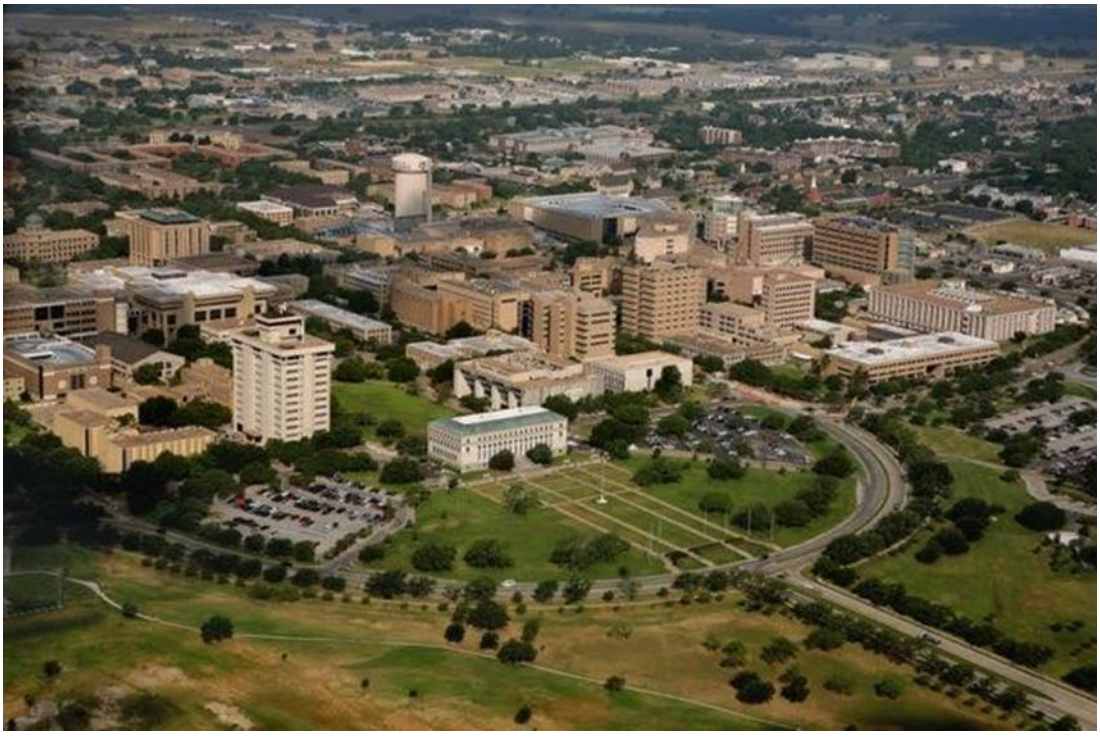
The 97th Annual Meeting of the American Society of Parasitologists



The George and Cavalry Court Hotels

College Station, Texas, JULY 9-12, 2022

Program & Abstracts

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

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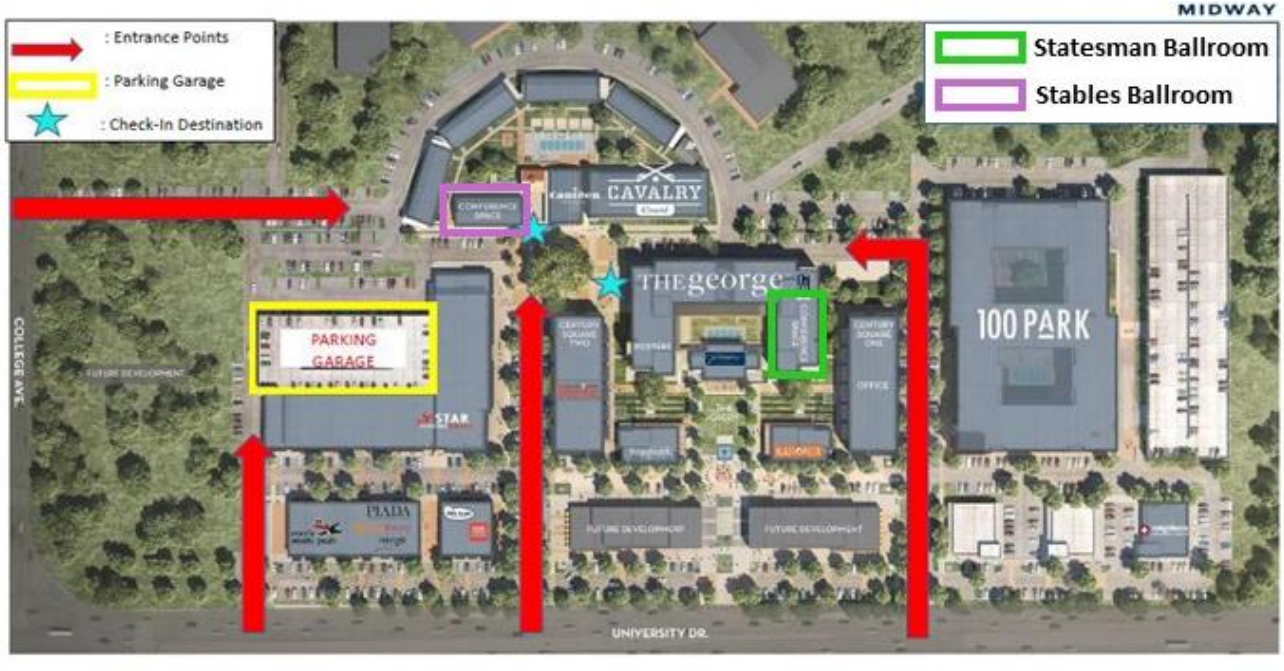
The American Society of Parasitologists

Welcome

We would like to welcome you to the 97th annual meeting of the American Society of Parasitologists (ASP). The ASP is a diverse group of over 800 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.

Maria G. Castillo and Judith Humphries, Scientific Program Officers

1. **Aerial view of The George and Cavalry Court Hotels**



CENTURY SQUARE

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. Sara Brant, sbrant@unm.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.

General Schedule

Day/Times	Activity/Function	Room/Space
Friday, July 8		
2:00–6:00 pm	Registration	The George Lobby
Saturday, July 9		
7:00 am–5:00 pm	Registration	The George Lobby
8:00 am–Noon	ASP Council Meeting	Statesman I
2:00–3:15 pm	Ecology & Evolution I	Statesman II
	Taxonomy, Systematics, & Phylogeny I	Stables I
	Host-Parasite Interactions I	Stables II
3:15–3:45 pm	Coffee Break	The George Lobby/Library
3:45–5:00 pm	Ecology & Evolution II	Statesman II
	Taxonomy, Systematics, & Phylogeny II	Stables I
	Host-Parasite Interactions II	Stables II
7:00–10:00 pm	Welcome Reception	Stables Ballroom & Parade Green
Sunday, July 10		
7:00 am–5:00 pm	Registration	The George Lobby
8:30–10:30 am	ASP President's Symposium	Statesman Ballroom
10:30–11:00 am	Coffee Break	The George Lobby/Library
11:00 am–Noon	ASP Student Business Meeting	Stables I
Noon–1:00 pm	Editorial Luncheon	Statesman I
1:15–3:00 pm	Ecology & Evolution III	Statesman II
	Taxonomy, Systematics, & Phylogeny III	Stables I
	Host-Parasite Interactions III	Stables II
3:00–3:30 pm	Coffee Break	The George Lobby/Library
3:00–6:00 pm	Auction Set Up	Statesman Ballroom
3:30–5:30 pm	ASP Students' Symposium	Stables Ballroom
5:30–6:30 pm	ASP Student Social	The George Lobby/Library
6:00–7:00 pm	Auction Preview	Statesman Ballroom
7:00–9:00 pm	31st Annual ASP Student Auction	Statesman Ballroom
Monday, July 11		
7:00–11.00 am	Registration	The George Lobby
8:15–10.30 am	Arthropods & their Pathogens Symposium	Statesman Ballroom
9:30–10:30 am	Ecology & Evolution IV	Stables I
10:30–11:00 am	Coffee Break	The George Lobby/Library
11:00 am–Noon	ASP President's Address	Statesman Ballroom
Noon–3:00 pm	Poster and Palettes & Parasites Set Up	Statesman Ballroom
1:00–2:00 pm	Genomics & Molecular Biology	Stables I

	Life Cycles & Epidemiology I	Stables II
2:00–3:00 pm	Vector Biology	Stables I
	Life Cycles & Epidemiology II	Stables II
3:30–5:30 pm	Poster Session, 2nd Annual Palettes & Parasites Contest	Statesman Ballroom

Tuesday, July 12

8:15–9:30 am	Parasites and Pedagogy Symposium	Statesman Ballroom
8:30–9:30 am	Taxonomy, Systematics, & Phylogeny IV	Stables I
	Host-Parasite Interactions IV	Stables II
9:30–10:00 am	Coffee Break	The George Lobby/Library
10:00–11:00 am	Ecology & Evolution V	Statesman Ballroom
10:00–11:15 am	Taxonomy, Systematics, & Phylogeny V	Stables I
10:00–10:30 am	Chemotherapy & Drug Resistance	Stables II
1:00–2:00 pm	H. B. Ward Medal Lecture	Statesman Ballroom
2:15–415 pm	ASP Business Meeting*	Statesman Ballroom

*Awards being presented include the Ashton Cuckler New Investigator Award, the Clark P. Read Mentor Award, Marc Dresden Student Travel Grants, and Best Student Presentations.

Detailed Schedule

Friday, July 8, 2022

2:00 pm–5:00 pm Registration

Location: The George Lobby

Saturday Morning, July 9, 2022

7:00 am–5:00 pm Registration

Location: The George Lobby

8:00 am–Noon ASP Council Meeting

Location: Statesman I (The George)

Saturday Afternoon, July 9, 2022

2:00–3:15 pm Ecology & Evolution I

Location: Statesman II (The George)

Presiding: **Jenna Hulke,** Texas A&M University

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

2:00 (1) † **Jenna M. Hulke**, Charles D. Criscione. TESTING AN ASSUMPTION AND PREDICTION OF THE MATING SYSTEM MODEL FOR COMPLEX LIFE CYCLE EVOLUTION IN THE TREMATODE *ALLOGLOSSIDIUM RENALE*.

