suggested that during migration within the fish host, metacercariae of *P. minimum* may have the capacity to sense existing infections and prolong their migration as a result. This phenomenon should manifest in distributions of encysted metacercariae that differ based upon the infection status of a newly infected host. Wild-caught bluegill sunfish were exposed to varying numbers (25, 50, 100, or 200) of cercariae in a single exposure event, and necropsied after 14 days to evaluate the relationship between infective dose and distribution of metacercariae in the fish. There was a positive relationship between the number of cercariae used for the exposure, and the number of locations from which metacercariae were recovered. In a separate experiment, bluegill sunfish were exposed to a total of 200 cercariae of *P. minimum* either in a single dose, or spread out equally across 2, 4, or 8 exposure events separated by 24 hours. Although spreading out the dose had little observable effect on the infrapopulation structure of *P. minimum* when exposed to 200 cercariae over 1-4 exposure events, the proportion of metacercariae recovered was substantially higher when the 200 cercariae were divided across 8 exposure events, and the proportion of metacercariae recovered from the liver was reduced. The results suggest that the timing of exposures has the potential to alter the distribution of metacercariae of *P. minimum* and potentially influence survivorship during the initial infection phase.

(119) Parasite avoidance behavior is remarkably adaptive for the Caribbean spiny lobster but has indirect consequences and a questionable future in our changing ocean

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Seawater is very effective at distributing parasites. The same properties of seawater that lend it so well to parasite transport also make it effective for transporting chemosensory cues. Marine organisms, and particularly crustaceans, have developed sensitive chemosensory receptors and use them for a multitude of ecological functions that include avoiding predators and competitors, locating mates and conspecific aggregations, foraging and, for spiny lobsters at least, avoiding infection. The Caribbean spiny lobster *Panulirus argus* is normally social, sharing crevice shelters with healthy conspecifics during the day. This behavior is mediated by chemical cues found in lobster urine and confers typical advantages of sociality such as reduced predation risk. However, the Caribbean spiny lobster is also able to detect and avoid urine-based cues from conspecifics infected with the lethal virus PaV1 (*Panulirus argus* Virus 1). This behavior reduces the infection risk for individuals and potentially reduces the likelihood of an epizootic. Despite its adaptive value, the avoidance of infected conspecifics has indirect consequences for spiny lobsters by limiting the availability of suitable shelters and driving the spatial distribution of their populations. Moreover, as the ocean warms, becomes more acidic, and is impacted by extreme rainfall events, these physical and chemical changes threaten the functionality of chemosensory-driven behaviors, such as avoidance of PaV1 infection by healthy lobsters. Although reports of parasite avoidance behavior among marine animals remain relatively rare, it has remarkable consequences for Caribbean spiny lobsters and similar behaviors likely exist in other marine parasite-host systems, but they simply remain undetected.

(120) Role of ecosystem characteristics in the evolution of complex helminth lifecycles

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Multi-host lifecycles feature prominently in many parasite groups, thus indicating selective advantages for complex lifecycles under wide-ranging conditions. Trophically transmitted generalist parasites are considered most prone to developing such lifecycles, as transitions from smaller hosts to larger ones offer increased space for growth and reproduction, which provides a selective advantage. However, the number of

hosts in a lifecycle varies considerably and mechanisms that determine the length of these multi-host lifecycles remain unclear. Here we took a macroecological view of complex lifecycle evolution to determine the role ecosystem characteristics play in developing multi-host helminth lifecycles. Using a dataset of 8,604 helminth records with species that exhibit at least partial trophic transmission, we posed two key questions: 1) Do lifecycle lengths differ across ecosystems? and 2) Is lifecycle length related to either host availability, as indicated by latitudinal biodiversity gradients, or trophic interaction opportunities, as reflected by free-living food chain length? We determined the maximum known number of hosts per helminth lifecycle and noted if lifecycles were terrestrial, freshwater, or marine. The mean latitude of each helminth species' range was obtained using the London Museum of Natural History's Parasite-Host Database, and mean number of free-living trophic interactions at that latitude was derived from iDiv's Global Database of Traits and Food Web Architecture, resulting in a subset of 803 georeferenced helminth records linked to localized food webs. Pairwise comparisons using rank sum tests with continuity correction found significant differences in the mean number of hosts across ecosystems (x^2=622.26, df = 2, p < 0.001) in the full dataset, with marine lifecycles possessing the most hosts, followed by freshwater, then terrestrial ones. Randomization tests also revealed significant differences in free-living food chain length between ecosystems (p < 0.001). However, generalized linear models using the georeferenced subset indicated that ecosystem type and latitude were the best predictors of helminth lifecycle length. These findings indicate that both ecosystem of origin and latitude where a lifecycle evolves significantly influence how many hosts are incorporated into it. This suggests that energy flow through ecosystems and available host biodiversity play key roles in the evolution of complex helminth lifecycles.

(121) Multipathogen interactions and the fecal microbiome of passerines in the Greater Yellowstone Ecosystem: Phase I

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Understanding how co-infecting pathogens interact with the host microbiome is vital for advancing the field avian disease ecology. This research investigates the relationships among multiple pathogens and gut microbial communities across approximately 55 passerine species in the Greater Yellowstone Ecosystem (GYE). Emphasizing the role of the microbiome in shaping infection dynamics, I integrate field-based disease surveillance of West Nile virus (WNV), Saint Louis Encephalitis virus (SLEV), avipoxvirus, haemosporidia causing malaria (*Plasmodium* spp., *Leucocytozoon* spp., *Haemoproteus* [*Parahaemoproteus*] spp.), coccidia, and pathogenic bacteria across passerines with high-throughput sequencing and ecological modeling. Fecal samples (n = 441) were aseptically collected in the field and sequenced at the University of New Hampshire's Hubbard Center for Genome Studies. I amplified the V4/V5 region of the 16S rRNA gene (primers 515F–926R) and conducted 250 bp paired-end sequencing on an Illumina NovaSeq platform. Sequences were processed using QIIME2. Diversity analyses included Shannon's Entropy, Faith's Phylogenetic Diversity, and Pielou's Evenness. To reduce bias from rare taxa, I normalized data using a 1,000-read threshold. I found that 3.7% of fecal samples were positive for *Mycoplasma gallisepticum*, based on microbial community profiling and clinical signs. Furthermore, potentially immunomodulating bacteria such as *Akkermansia*, *Bifidobacterium*, *Enterococcus*, *Faecalibacterium*, *Lactobacillus* were found in 15.23% of individuals, less than I had predicted. Individuals exhibiting active flavivirus (WNV and/or SLE) infection at the point of capture tended to have lower values of both Shannon's Entropy and Pielou's Evenness, suggesting potential disruption of microbial diversity during acute infection. Furthermore, alpha diversity metrics varied significantly across bird species, supporting species-specific microbial baselines and potential immunological trade-offs. These findings highlight the power of metabarcoding approaches for characterizing gut microbial dynamics in wild birds and underscore the importance of the microbiome in mediating susceptibility to infection. That said, microbial taxon-specific presence or abundance, which may be masked by alpha diversity metrics, may be more illustrative of any immune modulation. By linking microbial diversity with infection status for viruses, bacteria, and protist parasites, this research offers novel insights into host–pathogen–microbiome interactions and their implications for disease ecology in free-living avian communities.

(122) Current knowledge of parasitic nematodes of fish in Senegal

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Located on the extreme western tip of the African continent, Senegal covers an area of 196,722 km² and has enormous potential for ground and surface water. With 700 km of coastline and a hydrographic network comprising the Senegal, Gambia and Casamance rivers, The Sine, Diomboss and Saloum inlets, the Guiers lake, the Kayanga river and its tributary the Anambé, Senegal has a wide range of fishery resources, including fish, which form a major part of its economy. Parasitism is a form of life acquired by certain nematodes during the course of evolution, essentially by penetration of the skin or ingestion by the host, with various models throughout the phylogenetic diversification of nematodes having plants, invertebrates and vertebrates as host. Among the latter, fish are important group that host nematodes in various organs. In Senegal, the study of nemathelminth parasites of marine and freshwater fish has evolved very little since the work of Campanat-Rouget and Vassiliades. It would be useful, at a time when these studies are becoming increasingly important, and serve as a basis for further work, to draw up an inventory of the nematodes reported to date in Senegalese fishes, adding to the bibliographical data a few personal determinations. For this purpose, a documentary search was carried out in the central library of Cheikh Anta Diop University and the libraries of the Institut Fondamental d'Afrique Noire and the Ecole Inter-Etat des Sciences Vétériniaires of Dakar, the Senegalese Institute of Agricultural Research, and on the web. The results of this inventory reveal the presence of 24 genera of nematodes in marine fish and 19 in freshwater fish, with 6 genera common to both environments. Histological and ecological studies were used to characterize nematode communities and understand the effects on their host. Nematode parasites of fish in Senegal represent a major health and economic issue. Studying them provides a better understanding of their impact on fish and highlights the need for increased surveillance to protect the health of aquatic ecosystems and fishing activities.

(124) On the re-discovery of the North American medicinal leech, *Macrobdella decora* (Say, 1824) in northern Mexico

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Macrobdella decora (Say, 1824), is well-known for its blood feeding preferences and its ability to feed on the blood of a wide variety of vertebrates, including humans. This species has a widespread distribution including 26 US states, eight Canadian provinces, where it is relatively common in the shallows of lakes, rivers, swamps, ponds, and streams. A single occurrence record of *M. decora* in one state in northern Mexico represented a significant southern extension of the species distribution. The genus *Macrobdella* includes five species restricted to North America, with *Macrobdella mimicus* as the sister species of *M. decora*. A recent phylogeographic study including samples of *M. decora* from a substantial proportion of its natural distribution, failed to recover geographic structure among populations, despite the presence of well-recognized biogeographic barriers. In that study, no samples from Mexico were included despite extensive efforts to collect new specimens suitable for DNA extraction. The only published report of *M. decora* from Nuevo León, Mexico, was made by Eduardo Caballero in 1952. At least three field expeditions to Nuevo León were conducted between 2014–2015, all without success. However, in September 2024, 10 specimens were finally collected. To investigate its phylogenetic affinities, we generated DNA sequences of four loci (mitochondrial cytochrome c oxidase subunit I [COI] and NADH dehydrogenase I, as well as the nuclear ribosomal 18S rRNA and 28S rRNA). Phylogenetic analyses using both Parsimony and Maximum Likelihood approaches recovered samples from Nuevo León as a well distinct clade, sister to the other samples of

M. decora, and those together, sister to M. mimicus. Genetic distances between *M. decora* samples from Nuevo León and the USA and Canada reach 3%, and more than 5% when compared to *M. mimicus*. Here, we discuss whether specimens from Nuevo León represent an isolated southern population of *M. decora* or constitute a new species. The phylogenetic/phylogeographic patterns recovered here are congruent with the Pleistocene refugia hypothesis. The distribution of *M. decora* populations and closely related forms represent a new example of the impact of geological and climatic changes on the current distribution of this charismatic blood feeding leech.

(125) The origin of digenetic trematodes: Did the journey begin with the blood flukes?