2:15 (2) **Charles D. Criscione**, Cameron Goater. NASCENT LINKAGES BETWEEN PARASITE TRANSMISSION, PARASITE MATING SYSTEMS, AND CLONEMATE ABUNDANCE DISTRIBUTIONS IN TREMATODES.

2:30 (3) **Derek A. Zelmer**. THE EFFECT OF ABUNDANCE TRANSFORMATIONS ON BRAY-CURTIS NMDS ESTIMATION OF PATTERNS OF PARASITE INFRA- AND COMPONENT COMMUNITY SIMILARITY.

2:45 (4) **Mary J. Janecka**, Charles D. Criscione, Jan E. Janecka. WHAT DRIVES PARASITE GENE FLOW IN RIVERINE HABITATS? INTERACTIONS BETWEEN STREAM DRIFT, RIVER BIFURCATIONS AND HOST DISPERSAL.

3:00 (5) † **Daniel C. G. Metz**, Ryan F. Hechinger. INTRAMOLLUSCAN TREMATODES AS CLOSED POPULATIONS: PROJECTION MATRIX MODELS REVEAL INFRAPOPULATION DYNAMICS AND HELP RESOLVE QUESTIONS ABOUT TREMATODE SOCIALITY.

2:00–3:15 pm Taxonomy, Systematics, & Phylogeny I

Location: Stables I (Cavalry Ct)

Presiding: **Stephen Bullard,** Auburn University

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

2:00 (6) † **Haley R. Dutton**, Louis H. Du Preez, Edward C. Netherlands, Stephen A. Bullard. A SPECIES OF *DENDRITOBILHARZIA* (DIGENEA: SCHISTOSOMATIDAE) INFECTING THE HEART LUMEN OF WHITE-BACKED DUCK, *THALASSORNIS LEUCONOTUS* (ANSERIFORMES: ANATIDAE) FROM NAMIBIA: A FIRST GLIMPSE OF AVIAN SCHISTOSOME DIVERSITY WITHIN THE UN-SURVEYED NAYE-NAYE CONCESSION AREA OF SOUTHERN AFRICA.

2:15 (7) **Vasyl V. Tkach**, Taylor P. Chermak. MORPHOLOGICAL RE-EVALUATION AND PHYLOGENETIC ANALYSIS OF THE RENSCHETREMATIDAE.

2:30 (8) † **Haley P. Knudson**, Haley R. Dutton, Stephen S. Curran, Stephen A. Bullard. A SURVEY OF THE INTESTINAL TREMATODES INFECTING TWO FRESHWATER TURTLES FROM THE MEKONG RIVER BASIN, VIETNAM, WITH FIRST PHYLOGENETIC INVESTIGATION OF GENUS *ENCYCLOBREPHUS*.

2:45 (9) **Florian B. Reyda**, Margaret L. Doolin, Anindo Choudhury, Herman Wirshing, Anna J. Phillips. PHYLOGENETIC ANALYSIS OF NORTH AMERICAN SPECIES OF *NEOECHINORHYNCHUS* STILES & HASSALL, 1905.

3:00 (10) **Charlayna A. Cammarata**, Wesley J. Neely, Vasyl V. Tkach, Norman O. Dronen. FIRST REPORT OF TURTLE BLOOD FLUKES (DIGENEA: SCHISTOSOMATOIDEA) FROM APALONE SPINIFERA SPP. (TESTUDINES: TRIONYCHIDAE) IN TEXAS.

2:00–3:00 pm Host-Parasite Interactions I

Location: Stables II (Cavalry Ct)

Presiding: **Kelly Weinersmith,** Rice University

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

2:00 (11) **Omar Amin**. DENTAL SOURCES OF DELUSIONAL PARASITOSIS (NEURO-CUTANEOUS SYNDROME); A NEW TOXICITY DISORDER.

2:15 (12) † **Jordan Salomon**, Nadia A. Fernández-Santos, Italo B. Zecca, José G. Estrada-Franco, Edward Davila, Gabriel L. Hamer, Mario A. Rodríguez-Pérez, Sarah A. Hamer. BROWN DOG TICK (*RHIPICEPHALUS SANGUINEUS SENSU LATO*) INFECTION WITH ENDOSYMBIONT AND HUMAN PATHOGENIC *RICKETTSIA* SPP., NORTHERN MEXICO.

2:30 (13) † **Justin Wolz**, Elliot A. Zieman. ANALYSIS OF CYTOKINE PROFILES IN DOMESTIC CATS (FELIS CATUS) INFECTED WITH *CYTAUXZOON FELIS*.

2:45 (14) † **Sara Fresard**, Sophio Kirimlishvili, Russell Thomson, Jayne Raper. TLF3: IDENTIFICATION OF A UNIQUE PRE-BETA HIGH-DENSITY LIPOPROTEIN AS A THIRD TRYPANOSOME LYTIC FACTOR.

3:15–3:45 pm COFFEE BREAK The George Library/Lobby

3:45–5:00 pm Ecology & Evolution II

Location: Statesman II (The George)

Presiding: **Ryan Hechinger,** University of California

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

3:45 (15) † **Daniel C. G. Metz**, Emma M. Palmer, Ryan F. Hechinger. CERCARIA EMERGENCE RATES LET US CALCULATE TREMATODE PARTHENITA WITHIN-HOST DYNAMICS.

4:00 (16) **Roy N. Platt II**. HYBRIDIZATION BETWEEN HUMAN AND LIVESTOCK SCHISTOSOMES – RAMPANT OR RARE?

4:15 (17) **Eric S. Loker**, Erika T. Ebbs, Sara V. Brant. THE GASTROPOD HOSTS OF SCHISTOSOMES: PATTERNS, PROCESSES AND MECHANISMS.

4:30 (18) **Christina Anaya**. PHYSID SNAILS AS SENTINELS: THEIR STATUS 25 YEARS LATER.

4:45 (19) **John F. Shea**, Chirstyn Okuno, Jack H. Cook, Chase Howard, McKay Carstens. LARVAL TREMATODE DIVERSITY AND ITS CORRELATION WITH AQUATIC INVERTEBRATE DIVERSITY AND WATER QUALITY OVER FIVE YEARS AT THREE SITES IN OGLALA LAKOTA COUNTY, SD.

3:45–5:00 pm Taxonomy, Systematics, & Phylogeny II

Location: Stables I (Cavalry Ct)

Presiding: **Haley Dutton,** Auburn University

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

3:45 (20) **Kirsten Jensen**, Janine N. Caira. LIGHT AT THE END OF THE ALIMENTARY CANAL: ADVANCING GENERIC DIVERSITY OF ELASMOBRANCH TAPEWORMS.

4:00 (21) **Stephen A. Bullard**, Micah B. Warren. SHARKS AS DISPERSAL PLATFORMS FOR REMORA-INFECTING MONOGENOIDS (MONOGENOIDEA: DIONCHIDAE: *DIONCHUS*)?: MORPHOLOGICAL AND NUCLEOTIDE EVIDENCE OF *DIONCHUS POSTONCOMIRACIDIA* INFECTING THE SKIN OF THE BLACKTIP SHARK, *CARCHARHINUS LIMBATUS*.

4:15 (22) † **Micah B. Warren**, Larisa G. Poddubnaya, Alexander Zhokhov, Stephen A. Bullard. REDESCRIPTION OF A LITTLE STUDIED FRESHWATER FISH BLOOD FLUKE (DIGENEA: APOROCOTYLIDAE: *SANGUINICOLA*) INFECTING THE TYPE HOST (SABREFISH, *PELECUS CULTRATUS*) FROM THE UPPER VOLGA RIVER, RUSSIA, AND THE FIRST PHYLOGENETIC ANALYSIS INCLUDING A SPECIES OF *SANGUINICOLA* ACCOMPANIED BY ADULT VOUCHER SPECIMENS.

4:30 (23) † **Jakson R. Martens**, Tyler J. Achatz, Vasyl V. Tkach, Taylor Chermak. NEW SPECIES FOR AN OLD GENUS.

4:45 (24) **Stephen S. Curran**, Stephen A. Bullard. RECONSIDERING THE IDENTITY OF SPECIES BELONGING IN *DIPLOMONORCHIS* HOPKINS, 1941 FROM THE NORTHERN GULF OF MEXICO.

3:45–4:45 pm Host-Parasite Interactions II

Location: Stables II (Cavalry Ct)

Presiding: **Nicolas Wheeler,** University of Wisconsin

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

3:45 (25) † **Steven P. Ksepka**, Stephen A. Bullard. PATHOLOGY OF *HUFFMANELA* CF. *HUFFMANI* (NEMATODA: TRICHOSOMOIDIDAE) INFECTIONS IN SWIM BLADDER, PERITONEUM, AND GONAD OF VARIABLE PLATYFISH, *XIPHORUS VARIATUS* (CYPRINODONTIFORMES: POECILIIDAE) AND EASTERN MOSQUITOFISH, *GAMBUSIA HOLBROOKI* (POECILIIDAE) FROM FLORIDA.

4:00 (26) † **Matthew A. Walker**, Matthew G. Bolek, Elliott A. Zieman, Gabriel J. Langford, Jason L. Brown, Agustín Jiménez. GENETIC AND TRAIT VARIABILITY OF *GYRINICOLA BATRACHIENSIS* (NEMATODA: OXYURINA) ACROSS NORTH AMERICA WITH NOTES ON CURRENT TAXONOMIC PLACEMENT).