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Digenetic trematodes are one of the most successful groups of metazoan parasites, one with considerable medical, veterinary, wildlife and ecological relevance. The origins of their endoparasitism, trademark complex life cycles involving alternating sexual and asexual reproduction and unique production of cercariae have long provoked curiosity. Building on recent molecular phylogenetic results hypothesizing that ectoparasitic polyopisthocotylean monogeneans are the sister group of the trematodes, a new version is offered for how digeneans and their life cycles may have first evolved featuring a central role for blood flukes (Schistosomatoidea) in the process. In support, extant blood flukes: 1) appear as sisters with brachylaimoids in both 28S and mitogenome phylogenies to the remaining diplostomidans which in turn as a group are sisters to the remaining digeneans, the plagiorchiidans; 2) fErom early branching lineages exploit extant representatives of ancient, early branching vertebrate lineages suggestive of long periods of association; 3) collectively exploit a broader range of first intermediate hosts (annelids, bivalves and gastropods) than any other digenean group, suggestive of long periods of experimentation; 4) share blood-feeding habits and associated traits with polyopisthocotyleans, the common ancestor for which may have transitioned to endoparasitism indicating a “vertebrate first” digenean life cycle; 5) have two-host life cycles; 6) exhibit a variety of transitional intramolluscan larval and cercarial forms; 7) suggest a possible origin of the cercarial tail starting from a tiny knob to culminating in forked tails seen widely among digeneans; and 8) provide via the selection-responsive cercarial tail a path to other digenean life cycles. Also discussed is the ground-breaking role of modern functional genomics studies focused on stem cells in helping to elucidate the complexities posed by asexual reproduction in the digenean life cycle. Some alternative possibilities are discussed and needs for future studies highlighted.

(126) Decoding coccidia: Mitogenome diversity informs species identifications and evolutionary histories

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The mitochondrial genomes of apicomplexan protists have become central in the molecular differentiation of species of coccidia and provide useful genetic loci for inferring evolutionary relationships among these parasites. The mitochondrial genomes of Apicomplexa are compact (6-12kb), typically circular-mapping, with greatly reduced gene content compared to other eukaryotic mitochondria, retaining only 3 CDS (cytochrome c oxidase subunits I and III, and cytochrome B). Interspersed among the CDS are a varying number of small and large subunit ribosomal DNA fragments ranging from 16 to >180 bp in length that are highly conserved compared to CDS sequences. The sequence conservation of the rDNA fragments suggest that they remain ‘functional’ in some way; deep sequencing of small ‘non-coding’ ncRNA fragments from sporozoites of *Eimeria tenella* have demonstrated that these fragmented rDNAs are indeed transcribed into poly-adenylated RNA. At the species level, sequence diversity in the CDS regions is generally sufficient for differentiation of closely related coccidia; the adjoining conserved rDNA regions provide useful PCR targets for amplification of these CDS regions for DNA barcoding. For eimeriid coccidia in the genera *Eimeria*, *Isospora*, *Caryospora*, or *Lankesterella*, the content and organization of the mt genome is well conserved

but becomes widely varied in non-eimeriid coccidia of amphibia, fish or reptiles, and even more diversely organized in heteroxenous and monoxenous adeleid coccidia such as species of *Haemogregarina*, *Hepatozoon*, *Klossiella* and *Klossia*. The high copy number and PCR-friendly nature of CDS regions make these genetic targets highly suited for species-level diagnostics (e.g. ddPCR or amplicon NGS for mixed parasite infections) and for molecular phylogenetics. Site saturation of CDS sequences likely impacts utility of CDS sequences beyond the familial level but other loci, such as nu 18S rDNA, can resolve these more ancient relationships. Even using such concatenated molecular datasets, molecular phylogenetic reconstructions may support evolutionary relationships that conflict with morphology-based taxonomies; for example, the genera *Eimeria* and *Isospora* have been shown to be paraphyletic and that oocyst configuration (number of sporocysts and sporozoites per sporocyst) are unreliable characters for inferring relationships. Expanding the sequence databases may provide the necessary information to resolve conflicts between taxonomies and phylogenies.

(127) Host community diversity and river structure shape parasite evolutionary potential in a complex river system

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The coevolution of hosts and their parasites is fundamentally shaped by differences in evolutionary potential between them. Relative gene flow and genetic diversity are two of the most important factors affecting the dynamics of host-parasite coevolution, and each can vary dramatically across heterogeneous landscapes. Understanding how such landscapes shape gene flow and genetic diversity is therefore key to understanding host-parasite coevolution and disease dynamics in natural systems. Rivers are ideal habitats to examine the landscape evolutionary ecology of host-parasite systems because their discrete structures allow for targeted hypothesis testing: fish community composition changes predictably along their continua, and connectivity between host populations is often predictable from river structure. We leverage these characteristics using population genomics to compare the gene flow and genetic diversity of two *Gyrodactylus* spp. species infecting guppies, *Poecilia reticulata*, across the river networks in Trinidad's Northern Range mountains. We examined how host community composition may affect parasite population genetic structure by comparing the generalist *G. bullatarudis* to the guppy specialist *G. turnbulli*. For parasites that differ in host range, dispersal limitations for host-specific parasites, such as *G. turnbulli*, should restrict gene flow and differentially shape the population genetic structure relative to parasites with a broader host range, such as *G. bullatarudis*. Thus, the dispersal of generalist parasites capable of infecting hosts with greater vagility should exhibit reduced population substructure. We used a co-structure analysis between parasites and the guppy to assess how much the river network and host community composition may affect evolutionary potential in this system. We found that the generalist parasite dominated infections on guppies in the more species-diverse lower course fish communities and exhibited higher gene flow and higher genetic diversity across the landscape than the guppy. In contrast, the guppy specialist *G. turnbulli* was prevalent in less species-diverse upper course fish communities. *G. turnbulli* exhibited low genetic diversity and low gene flow among populations that more closely mirrored that of its host. Our results are consistent with the predicted distribution of parasite population structure and genetic diversity; however, the host community composition was strongly associated with which parasite species infected the guppy hosts.

(128) Morphological and molecular description of a new species of *Heterorchis* (Digenea: *incertae sedis*) parasite of marbled lungfish, *Protopterus aethiopicus* from Lake Kanyaboli, Kenya

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The trematodes belonging to genus *Heterorchis* Baylis, 1915 have been reported infecting fish species of

the family Protopteridae. The genus comprises four species described exclusively from Africa, though two of these taxa are currently regarded as *species inquirenda*. The present study material was collected from the intestine of Marbled lungfish, *Propterus aethiopicus* Heckel, 1851 in Lake Kanyaboli, Kenya between May and October 2023. An integrated systematic approach was employed in studying the trematode. Morphological analyses of the trematode revealed to be an unknown species with a unique set of distinctive characteristics such as longer body length, extent of the intestinal caeca in the post-excretory vesicle field, cirrus-sac reaching the level of the seminal receptacle, and the larger oral to ventral sucker length ratio differing from the known species. Phylogenetic trees through Bayesian Inference and Maximum likelihood analyses of the 28S rDNA dataset formed a separate clade comprising sequences of *Heterorchis* spp. The interspecific distance of 2% (25 bp) was calculated between new *Heterorchis* species to the available sequence on GenBank, MW586924, for *H.* cf. *crumenifer*. The infection indices were recorded as prevalence P = 46.7%, mean intensity MI = 1.25 and mean abundance MA = 0.58. This study was partly supported by the DSTI-NRF SARChI Chair (No.101054).

(130) A checklist in the diversity, distribution, and host interactions of *Trichuris* spp. (Nematoda: Trichuridae), with a meta-analysis in the intraspecific morphological similarities and variation in diagnostic traits in the genus

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The species in *Trichuris* are monoxenous geohelminths that parasitize mammals. Their taxonomy has been complicated by the reduced number of morphological traits and their irregular use in the characterization and differential diagnoses. The present work provides a compendium of the existing, valid and available species in the genus, considering approaches used in the identification by species, geographical distribution, host interactions, and molecular material, with a list of the morphological characters used in the descriptions. For this, a systematic search was performed following the Prisma criteria for systematic reviews, and a series of keywords in metasearch engines and taxonomic literature was also used. The results include 114 *Trichuris* species erected in 89 articles plus 111 articles representing complementary information such as new records, new host associations, genetic diversity. We consider 109 species valid, 3 represent synonyms, 1 *inserta saedis* (*Trichuris lama*), 1 *nomen dubium* (*Trichuris castoris*). *Trichuris* is found in five continents, parasitizing around 97 species of mammals, with five species demonstrating intercontinental distribution 33 with specific patterns of association and 79 that infect more than two hosts (generalists). Of the 114 species, 45 have pointed diagrams, 22 used light microscopy, 13 SEM, and 5 analyze morphological characters using multivariate statistics. Likewise, only 23 species are included in a phylogenetic context, 10 with a mitogenome, and three with complete sequenced genomes. A search term and meta-analysis was conducted based on the key question, “What is the most representative trait and variation in the genus?” yielding between 67 and 84 studies with information on reproductive and non-reproductive traits. Our results showed that spicular length is the most representative trait across species and the one that shows the most significant differentiation among them. Morphological similarities among the 84 species resulted in the formation of morphological groups (clusters), which are significant as they provide a basis for further taxonomic studies and understanding of the diversity within the genus. The taxonomic, morphological, and geographic information gathered here may contribute as a first step in resolving taxonomic problems in the group. Future studies, such as the phylogenetic context in the genus, need to be addressed.

(131) Diversity and interrelationships of diplostomids (Digenea: Diplostomoidea) parasitic in kingfishers

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Kingfishers are definitive hosts to a diversity of digeneans that use fish as second intermediate hosts. Many of these digeneans belong to the family Diplostomidae. Their larvae are a well-known cause of fish health problems throughout the world, including “black spot disease”. While most prior studies have focused on

larval stages, a few have examined adult stages from kingfishers. We provide a summary of recent taxonomic and systematic discoveries based primarily on adult stages of these kingfisher digeneans. The material discussed includes members of 11 genera (9 exclusively in kingfishers) from 5 continents. The combination of morphological and molecular data allowed the description of several new genera and species from around the world. Molecular phylogenies suggest multiple evolutionary host switches of diplostomids from other hosts to kingfishers, including the formation of one highly diverse clade, as well as multiple dispersal events between continents.

(132) Diversity and host specificity of *Kudoa* species (Myxosporea: Multivalvulida) in fishes of the world

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Kudoa species (Myxosporea: Multivalulida) are found in a wide range of marine fishes worldwide. Most infect the skeletal muscle of their hosts, while others infect various tissues including cardiac muscle, brain, intestine, and ovaries. In some cases, infections are associated with post-mortem myoliquefaction, impacting the value of food fishes. Some *Kudoa* species have only been reported once when described, while others like *Kudoa thyrsites* have been documented in 40 hosts and from many localities. Given their broad distribution and host range, we set out to document and evaluate the occurrence of *Kudoa* species in relation to their host habitat type and the taxonomic relatedness of their hosts. We identified 141 *Kudoa* species from 418 host across 316 different fish host species. The majority of *Kudoa* species (89/141, 63%) are reported from a single host species, while 18 (13%) are reported from 2 host species, 12 (9%) from 3 host species, and 22 (16%) from more than 4 host species. For those with greater than 2 host species, we calculated indices of host taxonomic specificity (S_{TD}). A weak positive correlation was observed between the number of host species and S_{TD}. *Kudoa* species with many hosts infect fish from various orders, and this is even observed in a few species that infect only 2 host species. For the latter, we propose that these species have the potential to infect taxonomically different hosts, and a lack of sampling and reporting explains why so few are reported. For example, *Kudoa megacapsula* is known to infect 2 hosts which are from different fish orders resulting in a relatively high $S_{TD} = 4$. Among *Kudoa* species infecting 7 or more hosts, *Kudoa gunterae* ($S_{TD} = 2.31$) and *Kudoa ovivora* ($S_{TD} = 2.29$) exhibit relatively low S_{TD} values, suggesting specificity to a few fish families. Regarding fish host habitat, 56.3% of host species are benthopelagic, 23.4% pelagic, and 20.3% benthic. Several *Kudoa* species infect fishes from all these habitats. Our data suggest that there are no clear patterns of host specificity for *Kudoa* species toward certain fish families or habitat types.