4:15 (27) **Dana Marie Calhoun**, Jamie Curtis, Clara Hassan, Pieter T. J. Johnson. NO PLACE LIKE HOME: USING HEATMAPS AS TOOL TO INVESTIGATE HABITAT SELECTION OF METACERCARIAE IN *PSEUDACRIS REGILLA*.

4:30 (28) † **Katrina D. Keith**, McKenna Sanchez, Gary Voelker. AVIAN MALARIA PREVALENCE ACROSS IMPORTANT BREEDING GROUNDS OF NORTHERN MEXICO AND TEXAS.

Saturday Evening, July 9, 2022

7:00–10:00 pm Welcome Reception

Location: Stables Ballroom & Parade Green (Cavalry Ct)

Sunday Morning, July 10, 2022

7:00 am–5:00 pm Registration

Location: The George Lobby

8:30–10:30 am ASP President's Symposium

Location: Statesman Ballroom (The George)

Presiding: **Matthew Bolek**, Oklahoma State University

Theme: "Snails in Parasitology: Taxonomy, Biogeography and Host Parasite Interactions."

8:30 **Matthew Bolek**. Introduction.

8:40 (29) **Jillian T. Detwiler.** IS IGNORANCE BLISS? THE VICISSITUDES OF SNAIL TAXONOMY FOR PARASITOLOGISTS.

9:15 (30) **Erika T. Ebbs**, Eric S. Loker, Sara V. Brant**.** COMPARATIVE INVASION HISTORIES OF TWO NORTH AMERICAN FRESHWATER SNAILS: APPROACHES TO IMPROVING OUR UNDERSTANDING OF SNAIL-TREMATODE INVASION DYNAMICS.

9:50 (31) **Ben Hanelt.** PARATENIC HOST TRANSFER AND TROPHIC TRANSMISSION: A ROLE FOR AQUATIC SNAILS IN THE GORDIID (PHYLUM NEMATOMORPHA) LIFE CYCLE.

10:25 Questions. Closing Remarks.

10:30–11:00 am COFFEE BREAK The George Library/Lobby

11:00–Noon ASP Student Business Meeting

Location: Stables I (Cavalry Ct)

Presiding: **Kayleigh Chalkowski,** Auburn University

Sunday Afternoon, July 10, 2022

Noon–1:00 pm Editorial Board Luncheon

Location: Statesman I (The George)

1:15–3:00 pm Ecology & Evolution III

Location: Statesman II (The George)

Presiding: **Janine Caira,** University of Connecticut

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

1:15 (32) **Abbe Pannucci**, Sarah Pangburn, Kelly Kroft, Rachel Joakim, Jimmy A. McGuire, Susan Perkins. LIZARD PLASMODIUM PREVALENCE AND EVOLUTIONARY HISTORY ACROSS SULAWESI.

1:30 (33) **Chris A. Hall**. DISEASE ECOLOGY OF *TRYPANOSOMA CRUZI* IN THE SOUTHEASTERN UNITED STATES.

1:45 (34) **Rachael Joakim**, Susan Perkins. THE AVIAN MALARIA COMMUNITY OF SULAWESI: ISLANDS ON AN ISLAND.

2:00 (35) **Joanna J. Cielocha**. GREGARINES OF GRASSHOPPERS FROM EASTERN KANSAS, U.S.A.

2:15 (36) † **Christopher Marshall**, Joseph Connolly, Patrick Hudson. DISTRIBUTION AND ECOLOGY OF *ERGASILUS COTTI* (KELLICOTT 1892) FROM MOTTLED SCULPIN AND RAINBOW DARTER.

2:30 (37) **Stephen A. Bullard**, Haley R. Dutton, Steven P. Ksepka, Justin D. Krol, Micah B. Warren, Triet N. Truong, Stephen S. Curran, John H. Brule, Haley P. Knudson. TAXONOMIC EXPERTISE IS EXCEEDED BY DEMAND FOR IT: THE FUNDAMENTAL NECESSITY OF TAXONOMY IN THE MANAGEMENT AND UNDERSTANDING OF FISH DISEASES, AQUATIC INVASIVE SPECIES, AND CRYPTIC SPECIES IN THE SOUTHEASTERN UNITED STATES.

2:45 (38) † **Genevieve M. Ivec**, Karin E. Limburg, Christopher M. Whipps. OTOLITH MICROCHEMISTRY ANALYSIS OF TRACE ELEMENTS IN RELATION TO PARASITISM IN TWO FISH SPECIES IN A LENTIC SYSTEM.

1:15–3:00 pm Taxonomy, Systematics, & Phylogeny III

Location: Stables I (Cavalry Ct)

Presiding: **Vasyl Tkach,** University of North Dakota

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

1:15 (39) † **John H. Brule**, Micah B. Warren, Haley R. Dutton, Cole R. Harty, Stephen A. Bullard. PARASITOLOGICAL SURVEY OF SILVER CARP, *HYPOPHTHALMICHTHYS MOLITRIX* (VALENCIENNES, 1844) (CYPRINIFORMES: CYPRINIDAE) REVEALS THE FIRST RECORD OF AN ECTOPARASITE, *DACTYLOGYRUS* CF. *SKRJABINI* (MONOGENOIDEA: DACTYLOGYRIDAE) FROM THIS HOST IN NORTH AMERICA.

1:30 (40) **Tyler J. Achatz**, Jakson R. Martens, Taylor P. Chermak, Vasyl V. Tkach. UNTANGLING THE SYSTEMATICS OF THE DIPLOSTOMIDAE.

1:45 (41) † **Ali Z. Lira Olguin**, Roxana Acosta Gutierrez, Carl Dick. TAXONOMIC REVISION OF THE GENUS *MEGISTOPODA* MACQUART, 1852 (DIPTERA: STREBLIDAE) AND PRELIMINARY RESULTS OF THEIR SPECIES DELIMITATION.

2:00 (42) **Omar Amin**. ANATOMICAL VARIABILITY IN THE ACANTHOCEPHALA (# 1 OF 2 PARTS).

2:15 (43) **Omar Amin**. STRUCTURAL-FUNCTIONAL RELATIONSHIPS AND CURIOSITIES IN THE ACANTHOCEPHALA (# 2 OF 2 PARTS).

2:30 (44) † **Kara Heilemann**, Janine N. Caira. A CLASH OF CLADES: CONFLICT IN PHYLOGENETIC SIGNAL BETWEEN SCOLEX MORPHOLOGY AND PROGLOTTID ANATOMY.

2:45 (45) **Christina Anaya**, Kurt E. Galbreath, Matthew G. Bolek. MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION OF ADULT HAIRWORMS (PHYLUM NEMATOMORPHA) FROM ICELAND AND THE FAROE ISLANDS AND DOCUMENTATION OF THEIR NON-ADULT STAGES AND HOSTS.

1:15–3:00 pm Host-Parasite Interactions III

Location: Stables II (Cavalry Ct)

Presiding: **Chen-Hua Li,** University of Calgary

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

1:15 (46) Olwyn C. Friesen, Chen-Hua Li, Ellen M. E. Sykes, Jake M. Stout, Harold M. Aukema, Ayush Kumar, **Jillian T. Detwiler**. CHEMICAL CUES DRIVE DENSITY DEPENDENT PROPHYLAXIS IN FRESHWATER SNAILS.

1:30 (47) **Adebayo J. Molehin**, Sean A. Gray, Darrick Carter, Afzal A. Siddqui. PROCESS DEVELOPMENT OF SJ-P80: A LOW-COST TRANSMISSION-BLOCKING VETERINARY VACCINE FOR ASIATIC SCHISTOSOMIASIS.

1:45 (48) † **Deblina Misra**, Maria G. Castillo. MODULATION OF THIOESTER-CONTAINING PROTEINS (TEPS) UPON IMMUNE STRESS IN THE *BIOMPHALARIA GLABRATA* EMBRYONIC (BGE) CELL LINE.

2:00 (49) † **Dayani Buddhika Maheshini Patuwatha Withanage**, Lien Luong. HOST PREFERENCE OF *PHASMARHABDITIS CALIFORNICA* ON THREE PEST SLUG SPECIES.

2:15 (50) † **Kelsey L. Froelich**, Brooke McPhail, Ronald L. Reimink, Sydney P. Rudko, Patrick C. Hanington. MINIMAL DEFINITIVE HOST PRESENCE IS SUFFICIENT TO SUSTAIN AVIAN SCHISTOSOME POPULATIONS.

2:30 (51) † **Adriana M. Perrucci**, Kristin K Herrmann, Charles R Randklev. PARASITE COMMUNITIES OF FRESHWATER MUSSELS OF TEXAS.

2:45 (52) † **Anai Novoa**, Ryan F. Hechinger. LATITUDINAL GRADIENTS IN PARASITE DIVERSITY OF THE STRIPED SHORE CRAB, *PACHYGRAPSUS CRASSIPES*, THROUGHOUT ITS TWO COASTAL HABITATS.

3:00–3:30 pm COFFEE BREAK The George Library/Lobby

3:00–6:00 pm Auction Set Up

Location: Statesman Ballroom (The George)

3:30–5:30 pm ASP Students' Symposium

Location: Stables Ballroom (Cavalry Ct)

Presiding: **Kayleigh Chalkowski,** Auburn University

Theme: "Communicating Complexity: Integrating Art, Story, and Parasitology."

3:30 **Kayleigh Chalkowski**. Introduction.

Time (Abstract No.)

3:40 (53) **Caroline Hu**. TELLING SCIENCE STORIES THROUGH COMICS.

3:55 (54) **Mona Luo**. AESTHETICS AND ABSTRACTION IN MAKING PARASITE ART.

4:10 (55) **Kelly Weinersmith**. FINDING A NICHE: HOW SYMBIOSIS HELPED ME FIND MY PLACE IN THE WORLD OF SCIENCE COMMUNICATION (SCICOM).

4:25 Panel Discussion

5:25 Questions. Closing Remarks.