(133) Mitochondrial genome sequencing of rhinebothriidean and phyllobothriidean tapeworms

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Advances in DNA sequencing and bioinformatics has rendered sequencing of complete mitochondrial DNA (mtDNA) to be relatively inexpensive. Our study expands the number of complete mtDNA genomes for species in the genera *Anthocephalum* (Order Rhinebothriidea) and *Scyphophyllidium* (Order Phyllobothriidea). An attempt was made to generate mtDNA genomes for species across the phylogenetic tree space for these two genera. DNA extractions were performed for 15 species of *Anthocephalum* and 18 species of *Scyphophyllidium*. Samples were sent to NOVOGENE for short read extractions. Sequencing was successful for a total of 30 samples - 15 samples of *Anthocephalum* and 15 samples of *Scyphophyllidium*. These mitochondrial genomes were aligned to existing genomes of *Anthocephalum* and *Scyphophyllidium* from Genbank. Mitochondrial gene order was conserved for the two genera and compares to that found by Trevisan et al. (2021). Analyses of individual mtDNA genes are ongoing and will include determination of their suitability for phylogenetic analysis. Thus far, we have determined that genetic distance statistics for CO1 and ND1 are closely comparable, and this is also the case when comparing distance estimates between *Anthocephalum* and *Scyphophyllidium*. We are ultimately interested in determining whether mtDNA can be useful in assessing the time of evolutionary origin for these tapeworm genera.

(134) Steppingstones to resolving "*Polypocephalus*"

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Members of the genus *Polypocephalus* Braun, 1878, with *Polypocephalus radiatus* Braun, 1878 as its type species, are highly recognizable by their possession of an apical organ divided into tentacles and four or six testes arranged in a single column. Collectively, the genus is known to parasitize a broad range of elasmobranchs including guitarfish, stingrays, and a shark. For nearly a decade, molecular sequence data has shown Polypocephalus to be not monophyletic. Moreover, a preliminary phylogenetic tree based on targeted gene capture data has placed specimens consistent with *Polypocephalus* in as many as 10 distinct clades, interspersed by multiple, non-tentacle bearing genera. We explored the feasibility of recognizing each of these clades as separate genera supported by morphological features. Specifically, we compared members of the sister clades Clade VIII, with six species—all new to science, and Clade IX, with one described and two new species. While members of both clades share the presence of six testes and acraspedote proglottids, the members of Clade VIII and Clade IX differ from one another in a number of respects, including the presence (or lack) of vitelline follicles anterior to the cirrus sac on the poral side, the arrangement of the vas deferens, and genital pore position. Furthermore, host associations are non-overlapping: members of Clade VIII parasitize eagle rays in the genus *Aetomylaeus*, and stingrays in the genera *Maculabatis*, *Neotrygon*, *Taeniura*, and *Urogymnus*, while those of Clade IX parasitize cownose rays in the genus *Rhinoptera* and stingrays in the genus *Pastinachus*. While molecular sequence data to place *P. radiatus* definitively in the phylogenetic framework are unavailable, membership in Clade VIII and Clade IX is highly unlikely based on pore position, possession of craspedote rather than acraspedote proglottids, and the use of rhinopristiform rather than myliobatiform hosts. While these efforts to dismantle "*Polypocephalus*" show promise, it remains to be determined if the remaining eight clades can be diagnosed similarly as distinct genera. Future work will also include developing methods for more consistent and thorough examination of scolex anatomy and ultrastructure.

(135) An investigation into cercarial morphology and anatomy using scanning electron and confocal microscopy

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Digeneans are the most diverse subclass of platyhelminths, yet their surface ultrastructure and internal organ architecture remains poorly studied, particularly in species of non-medical importance. This study aimed to characterize cercarial surface ultrastructure using scanning electron microscopy (SEM) and visualized muscle and nervous system structures using confocal microscopy (CM). Snails of the genus *Physa* were collected from Clinton Lake, Lawrence, KS, isolated, and monitored for cercarial shedding. Shed cercariae were fixed for light microscopy, SEM, and scanning laser CM. Morphological investigations with light microscopy showed the cercariae belong to the family Diplostomidae. With SEM, we observed a characteristic pattern of tegumental spines, including a dense crown of spines at the anterior end, followed by a double row and nine individual rows of spines interrupted dorsoventrally along the anterior 2/3 of the body. Concentrations of uniciliated sensory receptors with low tegumentary collars were also clearly visible on the anterior and posterior regions of the tail stem. For examination with CM, cercariae were stained with phalloidin (F-actin), anti-acetylated alpha-tubulin (AAAT) antibodies (acetylated tubulin), and DAPI (nuclei). Phalloidin staining confirmed the body musculature to be well organized into a wall with an outer layer of circular, a middle layer of longitudinal, and an inner layer of diagonal muscle fibers, with scattered dorsoventral muscle fibers providing internal support. In the tail, four prominent longitudinal muscle cords were observed, interconnected by circular fibers that taper into finer muscle fibers along the edges of the fins. Internally, a thick muscular basket surrounding the penetration organ, a weakly muscular pharynx, and a short gut caeca were visible. AAAT antibody staining showed the chaetotaxy and peripheral nerve projections of the cercariae. DAPI served as a nuclear counterstain, helping visualize where the cell bodies of the musculature and peripheral nerve projections are located. Future work will focus on characterizing the central nervous system and neuromuscular interactions using neurochemical mediator stains (anti-acetylcholine, anti-FMRFamide, and anti-serotonin antibodies), and extending these analyses to a second cercarial morphotype.

(136) From morphology to molecular: establishing a DNA barcoding framework for hairworm (Phylum Nematomorph) identification

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The phylum Nematomorpha, also known as horsehair worms, are an enigmatic group of parasites that infect arthropods that have both aquatic and terrestrial life cycles. Recent studies suggest hairworms are a cryptic species, therefore, DNA barcoding is a necessary tool in taxonomic and systematic investigations. DNA barcoding is a molecular method that can mediate the challenges of morphological-based identification. To date, there are 907 DNA sequences on GenBank representing six molecular markers, including mitochondrial (CO1, CytB) and nuclear (ITS1, ITS2, partial 28S, and 5.8S), representing only 9.17% of the 360 species described to date. This study provides a general guideline for hairworm samples and primer analysis in the genus *Gordius*. 13 polymerase chain reactions (PCRs) were performed with four sets of primers (COX1, CytB, 28S, ITS1, and ITS2) and annealing temperatures ranging from 44°C to 58°C, with 2°C intervals. Our analysis concluded that the mitochondrial molecular marker (COX1, CytB) showed optimal PCR annealing temperatures at 50°C and 46°C. For the nuclear molecular markers (partial 28S, ITS1, and ITS2), the optimal annealing temperatures for PCR were 52°C and 50°C. This study hopes to shorten the troubleshooting stage of polymerase chain reaction (PCR) for hairworm samples and allocate more time to process more hairworm sequences to the limited database. In the process, we will find new species and investigate additional incidences of cryptic species as we continue to extract and report sequences.

(137) Cysticercosis/*T. solium* taeniasis, a potential public health concern in non-endemic country, Kuwait: a new diagnostic method to screen *T. solium* taeniasis carriers among the expatriate population

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Kuwait is non-endemic for *Taenia solium* infection due to strict restriction on pig-farming and pork consumption however, several cases of cysticercosis and neurocysticercosis were detected among Kuwaiti nationals with no history of travel to endemic countries. Infected domestic helpers/food handlers from endemic countries who may have escaped detection of infection by microscopy at the time of their arrival into Kuwait were suspected as the possible source of infection. This study determined the seroprevalence of *T. solium* among domestic helpers/food handlers by screening of their blood using a sensitive taeniasis-specific anti-rES33 antibody assay. Newly arriving domestic helpers (n = 500) and food handlers (n = 500) from endemic countries were enrolled during 2015 - 2017. *T. solium*-specific rES33 antigen was expressed and purified from human embryonic kidney (HEK) 293-6E cells using the pTT5 mammalian expression vector. Stool samples were processed for microscopy, and blood samples were screened to detect anti-*T. solium* taeniasis-specific IgG antibodies by ELISA. All stool samples were negative for *Taenia* parasite eggs by microscopy. However, 42 individuals (4.2%) tested positive for *T. solium* taeniasis-specific IgG antibodies. Though statistically not significant, the IgG seropositivity was higher among individuals with lower education levels, low-income background, and higher frequency of hand washing. This is the first report from Kuwait and the Middle East on the detection of anti-*T. solium* taeniasis-specific serum IgG antibodies among the high-risk expatriate population. The results emphasize the importance of efficient and sensitive screening of *T. solium* carriers and thus the prevention of infection transmission and development of cysticercosis in the local population.

(138) Transcriptomic, behavioral, and morphometric differences between *Schistosoma mansoni* miracidia recovered from different host tissues

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Schistosomiasis is a tropical disease caused by human-infective parasitic flatworms of the genus *Schistosoma*. The larval stage, called miracidia, infects a snail intermediate host and matures into cercariae that are shed into water. Cercariae penetrate human skin and migrate to blood vessels connecting the intestines and liver. Here, mature parasites copulate, and females lay eggs that follow the flow of blood into the liver or against the flow through the intestinal wall and into the lumen. Intestinal eggs will mature, be defecated into fresh water, and

hatch to miracidia to continue the cycle of infection. In contrast, liver eggs have reached a dead end and will cause granuloma formation and clearance or destruction by the mammalian host immune system. *Schistosoma mansoni* is the primary lab model because the life cycle can be maintained in rodents. In day-to-day life cycle maintenance operations and in research experiments, the primary source of schistosome eggs is the rodent liver, which is harvested and processed to purify eggs or hatch miracidia, even though these eggs/miracidia would never naturally be excreted/hatch. Previous comparison of the liver and intestine eggs revealed distinct transcriptomic and antigenic differences, yet nothing is known about differences between miracidia derived from these eggs. We isolated infected mouse liver and intestines and hatched miracidia. These miracidia were measured morphometrically, their base swimming behavior was assessed, and their transcriptomes were sequenced. Interestingly, though there were relatively few differentially expressed genes, global transcriptome analysis showed distinct clustering of liver and intestine-derived samples. The role these genes play in differential development or behavior remains to be elucidated. Future directions include experiments to test for differences in their capacity to infect snails. These findings will lead to deeper insights about relevant differences between miracidia from different tissues and inform research and life cycle maintenance operations.

(139) Developing *Girardia dorotocephala* as a model organism for flatworm sensory biology

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Parasitic flatworms are a threat to human and animal health globally. All forms of parasitic flatworms, especially trematodes, engage in chemosensation to maximize the likelihood of successful infection and continuation of the life cycle. However, the molecular mechanisms that underly these behaviors are unknown, primarily because the molecular tools to study parasites are lacking. Understanding how flatworms find hosts to infect would help advance parasite control, but there is no good model for advancing these investigations. This study focuses on *Girardia dorotocephala*, a species of free-living planaria that we are developing as a flatworm model for sensory biology. While planaria are not parasites, they possess many of the same traits as parasites within the phylum. Because of the similarity between the two clades, we can use planaria as a model organism to better understand flatworm behavior. Planaria use chemoreceptors located in their auricles and eyespots on the head to sense and respond to their surroundings – these distinct sensory structures allow for precise manipulation and exploration of the molecular pathways employed by sensory cells. To initiate this project, we sought to establish base experimental, recording, and tracking parameters for high-resolution assessment of planaria behaviors. Worms were placed in controlled environments in which the light source could be modulated and chemical gradients derived from point sources could be induced. Separately, we are also working to sequence the genome of a clonal line of *G. dorotocephala*. A reference genome assembly combined with a precise and reproducible experimental platform will help identify genes involved in sensation, setting up the species as a model flatworm for sensory biology.