5:30–6:30 pm ***Social for ASP Students***

Location: The George Lobby

Sunday Evening, July 10, 2022

6:00–7:00 pm ***Auction Preview***

Location: Statesman Ballroom (The George)

7:00–9:00 pm ***31st Annual ASP Student Auction***

Location: Statesman Ballroom (The George)

Monday Morning, July 11, 2022

7:00–11:00 am ***Registration***

Location: The George Lobby

8:15–10:30 am ***Arthropods & their Pathogens Symposium***

Location: Statesman Ballroom (The George)

Presiding: **Julián Hillyer**, Vanderbilt University

Presiding: **Jose Pietri**, University of South Dakota

8:15 **Julián Hillyer**. Introduction.

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

8:20 (56) **Jose Enrique Pietri**, Rashaun Potts, Jamie Scholl, Lee Baugh. A COMPARATIVE STUDY OF BODY LICE AND BED BUGS REVEALS FACTORS POTENTIALLY INVOLVED IN DIFFERENTIAL VECTOR COMPETENCE FOR THE RELAPSING FEVER SPIROCHETE *BORRELIA RECURRENTIS*.

8:35 (57) † **Caroline Liang**, Lien Luong. PARASITIC MITES INDUCE NON-CONSUMPTIVE EFFECTS IN CACTOPHILIC FLIES.

8:50 (58) **Ryne Maness**, Clark Hall, Josh Gibson, Lisa Brown. SYNTHESIS OF REACTIVE OXYGEN SPECIES PROVIDES PROTECTION TO BACTERIAL INFECTION IN THE GUT OF CAT FLEAS (*CTENOCEPHALIDES FELIS*).

9:05 (59) † **Cole J. Meier**, Julián F. Hillyer. EFFECTS OF PHOTOSENSITIVE INSECTICIDES (PSIS) ON LIFE HISTORY TRAITS AND POPULATION SURVIVAL OF *ANOPHELES GAMBIAE* MOSQUITOES.

9:20 (60) † **Brenda Leal-Galvan**, Cristina Harvey, Donald B. Thomas, Perot Saelao, Adela Oliva Chavez. THE miRNA PROFILES OF A SPECIALIST, *RHIPICEPHALUS* (*BOOPHILUS*) *MICROPLUS*, AND GENERALIST, *IXODES SCAPULARIS*, TICK DURING FEEDING.

9:35 (61) **Julián F. Hillyer**, Yan Yan, Abinaya Ramakrishnan, Tania Y. Estevez-Lao. TRANSGLUTAMINASE-BASED MODULATION OF THE PHYSIOLOGICAL INTERACTION BETWEEN THE IMMUNE AND CIRCULATORY SYSTEMS OF MOSQUITOES.

9:50 (62) † **Chen-Hua Li**, Cameron P. Goater, James D. Wasmuth. PATTERNS OF GENE EXPRESSION IN WOOD ANTS INFECTED WITH LARVAE OF THE ICONIC MANIPULATOR *DICROCOELIUM DENDRITICUM*.

10:05 (63) **Staci Dreyer**, Jefferson Vaughan, Todd Molden, Marc Bauer, David Smith. IVERMECTIN FORMULATION AND BODY LOCATION AFFECT *ANOPHELES STEPHENSI* FEEDING RATE, SURVIVAL, AND REPRODUCTION WHEN FED ON TREATED CATTLE.

10:20 Questions. Closing Remarks.

9:30–10:30 am Ecology & Evolution IV

Location: Stables I (Cavalry Ct)

Presiding: **Joanna Cielocha,** Rockhurst University

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

9:30 (64) **Jasmine D. Hamilton**, Gilberto Flores, Cheryl Courtney-Hogue. CHARACTERIZATION OF FLATFISH GUT MICROBIAL COMMUNITIES, PARASITIC INFECTION LEVELS, AND HEALTH INDICES ACROSS A GRADIENT OF WASTEWATER EFFLUENT EXPOSURE IN SANTA MONICA BAY.

9:45 (65) **Victor M. Vidal-Martínez**, Frank A. Ocaña, Lilia C. Soler-Jiménez, Leopoldina Aguirre-Macedo. TAXONOMIC AND TRAIT-BASED APPROACHES IN THE ASSESSMENT OF FLOUNDER METAZOAN PARASITE COMMUNITIES AS INDICATORS OF CHEMICAL POLLUTION IN THE GULF OF MEXICO.

10:00 (66) † **Wesley J. Neely**, Gui Becker. HABITAT FRAGMENTATION INFLUENCES AMPHIBIAN SKIN MICROBIOME COMPOSITION, HELMINTH PARASITISM, AND DISEASE STATUS IN THE BRAZILIAN ATLANTIC FOREST.

10:15 (67) † **Ryan M. Weesner**, Gary Voelker. AVIAN HOSTS AND LANDSCAPE DRIVE PARASITE PREVALENCE IN THE CAUCASUS MOUNTAINS.

10:30–11:00 am **COFFEE BREAK** **The George Library/Lobby**

11:00 am–Noon ***ASP President's Address***

Location: Statesman Ballroom (The George)

Presiding: **Reginald Blaylock,** The University of Southern Mississippi

11:00 **John Janovy Jr.** Introduction of Matthew Bolek.

11:10 **Matthew Bolek. "**Parasites in the Driver's Seat: Understanding Parasite Natural History When the Parasites Lead Us in Asking the Questions."

Dr. Matthew Bolek. President of ASP.

Monday Afternoon, July 11, 2022

Noon–3:00 pm ***Poster and Palettes & Parasites Set Up***

Location: Statesman Ballroom (The George)

1:00–2:00 pm ***Genomics & Molecular Biology***

Location: Stables I (Cavalry Ct)

Presiding: **Winka Le Clec'h,** Texas Biomedical Research Institute

Time (Abstract No.)

1:00 (68) **Gabriel Mouahid**, Frédéric D. Chevalier, Salem Al Yafae, Mohamed A. Idris, Juliette Langand, Marina McDew-White, Grace-Ann Arya, Timothy J. C. Anderson, Hélène Moné. GENETIC MAPPING OF AN ADAPTIVE PARASITE TRAIT: LARVAL RELEASE TIME IN SCHISTOSOMES.

1:15 (69) **Egie E. Enabulele,** Emma K. Roberts, Winka Le Clec'h, Robert Bradley, Timothy Anderson, Roy N. Platt II. PROSPECTING FOR ZOONOTIC PATHOGENS IN MUSEUM SPECIMENS USING TARGETED DNA ENRICHMENT

1:30 (70) **Nicolas J. Wheeler**, Lenny R. Nunn, Paul M. Airs, Lyric C. Bartholomay, Mostafa Zamanian. MAKING SENSE OF SENSORY BEHAVIORS IN VECTOR-BORNE HELMINTHS.

1:45 (71) **Maureen A. Kelly**, Caroline Sobotyk, Neha Tyagi, Matthew Kulpa, Nancy McLean, Guilherme G. Verocai. PRELIMINARY VALIDATION OF A PROBE-BASED QPCR FOR DETECTION OF ZOONOTIC *ONCHOCERCA LUPI* IN CLINICAL SAMPLES OF COMPANION ANIMALS.

1:00–2:00 pm Life Cycles & Epidemiology I

Location: Stables II (Cavalry Ct)

Presiding: **Judith Humphries,** Lawrence University

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

1:00 (72) **Stacie D. Williams**, Lauren Wisnieski, Karen Gruszynski, Vina Faulkner, Charles Faulkner. A SURVEY OF PET CARETAKERS ON THE USE AND PERCEPTIONS REGARDING HEARTWORM PROPHYLAXIS FOR PREVENTION OF CANINE HEARTWORM DISEASE.

1:15 (73) **Ashley E. Steuer**, Michael Cruz-Penn, Jason Fritzler. TEXAS PANHANDLE COYOTES: A SURVEY OF PARASITES, WITH A FOCUS ON THOSE OF ZOONOTIC IMPORTANCE.

1:30 (74) † **Justin D. Krol**, Jennifer M. Hill, Peter R. Kingsley Smith, Elizabeth L. Gooding, Michael R. Kendrick, Corinne Fuchs, Stephen A. Bullard. SURVEY OF INVASIVE WILD-CAUGHT ASIAN TIGER PRAWN, *PENAEUS MONODON* (FABRICIUS, 1798) FROM THE GULF OF MEXICO AND NORTHWESTERN ATLANTIC OCEAN FOR WSSV (WHITE SPOT SYNDROME VIRUS), IHHNV (INFECTIOUS HYPODERMAL AND HEMATOPOIETIC NECROSIS VIRUS), AND TAURA SYNDROME VIRUS (TSV).

1:45 (75) † **Ian Daniel**, SaraBeth Boggan, Ashley Steuer, Jason Fritzler. DON'T MESS WITH TEXAS TICKS: TICKS AND THEIR PATHOGENS IN THE TEXAS PANHANDLE.

2:00–3:00 pm Vector Biology

Location: Stables I (Cavalry Ct)

Presiding: **Jose Pietri,** University of South Dakota

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

2:00 (76) † **Nicole A. Scavo**, Italo B. Zecca, Caroline Sobotyk de Oliveira, Meriam N. Saleh, Sarah K. Jeffreys, Mark Olson, Sarah A. Hamer, Guilherme Gomes Verocai, Gabriel L. Hamer. HIGH PREVALENCE OF CANINE HEARTWORM, *DIROFILARIA IMMITIS*, IN DOGS FROM LOW- AND MIDDLE-INCOME COMMUNITIES IN SOUTH TEXAS, U.S.A., WITH EVIDENCE OF *AEDES AEGYPTI* MOSQUITOES CONTRIBUTING TO TRANSMISSION.

2:15 (77) † **Rachel E. Busselman**, Alyssa C. Meyers, Italo B. Zecca, Andres H. Castro, Carolyn L. Hodo, Devin Christopher, Rachel Curtis-Robles, Ashley B. Saunders, Sarah A. Hamer. TRIATOMINES IN KENNEL ENVIRONMENTS: COLLECTIONS BY A TRAINED DOG, INFECTION WITH *TRYPANOSOMA CRUZI*, AND BLOOD FEEDING HOSTS.

2:30 (78) **Juan Pablo Fimbres-Macias**, Trevor Harris, Sarah A. Hamer, Gabriel L. Hamer. PHENOLOGY AND ENVIRONMENTAL PREDICTORS OF DISPERSAL ACTIVITY OF ADULT *TRIATOMA SANGUISUGA* – VECTOR OF THE CHAGAS PARASITE - IN CENTRAL TEXAS.

2:45 (79) **Stephanie C. Nordmeyer**, Timothy J. C. Anderson, Frédéric D. Chevalier, Winka Le Clec'h. THE IMPACT OF SCHISTOSOME INFECTION ON *BIOMPHALARIA GLABRATA* HOST SNAIL MICROBIOME.

2:00–3:00 pm Life Cycles & Epidemiology II

Location: Stables II (Cavalry Ct)

Presiding: **Ryan Hechinger,** University of California

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

2:00 (80) † **Ryan W. Koch**, Matthew G. Bolek. PICKY SNAIL HOSTS AND RESISTANT PARASITES: HOST SPECIFICITY OF ACANTHOCEPHALANS IN OSTRACOD AND SNAIL HOSTS.

2:15 (81) Julia Legiec, **Gabriel J. Langford**. DOES AN ORAL ROUTE OF INFECTION EXIST FOR *CYRTOSOMUM PENNERI* (NEMATODA: ATRACTIDAE) IN FLORIDA LIZARDS?

2:30 (82) † **Alexandria P. Nelson**, Daniel C. G. Metz, Ryan F. Hechinger. DESCRIPTION, REDESCRIPTION, AND LIFE CYCLES OF FOUR PHILOPHTHALMIDS (TREMATODA: DIGENEA) FROM THE CALIFORNIA HORN SNAIL, *CERITHIDEOPSIS CALIFORNICA* (GASTROPODA: POTAMIDIDAE).

2:45 (83) **Aura Kristina Valdez Flores**, Aimee Camacho Abdul. PREVALENCE OF SOIL-TRANSMITTED HELMINTH INFECTIONS AMONG CHILDREN IN SELECTED BARANGAYS OF KORONADAL CITY.

3:30–5:30 pm Poster Session, 2nd Annual Palettes & Parasites Contest

Location: Statesman Ballroom (The George)

(Abstract No.)

CELL BIOLOGY

84 **Jonathan E. Zirkiev**, Jyoti Pant, Jayne Raper. USING HEPG2 CELLS AS A HEPATOCYTE MODEL TO STUDY APOL1 SECRETION ONTO TLF COMPLEXES.

ECOLOGY & EVOLUTION

85 **Mary J. Janecka**, Rachael Kramp, David R. Clark, Ryan S. Mohammed, Mateusz Konczal, Jessica F. Stephenson. HOST COMMUNITY DIVERSITY AND PARASITE HOST RANGE HELP SHAPE PARASITE GENE FLOW IN COMPLEX RIVERS.

86 **Corinne L. Conlon**, Krysten L. Schuler, Christopher M. Whipps. SURVEILLANCE FOR *ECHINOCOCCUS MULTILOCULARIS*, AN EMERGING ZOONOTIC PARASITE IN WILD CANIDS IN NEW YORK STATE.

87 **Chelsea S. Thorn**, Autumn J. Smith-Herron, Tamara J. Cook. ENDOHELMINTH PARASITES OF ALLIGATOR GAR (*ATRACTOSTEUS SPATULA*) AND SPOTTED GAR (*LEPISOSTEUS OCULATUS*) FROM SABINE LAKE.

88 **Nicholas FitzGerald**, John Shea. UTILIZING INSECT DIVERSITY AND HORSEHAIR WORM PRESENCE TO MEASURE AN ECOSYSTEM'S HEALTH.

GENOMICS & MOLECULAR BIOLOGY

89 Joseph Spear, Isuru Gunarathna, **Tamar Carter**. PHYLOGEOGRAPHIC ANALYSIS OF *PLASMODIUM VIVAX* AND *P. FALCIPARUM* P47, P48/45, AND PIMMS43 AS MARKERS FOR PARASITE-VECTOR COMPATIBILITY IN INVASIVE MOSQUITO VECTOR SETTINGS.

HOST-PARASITE INTERACTIONS

90 **Maria Hendrickson**, Tamara Cook, Diane Neudorf. HELMINTH PARASITES AND BODY CONDITION IN BROWN-HEADED COWBIRDS (*MOLOTHRUS ATER ATER*).

91 **Jackson R. Snyder**, Ben Engle. ALTERATION OF BEHAVIOR IN AQUATIC SNAILS DUE TO LARVAL INFECTIONS OF *PARAGORDIUS VARIUS*.

92 **Ma. Leopoldina Aguirre-Macedo**, Linda Y. Marmolejo-Guzmán, Victor M. Vidal-Martínez. TEMPORAL DYNAMIC OF THE *OCTOPUS MAYA* PARASITE-FAUNA FROM CAMPECHE AND YUCATAN, MEXICO.

93 **James Pfaff**, Briahna Teaque, Ben Paul, Jake Strehlow, John Shea. *CHORDODES MORGANI* EFFECT ON HOST GROWTH AND ITS DEVELOPMENT TIME IN DIFFERING DIET AND TEMPERATURE CONDITIONS.

94 **Madeline N. Arszulowicz**, Robert C. Dowler, Nicholas J. Negovetich. PARASITES OF SPOTTED SKUNKS (*SPILOGALE* SP.) IN THE EASTERN AND CENTRAL UNITED STATES.

95 **Matthew G. Bolek**, Ryan W. Koch, Ryan P. Shannon, Allison Bryant, Kyle Gustafson, Heather Stigge, Christina Anaya. BIODIVERSITY OF PARASITES IN FRESHWATER SNAILS: HOW COMMON ARE NON-TREMATODE PARASITES IN FRESHWATER SNAILS?

96 **Adriana Perrucci**, Kristin K. Herrmann, Charles R. Randklev. THE EFFECT OF TREMATODE PARTHENITAE INFECTION ON THE REPRODUCTION AND MORTALITY OF FRESHWATER MUSSELS OF TEXAS.

97 **Daniel P. Lopes**, Bernardo Gonzalez-Baradat, Russell Thomson, Jayne Raper. CHARACTERIZATION OF TBCATL RECOMBINANT PROTEIN IN A CHO-S MAMMALIAN MODEL.

98 **Diane Roselyn Anderson-Aidoo**, Jeremy Sternberg. *IN VITRO* MODELS OF MACROPHAGE ACTIVATION IN *TRYPANOSOMA BRUCEI* INFECTION.

99 **Sophio Kirimlishvili**, Sara Fresard, Jayne Raper. UNDERSTANDING THE MECHANISM OF LYSING *TRYPANOSOMA BRUCEI* BY TLF AS FOLLOWED BY THE RELEASE OF THE VARIANT SURFACE GLYCOPROTEIN COAT.

LIFE CYCLES & EPIDEMIOLOGY

100 **Alex Gutierrez**, Jocelyn Munoz, Tamara J. Cook. THE SITE SPECIFICITY OF *BLABERICOLA HAASI* AND *PROTOMAGALHAENSIA WOLFI* (APICOMPLEXA: EUGREGARINIDA: BLABERICOLIDAE) PARASITIZING THE SPECKLED COCKROACH *NAUPHOETA CINEREA* (DICTYOPTERA: BLATTARIA: BLABERIDAE).

101 **Chris A. Hall**, Lilyann Jenkins, Madeline Phillips, Beth Falls, Hannah Atsma. MONITORING OF *TOXOPLASMA GONDII* IN MARINE SPECIES FROM THE INDIAN RIVER LAGOON, FLORIDA.

102 **Gul Ahmad**, Tyra Mollhoff. PREVALENCE OF *TOXOPLASMA GONDII* AMONG CAT POPULATIONS IN SOUTHEAST NEBRASKA.

103 **Daisy Porter**, Stephanie Bankong, Cameron Gonzalez, Makenzie Love, Tamara J. Cook. INFECTION PATTERNS OF TWO SPECIES OF EUGREGARINES (APICOMPLEXA: *EUGREGARINIDA: BLABERICOLIDAE*) PARASITIZING THE SPECKLED COCKROACH *NAUPHOETA CINEREA* (DICTYOPTERA: BLATTARIA: BLABERIDAE).

TAXONOMY, SYSTEMATICS, & PHYLOGENY

104 **Logan S. Elkin**, Jay Bowerman, Mike L. Kent, Anindo Choudhury. MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION OF *CREPIDOSTOMUM* SP. (TREMATODA: ALLOCREADIIDAE) FROM THE MOUNTAIN WHITEFISH (*PROSOPIUM WILLIAMSONI*) IN OREGON.

105 **Anindo Choudhury**, Carson Torhorst, Gerardo Pérez-Ponce de León. PARASITES OF HEPTAPTERID CATFISHES IN STREAMS OF SOBERANIA NATIONAL PARK, CHAGRES RIVER DRAINAGE, PANAMA.

106 **Emily Bulmer**, Morgan Fleming, Florian Reyda. A NEW SPECIES OF *NEOECHINORHYNCHUS* (ACANTHOCEPHALA) FROM TWO SPECIES OF REDHORSE (CATOSTOMIDAE: *MOXOSTOMA ERYTHRURUM* AND *MOXOSTOMA MACROLEPIDOTUM*) IN NORTH AMERICA.

107 **Lauren B. Morton**, Tyler J. Achatz, Jakson R. Martens, Vasyl V. Tkach. RE-EVALUATION OF THE DIVERSITY OF *PSILOCHASMUS LÜHE*, 1909 (DIGENEA: PSILOSTOMIDAE) AND DESCRIPTIONS OF TWO NEW SPECIES FROM EUROPE AND NORTH AMERICA.