(140) A novel device for high-throughput phenotypic screening of schistosome miracidia enables identification of transient receptor potential (TRP) channels modulators that impact miracidia behavior

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Schistosomiasis, a neglected tropical disease caused by three parasitic flatworm species, including *Schistosoma mansoni*, relies on freshwater snails as intermediate hosts. Interrupting the parasite's ability to locate snails could provide a novel strategy for disease control. Praziquantel (PZQ) is the current treatment of choice for human infections, and it exerts its effect by targeting transient receptor potential (TRP) channels on the parasite, debilitating the worms and leading to clearance by the host immune system. Despite its effectiveness in eliminating adult parasites, treated individuals remain susceptible to reinfection. Interestingly, TRP channels are classically recognized as key metazoan sensory receptors, involved in reception of a variety of chemical cues, though the mechanism of action of PZQ is not known to be related to sensation. Since TRP channels have been shown to be a rich source of anthelmintic drug targets, we hypothesized that they could also be targeted to disrupt the sensory behaviors involved in miracidia infection of snails. In this study, a high-throughput phenotypic screen was developed and used to identify bioactive compounds targeting the transient TRP

receptors in miracidia. A custom 96-well acrylic device – the ScreenChip – was designed for simultaneous wide-field imaging by a custom high-resolution, multi-camera imaging device. Miracidia were treated with 10 µM of compound, and the impact of each compound on miracidia behavior was assessed to identify potential hits. Our recording system and downstream analytical pipeline enabled precise observation of miracidia motility and orientation, allowing identification of compounds that disrupt general movement cause chemokinetic behaviors. Preliminary findings suggest that TRP channel modulators play a role in altering miracidia navigation, offering a promising avenue for disrupting the parasite's life cycle. Future investigations will establish the effective concentrations of hit compounds and test for potential inhibition of snail host-seeking, penetration, and infection.

(141) Tartrolon E: a new drug candidate against apicomplexan parasitic diseases

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Toxoplasmosis and Cryptosporidiosis are considered global endemic diseases caused by Apicomplexa parasites and have severe impacts in animal and human health. Toxoplasmosis is caused by the protozoan *Toxoplasma gondii*, responsible of severe neurological illness in patients with immunosuppression (HIV-AIDS, organ recipients), and congenital disorders when transplacental primo infection occurs during pregnancy. The animal industry is also severely affected by the reproductive impact of this agent. *Cryptosporidium parvum* is considered a relevant pathogen in cattle and the main cause of neonatal parasitic enteric infections in calves, with watery diarrhea outbreaks in neonatal ruminants severely affecting industry. Moreover, the agent is considered a major pathogen for human diarrheal disease in immunocompromised individuals and young children. Both diseases lack effective vaccines, as well as effective and safe treatment for the human and animal populations most at risk. The boronated polyketide Tartrolon E (trtE) has antiparasitic activity against different members of the Apicomplexa *phylum*. We determined that trtE exerts inhibitory activity against both extracellular and intracellular stages of *T. gondii*, blocking 80% of its infective capacity after only 30 minutes of tachyzoites exposure to compound (100 nM). Our results showed that, trtE rapid antiparasitic effect does not compromise early parasite viability or host cell attachment but has a significant impact of tachyzoites invasion capacity. These effects were found to be irreversible when parasites were allowed to infect host cells for a period 24 or 48 h after treatment (trtE,100 nM). We determined a rapid parasiticidal action on *T. gondii* and a delayed effect on viability and morphology at 8 h of exposure. TrtE against *C. parvum* orally infected INFgamma knock out mice significantly decreased the number of oocysts being shed in feces when a dose of 10 mg/kg starting 5 days postinfection was used. Our preliminary results on infected neonatal lambs, treated with 300 ug/kg of compound (5 doses) determined an average compound half-life of 6.1 h with no toxicity signs when administered. TrtE effective antiparasitic activity against both apicomplexan infections together with the lack of toxicity suggests that the compound could be a new therapeutic resource for Toxoplasmosis and Cryptosporidiosis.

(142) ***In vitro*** anti-leishmanial activity of *Nigella sativa* and *Zingiber officinale* against *Leishmania infantum*

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Species of *Leishmania* cause various clinical manifestations, ranging in severity from self-healing cutaneous lesions to life-threatening visceral diseases. The side effects of current drugs used in the treatment of leishmaniasis have highlighted the need for the development of agents with lower toxicity. The aim of this study was to investigate the anti-leishmanial effects of *Nigella sativa* and *Zingiber officinale* oils on *Leishmania infantum* using the Microcapillary Culture Method (MCM), a novel technique advantageous for parasite cultivation. *Leishmania infantum* promastigotes were cultured in RPMI 1640 medium supplemented with HEPES, gentamicin, and 10% inactivated fetal calf serum (FCS). MCM was used to assess antiparasitic efficacy, and 10^5 promastigotes were inoculated into each microtest tube. Inhibition percentages were determined by incubat-

ing *Leishmania infantum* promastigotes with the plant oil-medium mixtures, followed by parasite counting. IC_{50} values were calculated using linear regression analysis. *Nigella sativa* and *Zingiber officinale* oils reduced the viability of *Leishmania infantum* promastigotes after 72 hours of incubation, starting at concentrations of 250 µg/ml and 500 µg/ml, respectively. The calculated IC_{50} values were 420.077 µg/ml for *Nigella sativa* and 611.629 µg/ml for *Zingiber officinale*. The anti-leishmanial activities of *Nigella sativa* and *Zingiber officinale* oils against *Leishmania infantum* promastigotes at specific concentrations were demonstrated. Considering the challenges in the treatment of leishmaniasis, these findings may contribute to the development of alternative therapeutic agents.

(143) The nematode microbiome

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The parasite microbiome can influence parasite fitness, transmission, and host-parasite interactions. We conducted a literature review to consolidate what is known about the structure, diversity, and functional roles of nematode-associated microbiomes. Using publicly available data from four of the five major nematode clades and new sequence data for *Heligmosomoides bakeri*, we tested how factors like host species, nematode species, and parasite clade influence parasite microbiome composition. To collect *H. bakeri* for microbiome sequencing, we infected C57BL/6J lab mice (*Mus musculus*, n = 4) with *H. bakeri*. We then characterized the microbiome in host intestinal samples and parasites using 16s rRNA sequencing. The *H. bakeri* microbiome was distinct from that of the host, with consistently lower richness and evenness compared to surrounding small intestine contents. Both the host and *H. bakeri* had microbiomes dominated by Lactobacillus, consistent with previous studies. Further analysis of our *H. bakeri* data, and sequences from 16 previous studies on nematode microbiomes, reveals new insights into the factors structuring bacterial communities in Nematoda.

(144) Clinical phase-specific gut microbiota remodeling in *Plasmodium knowlesi*-infected macaques

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The role of the gut microbiota in *Plasmodium knowlesi* malaria pathogenesis, a zoonotic infection with prominent gastrointestinal symptoms, with the ability to undergo microvasculature sequestration linked to the expression of the SICAvar gene family, remains poorly understood despite its clinical relevance. Research in murine models has shown that the gut microbiome plays a significant role in malaria disease progression. However, there is limited understanding of how the gut microbiota influences infections in humans and non-human primates. This study delves deeper into *Plasmodium knowlesi*, a malaria parasite originating in primates that can infect humans and typically presents gastrointestinal symptoms. To investigate temporal shifts in gut microbial composition and function during *P. knowlesi* infection, shotgun metagenomics was applied to rectal swabs from longitudinally sampled, *P. knowlesi*-infected long-tailed macaques (*Macaca fascicularis*). To explore the factors influencing microbial population changes, we applied a functional metagenomic approach integrated with linear discriminant analysis. Our results revealed clinical phase-specific alterations: acute infection was marked by an increased relative abundance of mucosal-associated microbe Helicobacter macacae and bacterial motility genes related to flagellar function, suggesting opportunistic colonization during gut dysbiosis. In contrast, the chronic stage of infection featured a dominant enrichment of *Prevotella copri*, a taxon linked to malaria resistance in humans, alongside functional signatures indicative of microbiota recovery, such as metabolic pathway restoration. Differentially enriched enzyme commission and gene ontology profiles highlighted functional shifts reflecting microbial opportunism and host-microbe interactions. The study implicates gut microbiota dynamics in malaria pathogenesis, proposing that microbial taxa like *P. copri* may contribute to recovery or protection. At the same time, motility-enhanced pathogens like *H. macacae* could exacerbate acute-phase dysbiosis. These findings advance understanding of the complex tripartite interactions between *Plasmodium*, the host, and the gut microbiota, offering a foundation for exploring microbiome-targeted interventions in simian and human malaria.

(145) Specifications, bundles, and tokens—oh my! My journey into alternative grading

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Alternative grading systems offer a learner-centered approach where opportunities for improvement are built-in via feedback loops, and where final grades are linked to demonstrable evidence that the learning outcomes are met. Here, I share how I have implemented specifications grading in two distinct types of courses: a small upper-division parasitology course with 50 students, and a large-enrollment intro bio lab with 2000 students. In both case studies, the course structure was built around four core elements of specifications grading: (1) learning outcomes that are carefully defined, (2) grade bundles with clearly defined specifications that need to be met, (3) opportunities for assignment revision creating feedback loops, and (4) a token economy for added flexibility. I showcase how specifications grading can create a more equitable, learner-focused environment, and provide a framework for educators seeking to implement alternative grading approaches into their own courses.

(146) Integrated sensory behaviors of larval **Aedes triseriatus** and *Aedes aegypti*

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Mosquitoes are harmful, disease-carrying vectors that pose significant public health risks worldwide. *Aedes aegypti*, known for transmitting Zika Virus, Dengue, filarial nematodes, and yellow fever, poses a threat in urban locales across the world, while *Aedes triseriatus*—native to Wisconsin—transmits the La Crosse virus. While much is known about adult mosquito behavior and host-seeking, less is understood about the sensory behaviors of mosquito larvae in response to predators, competitors, conspecifics, or food. To address this gap, we have established and optimized approaches to investigating the sensory behaviors of *Ae. aegypti* and *Ae. triseriatus* larvae. We have refined protocols using the InVision device, a high-resolution camera system designed for tracking aquatic invertebrates, to monitor and quantify the behavior of mosquito larvae in response to chemical gradients emitted from a point source. The recording device uses four cameras to visualize two custom arenas that allow the formation of stable gradients of chemical cues. With these methodologies, we have first profiled the chemosensory behavior variations across mosquito larval stages for both *Aedes* species. Our preliminary findings suggest that L1 *Ae. triseriatus* and *Ae. aegypti* larvae do not rely on chemosensory modalities to locate food, but that sensory-induced foraging behavior increases in L2-L4 stages, suggesting a developmental shift in foraging strategies as larvae progress through these stages. Our recording device also supports backlighting with user-selected wavelengths and bidirectional RGB LED epi-illumination to generate light gradients of different wavelengths, allowing for precise adjustment of experimental parameters to explore multimodal sensation. Future directions will integrate chemosensory and photosensory behaviors and investigate the impact of widely used larvicides on these behaviors.