108 **Robert C. Jadin**, Sean King, Conrad R. Gausmann, Jason Leon, Sarah A. Orlofske. PARASITES LOST (AND FOUND): FILLING IN GAPS OF PARASITE DISTRIBUTIONS WITH NEWLY DIGITIZED COLLECTIONS.

109 **Gustavo A. Mendez**, Florian B. Reyda. A NEW SPECIES OF NEOECHINORHYNCHUS (ACANTHOCEPHALA) FROM WHITE SUCKER (CATOSTOMIDAE: CATOSTOMUS COMERSONII) FROM ONEIDA LAKE, NEW YORK.

110 **Jorge H. Medina-Duran**, Jordan Moore, Hojun Song. TOWARDS THE UNDERSTANDING OF GREGARINE DIVERSITY: DEVELOPMENT OF SINGLE-CELL WHOLE-GENOME SEQUENCING AND 18S BARCODING APPROACHES TO INFORM THE PHYLOGENY AND SYSTEMATICS OF GREGARINES (APICOMPLEXA) IN INSECTS.

VECTOR BIOLOGY

111 **Vina Faulkner**, Barbara C. Shock. IDENTIFICATION OF IXODID TICKS OF THE CUMBERLAND GAP REGION OF APPALACHIA (2016-2020).

112 **Jessica Eck**, Megan R. Wise de Valdez. DISTRIBUTION OF *DIROFILARIA IMMITIS* VECTORS AMONG NEIGHBORHOODS OF DIFFERENT SOCIO-ECOLOGICAL STATUS.

Tuesday Morning, July 12, 2022

8:15–9:30 am Parasites and Pedagogy Symposium

Location: Statesman Ballroom (The George)

Presiding: **Christina Anaya,** Florida Gulf Coast University

8:15 **Christina Anaya**. Introduction.

Time (Abstract No.)

8:20 (113) **Sarah A. Orlofske**, Robert C. Jadin, Kimberly M. Bates. IMPLEMENTING COURSE-BASED UNDERGRADUATE RESEARCH EXPERIENCES OF WATERFOWL PARASITOLOGY ACROSS THE CURRICULUM.

8:35 (114) **Christina Anaya**. INTEGRATING BOOK CLUB INTO PARASITOLOGY COURSES TO PROMOTE ACTIVE STUDENT LEARNING.

8:50 (115) Jeffrey Bell, James P. Bernot, Christopher Blanar, Nicole Chodkowski, Maggie Doolin, Makedonka Mitreva, Sarah Orlofske, J. Trevor Vannatta, **Elliot Zieman**. SHOWCASING EDUCATIONAL RESOURCES IN PARASITOLOGY.

9:05 (116) **Elliot Zieman**, J. Trevor Vannatta, Sarah Orlofske, Makedonka Mitreva, Maggie Doolin, Nicole Chodkowski, Christopher Blanar, James Bernot, Jeffrey Bell. BUILDING AN EDUCATIONAL NETWORK FOR SHARING RESOURCES IN ASP.

9:20 Questions. Closing Remarks.

8:30–9:30 am Taxonomy, Systematics, Phylogeny IV

Location: Stables I (Cavalry Ct)

Presiding: **Florian Reyda,** SUNY Oneonto

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

8:30 (117) † **Triet N. Truong**. DESCRIPTION OF A NEW SPECIES OF *PLAGIOPORUS* (DIGENEA: OPECOELIDAE) INFECTING THE INTESTINE OF TWO CATOSTOMIDS FROM THE EASTERN USA, INCLUDING AN EMENDED DIAGNOSIS, KEY TO NEARCTIC CONGENERS, AND PHYLOGENETIC ANALYSIS.

8:45 (118) **Tim Ruhnke**, Florian Reyda, Hannah Hudson. EVEN MORE SPECIES DIVERSITY IN THE GENUS *STILLABOTHRIUM*.

9:00 (119) † **Jessica C. Paul**, Janine N. Caira. UNDERAPPRECIATED DIVERSITY AND COMPLEXITY IN POTENTIALLY NOVEL ORDER OF CESTODES.

9:15 (120) **Janine N. Caira**, Kirsten Jensen, Elizabeth Jockusch, Jill L. Wegrzyn. CHAOS OUT OF ORDERS: IT'S JUSTIFIED!

8:30–9:30 am Host-Parasite Interactions IV

Location: Stables II (Cavalry Ct)

Presiding: **Ben Hanelt,** University of New Mexico

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

8:30 (121) † **Marisa Fonseca**, Gabriel Langford. INVASIVE PARASITES: A SURVEY OF ENDOPARASITES IN SALVATORMERIANAE POPULATIONS IN FLORIDA.

8:45 (122) **Ashley E. Steuer**, Kristin Scoggin, Alan T. Scoggin, Martin K. Nielsen. CYATHOSTOMINS AND MUCUS: EVALUATION OF THE HOST HISTOPATHOLOGIC CHANGES IN NATURALLY ACQUIRED INFECTIONS.

9:00 (123) **Kaylee R. Kipp**, Joe Luksovsky, Guilherme G. Verocai. RETROSPECTIVE EVALUATION OF GASTROINTESTINAL NEMATODES IN COMMERCIAL NORTH AMERICAN BISON HERDS. 2017-2021 AT THE TEXAS A&M UNIVERSITY PARASITOLOGY DIAGNOSTIC LABORATORY.

9:15 (124) **Sara B. Boggan,** Ethan Carpenter, Kristin K. Herrmann, Donald Beard, Guilherme G. Verocai, Heather A. Mathewson. INTESTINAL PARASITES OF JUVENILE AND ADULT FEMALE BISON OF THE TEXAS STATE HERD.

9:30–10:00 am COFFEE BREAK The George Library/Lobby

10:00–11:00 am Ecology & Evolution V

Location: Statesman Ballroom (The George)

Presiding: **Stephen Bullard,** Auburn University

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

10:00 (125) † **Heather R. Skeen,** Greg Dwyer, John Novembre. PERIODICITY AND DENSITY-DEPENDENT DYNAMICS OF MIGRATORY BIRD PATHOGENS.

10:15 (126) † **Jennifer A. Talbert,** Andy W. Jones, Autumn J. Smith-Herron, Kristin K. Herrmann. HELMINTH PARASITES IN MIGRATORY BIRD HOSTS OF THE FAMILY TURDIDAE

10:30 (127) † **Ethan S. Carpenter,** Sara B. Boggan, Heather Mathewson, Kristin K. Herrmann, Donald Beard, Guilherme G. Verocai. THE EFFECTS OF SEASONAL RAINFALL ON PARASITISM IN BISON.

10:45 (128) Ashley J. Pidwerbesky, Charlene N. Berkvens, Trent K. Bollinger, **Jillian T. Detwiler**. NON-INVASIVE SAMPLING REVEALED NOT ONE, BUT TWO PROTOSTRONGYLID PARASITES IN WHITE-TAILED DEER (*ODOCOILEUS VIRGINIANUS*) IN WESTERN MANITOBA.

10:00–11:15 am Taxonomy, Systematics, & Phylogeny V

Location: Stables I (Cavalry Ct)

Presiding: **Veronica Bueno,** University of Connecticut

Time (Abstract No.)
† denotes student presentation in the Best Student Presentation Competition

10:00 (129) † **Matthew R. Kulpa**, Guilherme G. Verocai. MULTI-LOCUS PHYLOGENETIC RELATIONSHIPS AMONG *ONCHOCERCA* ISOLATES FROM NEW YORK AND CALIFORNIAN UNGULATES.

10:15 (130) † **Hannah A. Danks**, Caroline Sobotyk, Meriam N. Saleh, Matthew Kulpa, Joe L. Luksovsky, Lee C. Jones, Guilherme G. Verocai. OPENING A CAN OF (LUNG)WORMS: MOLECULAR CHARACTERIZATION OF *DICTYOCAULUS* (NEMATODA; DICTYOCAULIDAE) INFECTING NORTH AMERICAN BISON (*BISON BISON*).

10:30 (131) **Richard E. Clopton**, Debra T. Clopton. THE EMERGING VIEW OF GREGARINE PHYLOGENY.

10:45 (132) † **Allison Bryant**, Matthew Bolek, Gabriel Langford. HIDING IN PLAIN SIGHT: WHAT CAN ENDOGENOUS DEVELOPMENT TELL US ABOUT COCCIDIAN DIVERSITY OF *ACROEIMERIA LINERI* AND OTHER COCCIDIANS FROM INTRODUCED POPULATIONS OF THE MEDITERRANEAN HOUSE GECKO, *HEMIDACTYLUS TURCICUS* AND THE TROPICAL HOUSE GECKO, *H. MABOUIA*?

11:00 (133) **Veronica M. Bueno**, Janine N. Caira. THE DISMANTLING OF THE "TETRAPHYLLIDEA'' SAGA: PROGLOTTIDS TO THE RESCUE!

10:00–10:30 am *Chemotherapy & Drug Resistance*

Location: Stables II (Cavalry Ct)

Presiding: **Nicolas Wheeler,** University of Wisconsin

Time (Abstract No.)

10:00 (134) **Winka M. Le Clec'h**, Frédéric D. Chevalier, Robbie Diaz, Amanda Strickland, Madison Morales, Timothy J. C. Anderson. MEASURING VARIATION IN DRUG RESPONSE IN SCHISTOSOME POPULATION USING THE SINGLE WORM ANALYSIS MOVEMENT PIPELINE (SWAMP).

10:15 (135) Sevan N. Alwan, Alexander B. Taylor, Stanton F. McHardy, **Philip T. LoVerde**. NOVEL THERAPEUTICS AGAINST HUMAN SCHISTOSOMIASIS.