(147) Temporal dynamics of midgut pH and serine protease activity in *Ctenocephalides felis*

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Cat fleas (*Ctenocephalides felis*) are important insect vectors that facilitate pathogen transmission from animals to humans. The gut environment is the first site of pathogen-vector interactions, influencing infection outcomes. Serine proteases, enzymes that play a crucial role in the digestive process, are essential for breaking down proteins and other nutrients in the bloodmeal. This enzymatic activity significantly impacts the pH levels in the gut, as the breakdown of blood releases various acidic or basic byproducts. Given that these proteases are a key component of the primary food source for fleas, understanding their concentration and the pH dynamics within the midgut is essential for assessing how digestion occurs in this species. It has been observed that a pH of 6.0-7.0 is the typical range in an unfed flea gut; however, digestion of blood meal is achieved by serine proteases, which have a pH optimum in the alkaline range. This study aimed to measure the pH and concentrations of serine proteases (trypsin) in the midgut over 48 hours post-blood meal ingestion. We hypothesized that pH would become more alkaline, with the highest concentrations of the serine protease occurring within the first 24 hours. Flea guts were dissected at 0, 6, 24, 30, and 48 hours after feeding, and pH and protease concentrations were measured using colorimetric and fluorometric assays. The results provide insights

into how flea gut pH and digestive enzymes fluctuate following blood meal ingestion, which could influence the transmission of flea-borne pathogens.

(148) Habitat degradation muddles sexual signals: disentangling infection, pollution, and sexual selection in *Lepomis* spp. in the Rio Grande Basin

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Anthropogenic changes have dramatically altered aquatic ecosystems, and aquatic ecosystems in arid habitats are particularly vulnerable. While mate selection is a vital fitness determinant influencing quality and quantity of offspring, our current understanding of sexual selection and host-parasite dynamics in anthropogenically-altered environments is limited. This study aims to address this knowledge gap by investigating the direct and indirect interactions between aquatic environments, parasite infection, and sexual selection in three species of sunfishes (*Lepomis* spp.) in the Rio Grande Drainage basin, including the most polluted (Rio Grande) and the most pristine (Devils) rivers in Texas. We will test the hypothesis that environmental condition jointly shapes sexual signals and parasite prevalence, intensity, and community, thereby altering the strength of sexual selection in polluted environments. For parasites, we predict highly polluted environments will have low species richness and low prevalence and intensity of infection due to reduced survival of free-living stages or disruption in complex life cycles due to low intermediate host densities. We expect sunfishes to have reduced variance in sexual signals and reduced sexual selection due to direct interactions between pollution and reduced host condition in polluted rivers. We predict there will be no correlation between sexual signal and parasite infection in the polluted rivers. In the pristine Devils River, we expect to find high parasite intensity and prevalence, high variance in host body condition and coloration, and increased sexual selection. We hypothesize there will be a significant negative correlation with expression of sexual signals and parasite infection in the Devils River. At each site, water quality will be measured and 30 sunfish from each species (810 total) will be collected pre- and post- breeding. Fish will be measured morphologically and spectrally, photographed and dissected for parasites. Gonadosomatic index (GSI) will be measured, and tissue samples analyzed for lead, mercury, and cadmium. Anthropogenic effects have yet to be fully understood in aquatic ecosystems in arid environments, and this study aims to elucidate the complex interactions between pollution, heavy metal contamination, parasite infection, and sexual selection in sunfishes. This poster will share preliminary results from the 2024 and 2025 field seasons.

(149) The importance of no data: Presence and absence data better inform ecological niche models of parasites

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Ecological niche modeling (ENM) is a powerful tool for understanding species distribution potential. This tool is widely used in diverse disciplines such as conservation, climate change, invasive species, and disease biogeography. In parasitology, ENMs face the additional complication that parasites require a host to develop (i.e, characterizations of environments that are suitable not only for the parasite but also for its hosts are needed). Nonetheless, this facet of ENM is increasingly important as parasites (pathogenic or not) move through populations. Parasite ENMs have been traditionally developed using presence records of their hosts or the parasites themselves. The lack of informative absence (non-detection) data in these models, however, limits their ability to discard environments and places that may not be suitable for the species of interest. Using parasite data from small mammal surveys in Mongolia, we investigate the effect of non-detection data on ENM prediction ability with an example for endo-parasites. Our mammal surveys utilized holistic sampling methods, resulting in a comprehensive dataset of mammal and parasite detections and non-detections for every host examined. We use data for the cestode *Paranoplocephala jarrelli* and their *Microtus* hosts (*M. oeconomus*, *M. fortis*, *M. mongolicus*, and *M. maximowiczii*). We build ENMs that use presence-only data, presence and background data, and presence and absence data. We found notable increases in the ability of models to assign lower suitability values to areas where parasites were sampled but not detected when presence-absence data is used. Our results reinforce the importance of holistic host sampling and standardized measures of effort and non-detection to better tune models aiming to characterize areas of parasite distributional potential.

(150) River otters (*Lontra canadensis*) consume many parasites, highlighting the role of directly transmitted parasites in the trophic transfer of energy

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Prior studies examining the roles of parasites in food webs primarily utilized infections from multi-host parasites, thereby not including directly transmitted parasites that might still make prey more likely to be consumed. We used a community-based genetic approach (i.e., metabarcoding) to identify parasites in the scat of river otters (*Lontra canadensis*) collected along the shore of a subestuary of the Chesapeake Bay. River otters are generalist apex predators with the potential to consume available parasites in a wide range of local prey. We extracted DNA from scat collected at river otter latrines and amplified the 18S gene to identify parasites, including those unlikely to be found using traditional approaches. We found parasite taxa occurred an average of 1.8 ± 1.0 SD times (range: 0-4) per scat with trematodes being the most frequently detected. Trematodes also had the highest sequence abundance with 99.5% (588,553/591,412) of sequences, though we also identified monogeneans, myxozoans, nematodes, and apicomplexans. While the nematodes (e.g. *Strongylida*) and some apicomplexans (e.g., *Cystoisospora*) identified likely parasitized the river otters, most parasitic taxa identified such as monogeneans (e.g., *Gyrodactylideans*), myxozoans (e.g., *Amyloodinium*), and some trematodes (e.g., *Plagiorchiida*) likely parasitized the prey items instead. Our results support that directly transmitted parasites are potentially playing a major role in coastal diets and suggest a wider role of parasites in ecosystem energy transfer.

(151) The effect of endoparasites on the thermal tolerance of small fishes

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CTmax, or Critical Thermal Maximum, is a temperature threshold beyond which an organism experiences loss of coordination or other critical failures that, if sustained, can lead to death. For ectothermic animals such as fishes, it can provide information on thermal tolerance and potential responses to a warming climate and more frequent heat waves. In many teleosts, approaching CTmax manifests as increasing agitation and muscle spasms. Experimentally, CTmax is non-lethally assessed at loss of equilibrium (LOE), where the fish cannot maintain vertical orientation. Biotic factors, including parasite infection, have been shown to modulate CTmax, although further investigation is necessary to better predict effects of thermal extremes on naturally infected fish populations and to understand underlying mechanisms. To this end, we are investigating possible mechanisms by which parasites change the thermal tolerance of a small freshwater fish, the Common Shiner (*Luxilus cornutus*) found naturally infected by *Posthodiplostomum* sp., *Bothriocephalus* sp., and larval nematodes. Preliminary experiments have focused on determining CTmax thresholds for individual fish, which are subsequently euthanized and examined for parasites. Individual fish were exposed to increasing water temperature at a ratio of 0.1 C min-1 increments until they experienced LOE, we determined that CTmax was reached at an average of 37.0 C, and ranged from 35.0 C to 38.1 C. CTmax is indeed modulated by parasitism: there was a significant negative relationship between CTmax and log-transformed parasite infection intensity ($R^2=0.51$, $F(1,9)=9.22$, $p=0.014$), indicating that heavier parasite infections decreased thermal tolerance of their host. To explore possible effects of temperature and parasite intensity on mitochondrial bioenergetics, we assayed the electron transport system (ETS) of isolated liver mitochondria under various substrates, uncouplers and inhibitors. We selected a titration protocol aimed to determine the proportion of mitochondrial O2 flux associated with ATP production (OXPHOS) to the O2 flux linked to proton conductance across the inner mitochondrial membrane (LEAK). Mitochondrial energy transduction efficiency is calculated from OXPHOS and LEAK respiratory states, which was later categorized according to parasite intensity and biomass. These results will be evaluated in the context of current water temperature trends throughout the range of this host species.

(152) Impact of mining-derived metal contamination on fish parasites at Tar Creek Superfund Site, Oklahoma

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The Tri-State Tar Creek Mining District, once a lead and zinc mining hub, now suffers from severe contam-

ination, with metals like lead, cadmium, and zinc leaking into the soil and water. This study examines how metal pollution influences fish parasitic loads and the relationship between fish and their parasites in these stressed environments. Studies suggest that parasites can be more sensitive to metals than fish, but specific adaptive mechanism are poorly understood. Moreover, little is known about how metal exposure affects parasite diversity. To overcome this lack of knowledge, we sampled four sites across the Grand Lake area in Oklahoma: two reference sites (Grand Lake Honey Creek & Sycamore Creek) and two polluted sites (Tar Creek E40 and Miami, OK). Water analysis showed a clear gradient of metal contamination, with zinc levels ranging from 1.1 µg/L at reference sites to 7,000 µg/L at polluted sites. Cadmium ranged from 0.10 µg/L at reference sites to over 12 µg/L at polluted locations, and lead levels were 1.8 µg/L at reference sites and 2.5 µg/L at polluted sites. Fish were examined for parasites, and parasite species richness and intensity was recorded. The most common parasite, the metacercariae stage of the trematode *Posthodiplostomum centrarchi*, was isolated for metal analysis. A pool of 50-75 metacercariae was dried and acidified for inductively couple plasma mass spectrometry analysis (ICP-MS). Preliminary results suggest fish persist even in highly contaminated sites, but parasite species richness is notably lower at polluted sites (Miami/E40: 2.2 ± 1.1/1.0 ± 0.7) compared to reference sites (GLHC/SYC: 2.4 ± 0.9/2.4 ± 0.547). Parasitic load differed, with fish from polluted sites hosting distinct parasite communities and an average of 109 parasites per fish, compared to 252 parasites per fish in fish from cleaner sites.

(153) Ecological parameters of nematode parasites of freshwater fish in the Senegal and Gambia rivers

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Apart from work carried out in 2010 by Koubková et al. and Šárka et al., knowledge of nematode parasites of freshwater fish in Senegal is long-standing. It mainly concerns systematics, with the description of many species. As far as the ecology of these parasites is concerned, to our knowledge no study has been undertaken, hence this present work, which aims to describe the ecological parameters of freshwater nematodes in Senegal. This study was conducted in the rivers of Senegal and the Gambia over three consecutive years, during both dry and wet periods. A total of 1216 fish were sampled during this period, with 551 from Gambia river and 665 from Senegal river. The fish were classified into 27 species. *Chrysichthys maurus* is the host fish with the broadest spectrum of parasites, with *Procamallanus* and *Contracaecum* being the most common genera of nematodes. *C. maurus*, *Clarias gariepinus*, *Synodontis annectens*, and *S. nigrita* exhibit the highest biodiversity indices, which vary depending on the seasons and sex of the fish. The overall prevalence of fish parasites varies by locality and sex. Only *Citharinus citharus* shows significant differences in weight and size, with respective values of 6.3e-08 and 0.01653. This study shows the ecological diversity of parasitic freshwater nematodes in Senegal and their sensitivity to abiotic and biotic factors. Depending on the species, their distribution is influenced by locality, season and the sex, weight and/or size of their hosts. Some nematodes could serve as biological indicators of the state of ecosystems. Further research integrating molecular approaches is essential to gain a better understanding of these interactions and to support the sustainable management of fish farming resources.

(154) From infection to connection: parasites in food webs

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In coastal and marine environments, waterbirds function as apex predators that link terrestrial and marine ecosystems, and their parasites can often bridge these systems too. Trophically transmitted parasites have complex dependencies within food webs, where changes in host populations, due to climate change, habitat loss, or overfishing, can disrupt parasite transmission and alter ecosystem connections. The disruption of these life cycles by the loss of one or more required hosts can extirpate a parasite from an ecosystem. Alternatively, the supplementation of novel or concentrated food items can manipulate and short-circuit the networks from which predators feed. Thus, the absence of parasites from a system indicates the functional or actual loss of intermediate hosts from a habitat. Conversely, the presence of parasites within a system indicates the persistence of an intact food web that supports sufficient transmission of a parasite. Here we test whether waterbirds foraging on aquaculture facilities circumvent traditional food webs as they consume farmed products through the

evaluation of their parasite communities. We obtained waterbird specimens from the USDA Wildlife Services (WS), culling nuisance predators from sportfish aquaculture in the southeastern United States. We scrutinized the gut contents for any animal parasites and preserved them for morphological identification. Following the identification of the parasites, we sourced intermediate host lists that had previously been reported for each parasite from peer-reviewed literature and online museum records. With these host-parasite accounts, we developed matrices for predator-prey interactions, developed trophic networks (i.e., food web models), and compared their topologies based on each host's parasite community. In doing so, we evaluated the trophic community that each waterbird effectively interacts with from an energetic standpoint. This research highlights the necessity of considering parasites in ecological studies and conservation planning, emphasizing their role as key players in maintaining biodiversity and ecosystem balance.

(155) Endoparasite communities of aquaculture-foraging waterbirds

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Aquaculture facilities offer a rich foraging habitat for wildlife, providing a concentrated food source that can support diverse endoparasite communities, which animals like waterbirds acquire during foraging activities. Although species richness can be limited in commercial operations, nearby aquatic systems offer more diverse food webs that often intermix with aquaculture operations. While foraging near aquaculture, waterbirds might encounter similar parasite communities; however, differences in their dietary habits can lead to specialized infracommunity composition. In this study, we compare the helminth communities of five waterbird species collected from aquaculture facilities in Florida and Alabama. To further investigate how diet and geospatial differences influence these dynamics, we analyzed stable isotopes (δ13C, δ15N, δ34S) of blood, liver, and muscle to assess dietary sources, trophic position, and habitat use of each host species throughout two collection seasons (June-October 2020 and 2021). We extracted parasite specimens from the lower gastrointestinal tract, identified and quantified them to construct community matrices for each host. We then used Principal Coordinates Analysis to compare the distance between hosts in ordinate space based on infracommunity composition given biogeochemical environmental metadata. Frequently recovered helminths included cestodes (e.g., *Glossocercus* sp.), trematodes (e.g., *Echinochasmus* sp.), nematodes (e.g., *Contracaecum* sp.), and acanthocephalans (e.g., *Polymorphus* sp.), many of which utilize aquatic intermediate hosts associated with aquaculture habitats. Our findings indicate that waterbirds foraging at shrimp aquaculture facilities exhibit distinct parasite assemblages, with four out of five taxa having limited ellipse overlap and one generalist species (Little blue Heron, *Egretta caerulea*) that overlapped in endoparasite community and isotopic signatures. These analyses reveal geographic and seasonal patterns in diet and provide insight into parasite transmission pathways. Understanding links between foraging behavior and parasite communities in waterbirds is vital for assessing their potential role as vectors of injurious parasites to aquaculture as well as aquaculture's ecological and health impacts on avian hosts.

(156) Observing parasitic diversity in Canadian coastal birds

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Because parasitism is such a common mode of heterotrophy and trophically transmitted parasites have complex life cycles, it is possible that co-occurring definitive hosts are infected by the same helminths because they consume the same prey species. We would expect birds that eat the same prey types to contain similar parasite communities. This study examines the parasitic diversity in two seabird species, the Common Eider (*Somateria mollissima*) and the Black Guillemot (*Cepphus grylle*), collected in the same region and season of Newfoundland and Labrador, Canada, to better understand their feeding ecologies. Using the collection of helminths infecting their gastrointestinal tracts, we compared their endoparasite prevalence and diversity. Each digestive tract was separated into distinct segments and dissected to find and identify parasitic animals. Dominant parasitic groups found included Acanthocephala, Platyhelminthes (Cestoda), and Nematoda (Acuaroidea). Preliminary findings suggest slight differences in community richness, and prevalence, with more

pronounced differentiation of intensity. Additionally, we detect some host specificity between the two species, potentially linked to variations in diet, migration patterns, and nesting habits. Additionally, we take note of parasites that could be a risk to human populations that consume muscle tissues or other organs that are likely to be accidental sites of infection. This study was performed using birds hunted for human consumption by an Inuit community. We intend to follow up with the community to perform additional surveys of hunter-collected specimens on fresh-caught birds for future analyses. This research contributes to the broader understanding of parasitic interactions within coastal avian communities and underscores the need for ongoing monitoring of seabird health in the face of environmental change.

(157) Comparative parasitology of marine and freshwater loons: what bycatch reveals about loon parasite diversity

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Commercial fishing is a major stressor to marine ecosystems, not only by increasing competition for resources but also by directly reducing predator populations through bycatch. Fishing gear unintentionally kills an estimated 645,000 marine mammals, 370,000 marine reptiles, and 720,000 seabirds annually, potentially inflicting severe ecological consequences. Nonetheless, it offers rare opportunities to study species that are otherwise difficult to access, particularly in the context of host-parasite interactions. Some seabirds caught as bycatch, such as loons, migrate between marine and freshwater habitats, allowing us to compare parasite communities across environments. To successfully mitigate the environmental shifts between salt and freshwater systems, these duoaquas birds utilize salt glands that shunt excess ions from their bloodstream to retain homeostasis. By analyzing salt gland histology, as well as sodium and potassium concentrations in bodily fluids, we can assess the condition of internal microhabitats where parasites reside. Unlike other seabirds, where the salt glands are encased within the skull, loon salt glands sit in supraorbital depressions, making them easier to extract and ideal candidates for histological research. In this study, we examined Common Loons (COLO) and Red-throated Loons (RTLO) collected from saltwater (NOAA, n=15; Loon Preservation Committee [LPC], n=10) and freshwater habitats (LPC and wildlife rehabilitation centers, n=12). We performed quantitative necropsies and collected gastrointestinal parasites, which we stained, mounted, and identified morphologically. Once identified, we tallied intensities and calculated prevalences of all parasites that occurred in at least 95% of hosts. We extracted eye fluid by syringe and digestate from the duodenum, jejunum, and ileum, which we analyzed for sodium and potassium concentrations using Inductively Coupled Plasma (ICP) spectroscopy. Results indicate that saltwater loons have lower intensities and parasite diversity (cestodes and nematodes). In contrast, freshwater loons hosted a higher diversity, including cestodes, nematodes, trematodes, and acanthocephalans. We explore potential causes of differences in parasite communities, including host salt gland condition, trophic network breadth of pelagic vs. freshwater systems, and coastal fisheries' impacts on food web dynamics. Future studies should examine the diets of bycaught birds. Frozen fish bait that is eaten by avian hosts could be a factor contributing to lower parasite diversity.

(158) First record of the subcutaneous avian mite *Hypodectes propus* (Nitzsch, 1861) (Acari: Hypoderatidae) in Taiwan

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The family Hypoderatidae is a small group of cosmopolitan astigmatid mites primarily associated with birds, with some species known to parasitize rodents. Hypoderatid mites are of veterinary importance since during its immature stage, the heteromorphic deutonymphs (also known as hypopi) behave as endoparasites and commonly found aggregating on subcutaneous tissues. In contrast, adult forms are free-living nidophiles (nest-dwellers). Despite its wide distribution, they are poorly reported in terms of their host associations and specific geographic accounts. In this paper, we present the first record of the hypoderatid mite *Hypodectes propus* (Nitzsch, 1861) in Taiwan, a species primarily associated with columbiform and ardeiform birds. Gross necropsy of four avian species (*Ardea cinerea*, *A. coromanda*, *Streptopelia orientalis*, and *S. tranquebarica*) collected

from eastern and southern Taiwan was performed for post-mortem evaluation. Upon dissection, several small aggregates of hypopi were observed and collected for preservation in vials containing 95% ethanol. Confirmation of hypopi identity was carried out using an integrative approach: morphological and molecular identification. During the dissection, no obvious symptoms were found. Furthermore, we provide updated global distribution records and a host index for *H. propus* across its range. Our study highlights the role of migratory birds as mechanical vehicles for parasite dispersion, as well as the importance of natural history accounts on understudied parasitic groups associated with avians.

(159) Seasonality of gregarine infections in *Enallagma civilie*

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Gregarines (Apicomplexa: Eugregainida) are ubiquitous parasites of invertebrates, especially insects. There have been 10 species described in damselflies in North America. There are two seasonal studies done on gregarine infections in odonates. Only one of them has the study system of damselflies and they focused only on adult damselflies, but they did find unimodal patterns in prevalence and intensity of infection. This study will investigate seasonal patterns of gregarine infections in *Enallagma civile* adults over the flight season, and larvae over an entire year. We know that *Hoplorhynchus* and *Steganorhynchus* dunwoodyi infect damselflies in the area that we are collecting. Sampling is done bi-weekly for larvae and adults, which would make about two collections a month for both larvae and adults. We record temperature and weather condition data when sampling and collected 20-30 every time we sampled. Preliminary data for the first three months of the year are for three months of larvae collection and one adult collection during the first flight emergence. On the 30th of January the prevalence of infection in the larvae was 67%, and after observing the slides the infections seem to be 100% *Hoplorhynchus*. In February the prevalence of infection in the larvae was 90% and observing the slides showed that the infections were also 100% *Hoplorhynchus*. In March the first adults started coming out and the prevalence of infection was 32% and the ones that were infected were also infected with a *Hoplorhynchus* species. For the larvae collection in March the prevalence of infection is 45%. Based on my first three months of data there may be a decrease in infections during the flight season of the adults. More data will tell if that is the case.

(160) Helminth parasites of native North Carolina pit vipers: diversity and host associations

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Parasites are an important yet understudied aspect of snake health and ecology. For example, an invasive pentastome is causing widespread mortality in native snakes in Florida, and this parasite is spreading northward rapidly. Most pentastome and helminth parasites are acquired through trophic transmission when the snake consumes prey. However, we still know little about the association between snake feeding preferences and endoparasite diversity. We investigated parasite load and diversity within three unique species of pit vipers native to North Carolina, each with distinct diet preferences and feeding frequencies: timber rattlesnake (z, n=17), copperhead (*Agkistrodon contortrix*, n=18), and cottonmouth (*Agkistrodon piscivorus*, n=11). Among these host species, we found 8 species of larval or adult endoparasites: 1 acanthocephala (*Macracanthorhynchus ingens*), 1 cestoda (*Ophiotaenia* sp.), 4 nematoda (*Capillaria* sp., *Ophidascaris ashi*, *Spirocera* sp., and *Spiroxys* sp.), 1 pentastomida (*Kiricephalus coarctatus*), and 1 trematoda (*Strigea* sp. metacercariae). Of the three species, rattlesnakes had the lowest prevalence of infection and parasite community diversity. In contrast, cottonmouths had the highest, reflecting the importance of feeding frequency and diet specialization on both parasite load and diversity. This poster examines the influence of prey items on the spectrum of parasites found in pit vipers, demonstrating how different dietary components shape parasite richness and composition. Understanding the link between snake diet and parasite burden is crucial for developing effective conservation and management strategies, particularly in light of ongoing invasive species introductions and habitat modifications.