Tuesday Afternoon, July 12, 2022

1:00–2:00 pm H. B. Ward Medal Lecture

Location: Statesman Ballroom (The George)

Presiding: **Sara Brant,** University of New Mexico

1:00 **Sam Loker.** Introduction of the 2022 H. B. Ward Medal Recipient

1:10 **Patrick C. Hanington.** "A bifurcated tale of schistosomes and snails."

Dr. Patrick C. Hanington. Recipient of the 2022 H. B. Ward Medal.

2:15–4:15 pm ***ASP Awards & Business Meeting***

Location: Statesman Ballroom (The George)

ASP AWARDS:

CLARK P. READ MENTOR AWARD LECTURE

Presiding: **Sara Brant,** University of New Mexico

2:15 **Joanna Cielocha**. Introduction of the 2022 Clark P. Read Mentor Award recipient

2:25 **Richard Clopton.** "Mentoring by Design."

Dr. Richard Clopton. Recipient of the 2022 Clark P. Read Mentor Award.

ASHTON CUCKLER NEW INVESTIGATOR AWARD

Presiding: **Sara Brant,** University of New Mexico

Dr. Tyler Achatz. Recipient of the 2022 New Investigator Award.

BEST STUDENT PRESENTATIONS AND MARC DRESDEN TRAVEL GRANT AWARDS

Presiding: **Debra Clopton**, Peru State College

ASP BUSINESS MEETING

Presiding: **Matt Bolek**, Oklahoma State University

Thank you for participating and making this another successful ASP meeting.

See you all next year July 13th – 16th in Kansas City!

Abstract Listings

1

Testing an assumption and prediction of the mating system model for complex life cycle evolution in the trematode *Alloglossidium renale.*

Jenna M. Hulke, Charles D. Criscione
Texas A&M University, College Station, TX, USA

Three-host life cycles have evolved among the digenetic trematodes, but subsequently several species in these lineages have evolved precociousness where they sexually mature in their second intermediate host. The question has been raised as to why precociousness is not more common given studies have found few constraints to truncating the third host from a life cycle. The mating system model of Brown et al (2001) argues that complex life cycles preclude inbreeding and thus, its costs (i.e., inbreeding depression) by concentrating potential mating partners. The model assumes a shorter life cycle results in inbreeding and predicts a shorter life cycle can only evolve if there is no inbreeding depression. We tested this assumption and prediction in the hermaphroditic trematode *Alloglossidium renale*, which has an obligate 2-host life-cycle with sexual reproduction occurring within the paired antennal glands of grass shrimp. We evaluated the mating system of *A. renale* from 3 different populations (Louisiana, Texas, and Mississippi) with a temporal replication in Mississippi (2014 and 2018). Using genetic estimates based on deviations from Hardy-Weinberg equilibrium (quantified via F_{IS}) and identity disequilibrium, all population samples had high levels of inbreeding. Assessing inbreeding depression is difficult in many parasite systems. Here, we provide a novel approach by estimating a lower-bound selfing rate using infection intensities. If this demographic estimate exceeds the genetic estimate of inbreeding, there would be evidence of inbreeding depression. The genetic estimates were on par or greater than levels of inbreeding based on the demographics of infections. Hence, we found no evidence of inbreeding depression from field-based data. Even though multiple *A. renale* may infect the same host, the high levels of inbreeding may be facilitated by the fact it infects a discrete paired organ (i.e., individuals in one gland cannot mate with individuals in the other gland). The lack of inbreeding depression in this precocious species also fits the prediction of the mating system model. Other work has suggested inbreeding depression may be manifested over generations. However, both temporal and spatial data indicate that high inbreeding with a lack of inbreeding depression is a common biological feature of *A. renale*.

2

Nascent linkages between parasite transmission, parasite mating systems, and clonemate abundance distributions in trematodes.

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Emergent properties of transmission (infection intensity and relatedness of co-infecting parasites) can affect the evolutionary mechanism of inbreeding in parasites, especially among self-compatible hermaphroditic endoparasites whose mating opportunities are restricted to within-hosts. Prior work by Criscione and colleagues has shown how the proportion of sibling parasite dyads (P_S) within hosts provides an eco-evolutionary link between parasite transmission and mating systems. As trematodes have the interesting feature of an asexual developmental stage that can produce genetically identical individuals (clonemates), we extend this approach to compare clonemate abundance distributions (CAD) in trematodes by using the proportion of clonemate dyads (P_C) within hosts. Previous CAD studies were innovative in comparing clone richness (number of clones) across life cycle stages in order to infer transmission processes. Nonetheless, P_C has several advantages as an ecological metric in that it is

unbiased by sample size, takes into account relative abundances, and has a direct transmission interpretation, i.e., the probability of co-transmitting clonemates. Moreover, we show an additional utility of P_C as an evolutionary metric as it can be used to estimate a potential clonemate mating rate. Clonemate mating in hermaphroditic species produces a genetic inbreeding signature identical to that of self-mating. We demonstrate the use of P_C in comparing CADs within and across two trematode developmental stages. Also, we show how genetic estimates of selfing at larval/juvenile stages can be compared to P_C estimated at the adult stage to assess the contribution of clonemate mating to apparent selfing. The eco-evolutionary links presented are generalizable to any level of relatedness. Thus, the framework presented herein will facilitate future field-based studies on the transmission and mating systems of parasitic flatworms.

3

The effect of abundance transformations on Bray-Curtis NMDS estimation of patterns of parasite infra- and component community similarity.

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Nonmetric multidimensional scaling (NMDS) of Bray-Curtis (B-C) dissimilarities has been shown to produce robust estimations of patterns of community similarity. A known issue with the Bray-Curtis measure is a tendency to weight dissimilarities by the most abundant species in a sample. For this reason, abundances often are transformed to reflect unit maxima or, more commonly, square root transformed prior to the generation of B-C distances. Patterns of parasite infracommunities were simulated based on varying exposure of individuals to a relatively fixed parasite species pool to model changes in exposure probabilities in older/larger hosts. Patterns of parasite component communities were simulated by modifying set (regional) distributions of abundances based on community position in a 2-dimensional space defined by orthogonal gradients affecting the abundances of a portion of the species in a community. Additional component community simulations were conducted with differing regional pools of parasites based on position within the 2-dimensional space. Preliminary Procrustes comparisons of NMDS patterns of similarity generated from raw and transformed data indicate that while the unit-maximum transformation outperforms the square root transformation, the most robust NMDS estimation of patterns of community similarity were produced by B-C distances generated from untransformed abundances.

4

What drives parasite gene flow in riverine habitats? Interactions between stream drift, river bifurcations and host dispersal.

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River systems are characterized by their dendritic structure and unidirectional stream flow. The structural characteristics of river systems are known to influence the ecology and evolution of their inhabitants at multiple scales, from determining community composition to altering the genetic structure of their inhabitants. However, the effects of the potentially important generative riverscape processes on shaping parasite geneflow are largely unknown. We examined the effects of unidirectional stream drift, dendritic ecological networks, and host dispersal on the population structure of *Renifer aniarum*, which infects three species of water snakes in a bifurcating river network in west-central Texas. We collected parasites from 13 sampling sites distributed along 250 miles of the Colorado and Concho rivers. Parasites were genotyped at 11 microsatellite markers. To examine the effects of unidirectional stream drift on parasite genetic diversity, we tested for correlations between river

distance and expected heterozygosity and allelic richness. To examine the effects of dendritic ecological networks, we assessed parasite population structure and employed mantel tests for isolation by river distance along network pathways. There was no significant increase in expected heterozygosity with distance downstream, however allelic richness was positively correlated with downstream distance. We found significant pairwise F_{ST} values for populations located on distal network bifurcations and at collection site located below the reservoir at the confluence of the two river branches. Patterns of geographic clustering and significant isolation by distance were found associated only with the Upper Colorado River. However, the lower Colorado and Concho Rivers exhibited little to no population subdivision and no isolation by distance despite similar network lengths. Thus, dendritic branching along network pathways may constitute an important feature of river systems in determining parasite population structure even when host dispersal abilities are high.

5

Intramolluscan trematodes as closed populations: projection matrix models reveal infrapopulation dynamics and help resolve questions about trematode sociality.

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Trematodes typically form a colony inside their first intermediate host mollusc, consisting of many individual bodies (parthenitae) cooperatively exploiting a resource (the host). A classic problem in trematodology is that these colonies are difficult to observe over time, as the typical host is protected by an opaque shell and observing the parasites requires killing the host. However, a generally unappreciated fact—that colonies are analogous to closed populations of free-living individuals—gives us power to probe the intra-colony dynamics of these recalcitrant parasites. We show here that nearly any colony, parasitic or not, can be simply and easily represented by a projection matrix model. The simplicity of these models and their foundation in real biological processes – birth, growth, and death rates – allows us to explore colony dynamics and the developmental biology of otherwise difficult-to-observe colonial organisms. We use this power to analytically reveal the demographic processes that can lead to two separate size classes in trematode colonies, as this bimodality has been tentatively linked to the existence of a soldier caste. Using matrix models parameterized with empirical data, we show that a trematode colony will have a bimodal size frequency distribution if the parthenitae have 1) continual births and deaths ("turnover"), 2) density-dependent developmental arrest of immature worms, and 3) relatively rapid transition from immature to mature once growth is initiated. These demographic mechanisms leading to discrete size classes within a colony could arise for reasons other than selection of a soldier caste, emphasizing the need for continued work that directly quantifies defensive function to determine whether colonies exhibit division of labor. In those colonies with such social organization, our work reveals a route by which trematodes can adaptively increase or decrease the size of the soldier caste. Further, with vital rates known, this model allows us to estimate how rapidly colonies could plastically increase the size of their standing army in response to perceived threats.

6

A species of *Dendritobilharzia* (Digenea: Schistosomatidae) infecting the heart lumen of white-backed duck, *Thalassornis leuconotus* (Anseriformes: Anatidae) from Namibia: a first glimpse of avian schistosome diversity within the un-surveyed Naye-Naye Concession Area of southern Africa.