(161) Snake eels (family Ophichthidae) as pseudoparasites of predatory fish

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Snake eels (Ophichthidae) are a globally distributed family of Anguilliformes found anywhere from the bottom of tidepools to depths of 1300 meters. Members of this family use their sharp bony tails to burrow into the sand, but when swallowed by predatory fish, they can burrow through the intestinal tract. Their mummified corpses have been found in organs and body cavities of predatory marine fishes. The few reports of this occurrence denote different species being observed each time and disagree about whether this should be considered pseudoparasitism. We found a snake eel in the body cavity of a Black Sea bass (*Centropristis striata*) collected in North Carolina. Extraction and sequencing of the snake eel DNA allowed us to identify the eel as *Ophichthus cruentifer*. This contribution adds to our knowledge of members of the family Ophichthidae as pseudoparasites of predatory fishes.

(162) Comparing the parasite fauna of cane toads (*Rhinella horribilis*) originating from three regions of Florida

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When non-native species enter a new ecosystem, they commonly transport their natural parasites from their native range which may spillover into native species. It therefore becomes necessary to develop baseline checklists of parasites in non-native species. The cane toad, *Rhinella horribilis*, is a common invasive species in Florida's urban ecosystems. It originally became established in the Miami-Dade area but has since rapidly expanded its range. In this study, we are developing a checklist and comparing the types of helminths from the respiratory and digestive systems of cane toads from central, southwest, and southeast Florida. If parasite fauna is different by region, we expect the rapid host movement and establishment to play a factor in the variation of parasite fauna by region. To accomplish this, we received cane toads from local contractors and homeowners from each region. In the laboratory, a necropsy was performed on each specimen by removing the lung tissue and digestive tract from the body cavity. Each organ was individually separated and lacerated to release the internal contents into a petri dish. Any parasites found were extracted and sorted via external characteristics. In the respiratory tract we found the trematode *Haematoloechus sp.*, the nematode *Rhabdias pseudosphaerocephala* and a pentastome in the genus *Raillietiella*. *Haematoloechus sp.* was only found in central Florida while the pentastome was only found in southeastern Florida. The prevalence of *R. pseudosphaerocephala* was 72% in southeast Florida but dropped significantly to 9% in central Florida. In the gastrointestinal tract, we found two nematodes (one in the genus *Cosmocercoides*), two trematodes, and a cestode species. The nematode *Cosmocercoides sp.* was found in all three regions while the cestode species was absent from central Florida. The mean abundance of the nematode *Cosmocercoides* sp. varied, with an abundance of 32.4 per host in southeast Florida and 23.69 per host in southwest Florida. Additionally, one nematode was found in the abdominal cavity. Cane toads throughout Florida harbor a variety of helminthic parasites, with those originating near the original establishment site exhibiting the greatest diversity of parasites. We are continuing to identify species using microscopy and molecular analysis.

(163) Survey of water mites parasitizing mosquitoes in central Florida

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Water mites (Acari: Trombidiformes: Hydrachnidia) are common members of freshwater communities whose larval stage parasitize aquatic arthropods. These mites can significantly impact the survival and reproduction of their hosts and therefore can alter the structure of their community. Despite their ecological importance, the diversity of these mites and their relationships with their hosts is vastly understudied. This study aims to describe the diversity of water mites infecting mosquitoes in central Florida and assess whether the mites demonstrate host or site specificity. A total of 280 mosquitoes, representing four genera, were collected from Lakeland, FL between June 2024 and April 2025. Only three individuals, one *Culex* and two *Anopheles*, were infected with water mites, indicating a low overall prevalence of approximately 1%. Infected individuals hosted

between 2–4 mites, with a mean intensity of 3.3. Mites were found attached to the ventral (2) and dorsal (4) side of the thorax and the lateral (2), ventral (1), and dorsal (1) region of the abdomen. Mites have preliminarily been identified to the genus *Arrenurus*, but additional analyses, both morphological and molecular, are being conducted to confirm this. Adult mites with similar morphology have also been collected from lakes adjacent to the mosquito collection sites. Molecular analyses will be used to confirm that the larval and adult mites are the same species. This work is ongoing, so collection will continue for the next year to increase our sample size.

(164) Initial detection of rat lungworm, a human pathogen, in invasive snails in Georgia

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Rat lungworm, *Angiostrongylus cantonensis*, is an invasive nematode that naturally parasitizes rodents, primarily rats. A variety of gastropod mollusks act as the required intermediate host of rat lungworm, including invasive apple snails (*Pomacea maculata*) and mystery snails (*Heterogen japonica*). Freshwater crustaceans may serve as paratenic hosts (i.e., a host where development does not occur, but transmission between snail and rodent can be facilitated). In some cases, infective nematode larvae may be found on vegetation exposed to water with infected snails. When infected snails or paratentic hosts are ingested by rats, the larvae reach brain where they mature into adults and then migrate to the lungs. Other mammals, as well as some bird species, may be accidentally infected if they ingest the nematode larvae. In humans, rat lungworm can cause severe pathology (including meningitis) or death. There has only been one previous study that reported rat lungworm in Georgia, which were from wild brown rats collected in the Atlanta Zoo. In the present study, we collected invasive apple and mystery snails from 8 sites across the state of Georgia (Lakes Oconee, Lanier, Chehaw, Allatoona, Ocmulgee River, Pipemakers Canal, St. Marys, and Kingsland). Snails were euthanized, necropsied and examined for rat lungworm. Collected nematodes were used for molecular screening. Based on data in GenBank, we sequenced a fragment of the cytochrome *c* oxidase subunit I (*cox*1) mtDNA gene. We identified rat lungworm from Lake Lanier, Ocmulgee River, Pipemakers Canal, St. Marys, and Kingsland, however, prevalence of these nematodes was extremely low (0.5-18.9% of snails per site). Based on our data, it is clear that rat lungworm is already broadly distributed throughout Georgia. Efforts should be taken to help mitigate potential public health risks associated with this invasive pathogen.

(165) Prevalence and distribution of parasites infecting canines and felines in Southwest Florida

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Parasites are found in almost all ecological systems and are found in a wide range of organisms. Our companion animals are often exposed to parasites and can develop diseases that are detrimental to their health. This poses risks to pet owners as parasites can be transmitted between pets and their owners, often unbeknownst to them. While many pet owners do use anti-parasite medications, helminth parasites are still quite prevalent in communities but are often unknown. The purpose of this study is to identify the prevalence of different parasite species found in canines and felines that were admitted as patients at local clinics, and the prevalence of each based on location and pet age. Fecal samples will be collected from multiple veterinarians from Lee and Collier counties in Southwest Florida. So far, we have received 665 samples, along with 23 IDEXX™ Laboratory reports, from two veterinary clinics in Collier County, Florida, for processing. Fecal floatation via centrifugation is being performed on a portion of each confirmed positive fecal sample, and the parasitic eggs found are counted and imaged. Collections and centrifugation of fecal samples will continue until the end of summer 2025. DNA Extraction and PCR will be performed on parasite eggs found through centrifugation to identify parasitic DNA in each positive fecal sample. So far, 37 canine samples and 7 feline samples were found to contain parasite eggs and/or cysts. Hookworm ova was the most prevalent parasite group, found in 24 canines and in 1 feline sample, specifically ova of the Ancylostoma genus in the majority of those samples. On the other hand, ova of the *Trichuris* genus were found in only 1 canine sample and is the least common parasite genus we found so far. The ages of the sampled pets ranged from 2 months to 16 years old. We are requesting feedback on the currently used methodologies and master's thesis practices for this ongoing project.

(166) A survey of the parasites of *Morone saxatilis* (striped bass) in the Hudson River, New York

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The Hudson River has been an area of much ecological distress, including the dumping of Polychlorinated Benzenes (PCBs) and the dredging of sediment in an effort to remediate the amount of toxins in the water. The PCBs are a bio-accumulator that most harm the species at the top of the food web. One such fish found in the river is striped bass, *Morone saxatilis*, the population of which has decreased substantially in recent years. Parasites are known indicators of environmental change and can be used to infer details about the population dynamics, community structure, food web structure, and biodiversity. The New York State Department of Conservation (NYS DEC) is monitoring the population health of *M. saxatilis* via routine gill net surveys throughout April and May of each year. The current project adds a parasitological element to the NYS DEC study of *M. saxatilis*. The fish were collected via gill net along different points of the Hudson River and subsequently measured, sexed, and dissected, with the intestinal tract examined for parasites with the aid of a stereoscope. This poster presentation will report on the preliminary parasitological results of the survey work being conducted during April and May 2025. At this point, we have encountered three species of intestinal helminth including a species of acanthocephalan *Pomphorhynchus*, a species of digenean, and a nematode. We have also encountered a species of nematode from the body cavities. These preliminary parasitological results are interpreted in the context of the known life cycles of each helminth encountered in order to clarify elements of the fish host biology including diet.

(167) First report of horsehair worms (Phylum Nematomorpha) from plethodontid salamanders in North America

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The Plethodontidae family are a lungless salamander group that are mostly found in the Western Hemisphere. They play a significant ecological role consuming terrestrial invertebrates and are a food source to many small mammals and other invertebrates. Horsehair worms are parasites with a complex life cycle that use larval aquatic invertebrates and terrestrial arthropods to complete their life cycle. Previously published reports in other salamander families have identified the presence of the cyst stage of nematomorphs but it is unclear whether salamanders play a role in the life cycle of the Nematomorpha. The purpose of this study was to examine horsehair worm cysts in lungless salamanders and determine how common they were. Four species of larval salamanders were collected from various sites in Northern Georgia, stored in 70% ethanol, and stored in a -20°C freezer until examined. Upon necropsy, the salamanders were measured snout to vent (mm) and, only the integument and the inner layer of muscles was examined for horsehair worms. The ventral and dorsal sections were examined for cysts by placing tissue on a microscope slide with coverslip and applying gentle pressure to flatten the tissue. The sections were then examined under an Olympus BX-51 compound microscope, at 100-400x magnification. Some samples had other sections examined (i.e., toes, head, and tail). We found 25/95 (26.3%) of salamanders contained horsehair worm cysts and had a mean intensity of 82.6 ± 108.7 (range 1-696) but this varied by salamander species and location. Because terrestrial insects are not likely to consume salamanders as prey, we suggest the Plethodontidae are accidental infections. To the best of our knowledge, this study is the first to identify horsehair worm cysts in the family Plethodontidae.

(168) Collaborative field collections of *Sorex* shrews in North Carolina uncover novel cestode diversity

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Shrews of the genus *Sorex* are definitive hosts to a wide diversity of hymenolepidid tapeworms (Cyclophyllidea: Hymenolepididae). Although this tapeworm family is globally distributed, prior study of cestodes of *Sorex* spp. in North America has left numerous regions under-sampled, including the Southeastern US. In this study we examined the intestinal contents of a total of 81 shrews, representing two species, *Sorex cinereus* and *Sorex fumeus*, from the Southern Appalachian Mountains of western North Carolina. The major aim was to

investigate the diversity of hymenolepidid tapeworms infecting shrews in this region and formally describe any new species uncovered based on a combination of molecular (28S rDNA sequences) and morphological data. Our examinations uncovered 14 tapeworm species within 7 genera, of which 12 are likely undescribed species. One of the new species is within the genus *Staphylocystis*, of which only 2 species have been previously described in North America, both from Northern regions of the USA. We present new mitochondrial genomes and comparisons of the 2 previously described species, *S. clydsengeri* and *S. schilleri*, our new species, as well as 1 Eurasian species (*S. furcata*). We integrate morphological and molecular data that clearly separates our new species from its congeners. Ongoing field collections within other regions of North Carolina will likely continue to reveal new diversity of Hymenolepidids within *Sorex* hosts, and community dynamics of these taxa across sites and seasons.

(169) Endoparasite community of the invasive grey-headed swamphen (*Porphyrio poliocephalus*)

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Native to southeast Asia, the Grey-Headed Swamphen (*Porphyrio poliocephalus*) is a recent invasive to south Florida. After escaping from captivity in 1996 from Pembroke Pines, they are expanding their invasive range northwards, along the east coast of Florida. In their invasive range, they consume primarily *Eleorchis cellulose* and *Panicum* seeds and occupy the same wetland marsh habitat as native Gruiform rails. A method in monitoring the progress of their invasion is to examine their endoparasite community. Endoparasites are acquired primarily through a host's diet preferences and secondarily through the local environment with many parasites requiring multiple host taxa to complete their lifecycle. Additionally, as parasites tend to be specialists in their choice of host, it takes time for them to adjust to the presence of a new host environment. This study aims to compare the endoparasite community of *P. poliocephalus* to nine native rail species. These hosts were chosen due to niche and phylogenetic similarities. *P. poliocephalus* specimens were caught and euthanized from Water Conservation Areas 2 and 3 via a partnership with FWC and non-swamphen carcasses are received frozen from six wildlife rehabilitation centers across south Florida. Dissections targeting the gastrointestinal tract are conducted. Parasite intensity, load, and species richness are recorded for each specimen. After dissection, parasites are stained in acetocarmine, mounted on slides, and identified to the lowest possible taxa. Thus far, native rails have an overall species richness of 19 and an infection prevalence of 76%. *P. poliocephalus* have been infected by *Hystrichis* sp. (Nematoda: Dioctophymidae) at a rate of 11%. In their endemic range, there are records of echinostome (Digenea: Echinostomatidae) infections. With the combined instances of rapid population growth and lack of parasitic infections, the enemy release hypothesis is evident in this system. Spillback, when native parasites infect nonnative hosts, is also occurring with the presence of the native generalist nematode, *Hystrichis* sp. Meanwhile spillover, when a nonnative host's endemic range parasites infect native hosts, does not appear to be active.

(170) Development and distribution of a pathogenic neogregarine (*Ophryocystis elektroscirrha*) in monarch butterflies

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The pathogenic neogregarine *Ophryocystis elektroscirrha* infects the hypodermal tissues of monarchs (*Danaus plexippus*). However, the life cycle, development, distribution, and pathology of this parasites is not well documented in monarch hosts. To evaluate this, we exposed 15 2nd instar monarch butterfly caterpillars with 200 oocysts of *O. elektroscirrha* obtained from monarchs collected in Stillwater, Oklahoma. Exposed 4th instar caterpillars and/or 8- and 11-day old chrysalises were fixed along with unexposed controls and processed for histology. Additionally, the abdomen of one infected and one unexposed control adult monarch butterfly was prepared for scanning electron microscopy (SEM). Our results indicate that we did not find any developmental stages of *O. elektroscirrha* in caterpillar stages, but we detected immature and mature oocysts of *O. elektroscirrha* in 8- and 11-day old chrysalises and/or adult stages of monarch butterflies. Both immature and mature oocysts were distributed on the cuticle of chrysalises and mature oocysts were distributed on the cuticle of adult butterflies. The majority of oocysts were located on the surface of the cuticle and below the scales but also surrounding the cuticle of the reproductive structures including the egg chamber

in female chrysalises and the aedeagus in male chrysalises and adult monarch butterfly. These observations provide a plausible mechanism for maternal and sexual transmission of this parasite. Additionally, our SEM investigation of the cuticle of adult monarch butterfly revealed many oocysts that were embedded in the cuticle indicating host pathology (cuticle damage). Because previous studies indicate that infected monarch butterflies lose weight more quickly than uninfected individuals, damage to the cuticle in adult butterflies by the oocysts of this parasite might explain the drastic weigh loss observed in infected adult monarchs. The implications of our hypotheses are discussed in terms of the unique biology of monarch butterflies and their conservation efforts.

(171) 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.

(172) *Cryptosporidium* in grey squirrels on Transylvania University campus, Lexington, KY

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Urban wildlife such as grey squirrels (*Sciurus carolinensis*) may serve as reservoirs for a range of gastrointestinal parasites, including protozoa of zoonotic concern. *Cryptosporidium* species are notable for causing gastroenteric disease in animals and humans. While frequently detected in rodents, their prevalence and transmission potential in synanthropic squirrel populations remain unexplored. This study aimed to investigate the presence of *Cryptosporidium* in grey squirrels inhabiting the Transylvania University campus in Lexington, Kentucky. Seventy grey squirrels were trapped across various campus sites using Sherman live traps baited with rolled oats and vanilla essence. Fecal samples were collected noninvasively from trap-lining sheets and preserved in 70% ethanol. Each animal was marked with non-toxic dye before release to prevent recapture. Stool samples were analyzed via the modified Telemann coprological method for microscopic detection of gastrointestinal parasites. In parallel, molecular identification of *Cryptosporidium* was initiated using PCR amplification of the 18S rDNA gene. Of the 70 fecal samples analyzed, 45 (64.3%) were microscopically positive for *Cryptosporidium* oocysts. At the time of reporting, only 20 samples had undergone molecular testing, with 10 (50%) returning positive for *Cryptosporidium* DNA. These preliminary findings suggest a high potential prevalence of *Cryptosporidium* in this urban grey squirrel population, indicating their possible role as wildlife reservoirs within shared human-animal environments such as university campuses. This study provides foundational data for future zoonotic surveillance efforts in urban ecosystems. Ongoing work includes the continued molecular screening of remaining samples and genotypic characterization of *Cryptosporidium* to assess host-specificity and zoonotic potential. These efforts will contribute to a deeper understanding of protozoan parasite

(173) A parasite survey of lizards on Andros Island, Bahamas: Do *Anolis* ecomorphs host different assemblages of parasites?

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Lizards are one of the most abundant terrestrial vertebrates on Bahamian islands, yet few studies have surveyed these hosts for parasites. The 4 species of *Anolis* on the island occupy different ecological niches and have different body types, and thus are considered different ecological morphotypes (ecomorphs). In addition to completing a baseline survey, we hope to determine if *Anolis* ecomorphs host different assemblages of parasites or if parasite species are shared among ecomorphs. In 2015 and 2017, we conducted parasite surveys to ascertain the prevalence, abundance, and distribution of parasites within 7 species of lizards commonly found on Andros Island, Bahamas: *Ameiva auber*i, *Anolis angusticeps*, *Anolis carolinensis*, *Anolis distichus*, *Anolis sagrei*, *Hemidactylus frenatus*, and *Leiocephalis carinatus*. We collected lizards from three regions of the northern section of Andros Island, then dissected and examined hosts for parasites at ForFar Field Station. We also made blood smears and preserved feces at ForFar for protozoans. We identified parasites at Florida Southern College, and we calculated prevalence, mean abundance and intensity of all parasites encountered. Our results suggest that the nematodes *Cyrtosomum* sp. and *Spinicauda spinicauda* were the most common parasites in lizards, whereas no blood protozoans have been located to date. We found that the ground- trunk lizard, *Anolis sagrei*, hosts nearly all species of parasites found in this study, whereas the canopy lizard, *Anolis smaragdinus*, and twig specialist, *Anolis angusticeps*, hosted relatively few parasite species. We will discuss differences between parasite parameters among locations, host species, and years. Overall, our study suggests that *Anolis* ecomorphs have different parasite assemblages, although some parasites are shared among most anoles.

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Notes

ASP Meeting History

1925	Kansas City MO
1926	Philadelphia PA
1927	Nashville TN
1928	New York NY
1929	Des Moines IA
1930	Cleveland OH *
1931	New Orleans LA
1932	Atlantic City NJ
1933	Boston MA
1934	Pittsburgh PA
1935	St Louis MO
1936	Atlantic City NJ
1937	Indianapolis IN
1938	Richmond VA
1939	Columbus OH
1940	Philadelphia PA
1941	Dallas TX
1942	No Meeting
1943	No Meeting
1944	Cleveland OH
1945	St. Louis MO
1946	Boston MA
1947	Chicago IL
1948	New Orleans LA *
1949	New York NY
1950	Cleveland OH
1951	Chicago IL *
1952	Ithaca NY ‡
1953	Madison WI ‡
1954	Memphis TN *
1955	Atlanta GA
1956	Storrs CT ‡
1957	Philadelphia PA *
1958	Bloomington IN ‡
1959	University Park PA ‡
1960	Los Angeles CA *
1961	Lafayette IN ‡
1962	Washington DC +
1963	Chicago IL *
1964	Boulder CO ‡
1965	Atlanta GA
1966	San Juan PR *
1967	Tucson AZ §
1968	Madison WI ‡
1969	Washington DC *
1970	Washington DC ¶
1971	Los Angeles CA
1972	Miami Beach FL *
1973	Toronto ON Canada
1974	Kansas City MO
1975	New Orleans LA *
1976	San Antonio TX
1977	Las Vegas NV
1978	Chicago IL *
1979	Minneapolis MN
1980	Berkeley CA
1981	Montreal QB Canada
1982	Toronto ON Canada ¶
1983	San Antonio TX *
1984	Snowbird UT
1985	Athens GA
1986	Denver CO *
1987	Lincoln NE #
1988	Winston-Salem NC
1989	Vancouver BC Canada
1990	East Lansing MI
1991	Madison WI
1992	Philadelphia PA
1993	Atlanta GA *
1994	Ft. Collins CO
1995	Pittsburgh PA ‖
1996	Tucson AZ **
1997	Nashville TN
1998	Kona HI
1999	Monterey CA ++
2000	San Juan PR **
2001	Albuquerque NM
2002	Vancouver BC Canada ¶ ss
2003	Halifax NS Canada
2004	Philadelphia PA ‖
2005	Mobile AL
2006	Glasgow ¶
2007	Merida Mexico ‡‡ ss
2008	Arlington TX
2009	Knoxville TN
2010	Colorado Springs CO
2011	Anchorage AK
2012	Richmond VA
2013	Quebec City QC Canada ¶¶
2014	New Orleans LA
2015	Omaha NE
2016	Edmonton AB Canada
2017	San Antonio TX ##
2018	Cancun Mexico
2019	Rochester MN
2020	Cancelled
2021	Virtual Online
2022	College Station TX
2023	Kansas City MO
2024	Denver CO
2025	Winston-Salem NC
2026	Orlando FL

* With the American Society of Tropical Medicine; since 1952, American Society of Tropical Medicine and Hygiene
+ With the Helminthological Society of Washington
‡ With the American Institute of Biological Sciences
§ With the American Microscopical Society
¶ With the International Congress of Parasitology; 1970 (ICOPA-II), 1982 (ICOPA-V), 2002 (ICOPA-X), 2006 (ICOPA-XI)
# With the Wildlife Disease Associaton
‖ With the American Association of Veterinary Parasitologists
** With the Society of Protozoologists
++ With the Society of Nematologists
‡‡ With the Parasitology Section of the Canadian Society of Zoologists
ss With the Sociedad Mexicana de Parasitología
¶¶ With the Quebec Molecular Parasitology meeting
With the International Coccidiosis Conference