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The 4 species of bird schistosomes comprising *Dendritobilharzia* are morphologically unique by lacking a gynecophoral canal, having a flat, elongate-ovoid body, having none or a weakly muscular oral sucker, lacking a ventral sucker, and having diverticulate ceca. One congener, *D. pulervulenta*, the only congener represented by publicly-available nucleotide sequences, infects the arterial system of waterfowl. Phylogenetic analyses considering the large subunit (28S) recover *Dendritobilharzia* as a distinct lineage sister to the clade that includes other waterfowl schistosomes (*Marinabilharzia*, *Gigantobilharzia* (paraphyletic), *Riverbilharzia*, and several nucleotide-based, innominate lineages). Most species of *Dendritobilharzia* are little studied. Given the unique morphology and phylogenetic position of this lineage, information on new infection reports from little surveyed areas remains valuable. During a research expedition to north-eastern Namibia in 2021, we discovered adult male and female schistosomes of *Dendritobilharzia* sp. infecting the lumen of the heart of several white-backed ducks, *Thalassornis leuconotus* (Anseriformes: Anatidae). We herein describe the morphological features of these specimens, present a phylogenetic analysis for the genus, and highlight the ecologically unique region comprising the Nye-Nye Pans (a rain/drought extreme ecosystem never surveyed for parasites). The present study comprises the 1st species of *Dendritobilharzia* reported from the white-backed duck and the 1st adult specimen of a species of *Dendritobilharzia* from Namibia and southern Africa. These are the first nucleotide sequences of *Dendritobilharzia* sourced from a blood fluke infection in a wild-caught bird.

7

Morphological re-evaluation and phylogenetic analysis of the Renschetrematidae.

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Renschetrematidae is a very small family containing only 2 genera and 4 species of digeneans parasitic in bats in southern and Southeast Asia. According to the original descriptions and the latest revision, its representatives are characterized by the presence of several highly unusual characters. Among them are the dorsal position of the genital pores, separate male and female genital pores, and the presence of an accessory sac (stylet pouch) associated with terminal genitalia and containing a stylet-like structure. Prior to our study, the phylogenetic relationships of the Renschetrematidae were unknown and DNA sequence data were absent from any of its representatives. We have discovered and described a new species of Renschetrema from bats in the Philippines and explored the phylogenetic affinities of the Renschetrematidae using newly obtained partial sequences of the 28S rRNA gene from Renschetrema specimens collected in the Philippines and Southeast China. Detailed examination of our material as well as museum specimens revealed significant errors in the current diagnoses of the genus Renschetrema and the Renschetrematidae, which required amendments of the diagnoses. Our phylogenetic analysis supports the status of the Renschetrematidae as an independent family within the superfamily Microphallidea basal to the remaining taxa in the superfamily. This study was funded in part by the National Science Foundation (grant 1852459), the National Institutes of Health (IDeA grant number P20GM103442) and the UND College of Arts and Sciences undergraduate research scholarship.

8

A survey of the intestinal trematodes infecting two freshwater turtles from the Mekong River Basin, Vietnam, with first phylogenetic investigation of genus *Encyclobrephus*.

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We herein report the results of 2 parasitological surveys (2015, 2018) targeting the intestine of 2 freshwater turtle species (Mekong snail eating turtle [*Malayemys subtrijuga*] and yellow-headed temple turtle [*Heosemys annandalii*]) from the Mekong River Basin, Vietnam. All trematode specimens were

rinsed in citrated saline before being heat-killed and formalin fixed for morphology as well as preserved separately in 95% EtOH for DNA extraction and sequencing of the large subunit ribosomal DNA (28S). Using conventional morphological keys and the trematode literature, we identified the following trematodes infecting these turtles: *M. subtrijuga* hosted 2 *Telorchis* spp., 2 *Encyclobrephus* spp., and Digenea sp. (juveniles); *H. annandalii* hosted Orientocreadiidae sp. (cf. Orientocreadium), and 2 species of Plagiorchiidae (cf. *Plagiorchis*). Only 3 parasites (2 Platt spp. and the leech, *Placobdelloides siamensis*) were known previously to infect M. subtrijuga; none of the trematodes we collected from *M. subtrijuga* had been known in that host previously. Likewise, all of those we collected from *H. annandalii* are new host records, with only 4 parasites (the blood flukes *Enterohaematotrema triettruongi* and *Ruavermis mikebargeri* plus the leeches *Placobdelloides siamensis* and *Placobdelloides sirikanchanae*) having been reported from this host previously. These results are based on only 2 field collections of few turtles, indicating that a large, hitherto undocumented diversity of digeneans infect these turtles in the Mekong River. Herein, we detail the morphology of these digeneans and highlight noteworthy aspects of their systematics, with special emphasis on the phylogenetic affinity of *Encyclobrephus* using 28S ribosomal RNA.

9

Phylogenetic analysis of North American species of *Neoechinorhynchus* Stiles & Hassall, 1905.

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Neoechinorhynchus Stiles & Hassall, 1905 is one of the most diverse genera of acanthocephalans. With >120 species worldwide, it represents ~10% of the diversity of Phylum Acanthocephala. In the USA and Canada, 8 species are reported from turtles and 27 species from fish. Towards a revision of the genus, our phylogenetic analyses presented here are based on nuclear DNA from the internal transcribed spacer (ITS) and large ribosomal subunit (LSU) regions of 19 described species from the USA and Canada and congeners from South America, Europe, and Asia after several years of field work. Multiple specimens of *Neoechinorhynchus* from the USA and Canada were included to address intra-specific and geographic variation. Specimens from 8 species in the analysis were collected from their respective type localities in the USA. Representatives of several other genera from Neoechinorhynchidae were also included to address paraphyly of *Neoechinorhynchus*. Our results recovered 3 novel lineages that correspond to putative new species of *Neoechinorhynchus*, requiring further morphological examination. For example, some of the clades recovered correspond to morphological characters that have been emphasized in species descriptions from the 20th Century, such as a markedly thicker dorsal body wall and markedly unequal lemnisci, while other characters, such as eggs with polar prolongations, appear not to. Specimens of European *Neoechinorhynchus rutili*, the type species of the genus, unexpectedly grouped with species from western North America and eastern Asia. The conspecificity of specimens from localities throughout eastern and central USA identified as *Neoechinorhynchus cylindratus*, a species reported from centrarchid fishes and multiple other fish families, was supported. However, some previously made records of this species are instead suspected to be *Neoechinorhynchus tenellus*. The four *Neoechinorhynchus* species from turtles from Oklahoma formed a monophyletic group whose position within the tree suggests that turtle parasitism is derived from fish parasitism within Neoechinorhynchidae. *Octospinifer macilentus*, a neoechinorhynchid from catostomid fishes, nested with a clade of multiple *Neoechinorhynchus* species also from catostomid fishes, augmenting evidence from a previous study that *Neoechinorhynchus* is paraphyletic. Future studies will build on these results by including more neoechinorhynchid genera, more samples from other continents, and additional DNA loci.

10

First report of turtle blood flukes (Digenea: Schistosomatoidea) from *Apalone spinifera* spp. (Testudines: Trionychidae) in Texas.

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Turtle blood flukes (Digenea: Schistosomatoidea: "Spirorchiidae") are considered important disease agents in turtles yet are severely underreported in many turtle species. In Texas, previous researchers documented blood fluke infections in only 3 of the 38 turtle species and subspecies. There are no reports in Texas from any species of *Apalone* Rafinesque (Testudines: Trionychidae). From 2017-2018, 4 *Apalone spinifera emoryi* (Agassiz) and 14 *Apalone spinifera pallida* (Webb) were collected from 9 locations in 6 counties across Texas and examined for blood flukes. *Vasotrema robustum* Stunkard, 1928, *Vasotrema longitestis* Byrd, 1939, *Vasotrema* cf *brevitestis* Brooks and Mayes, 1975 and 2 unidentified species of *Vasotrema* (Stunkard, 1926) Stunkard, 1928 were recovered from the heart, liver, lungs, spleen and kidneys of 8 hosts (1 *A*. *s*. *emoryi* and 7 *A*. *s*. *pallida*). Phylogenetic analysis of the large subunit rDNA (28S), combined with unique morphology and host associations suggests *Vasotrema* warrants consideration to be elevated to Family status once "Spirorchiidae" is formally split. This is the first report of blood flukes from *A*. *s*. *emoryi* and *A*. *s*. *pallida* and is part of the largest survey of blood flukes in Texas to date.

11

Dental sources of delusional parasitosis (Neuro-cutaneous Syndrome); a new toxicity disorder.

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We have been seeing an increasing number of patients with pathogenic bacterial and fungal infections associated with recurrent open skin sores/lesions and with crawling and tingling (pin prick) sensations, often interpreted as and confused with presence and movement of parasites under the skin and in body cavities. The presence of parasites could not be substantiated upon thorough testing. Patients were classified by health care practitioners as delusional. They were, however, found to be genuine clinical cases but not of parasitic infections. Our studies of about 1000 patients since 1996 have led to the description of a new disease, Neuro-cutaneous Syndrome (NCS), also previously reported as Morgellons, a dental toxicity disorder caused by the use of incompatible dental materials including, but not limited to, liners, bases, cements, sealants, adhesives, composites, bonding agents, root canal, denture, and etching materials during routine dental procedures.

12

Brown dog tick (*Rhipicephalus sanguineus* sensu lato) infection with endosymbiont and human pathogenic *Rickettsia* spp., Northern Mexico.

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Of the documented tick-borne diseases infecting humans in Mexico, Rocky Mountain spotted fever (RMSF), caused by the gram-negative bacterium *Rickettsia rickettsia*, is responsible for most fatalities. Given recent evidence of brown dog tick, *Rhipicephalus sanguineus* sensu lato, as an emerging vector of

human RMSF, we aimed to evaluate dogs and their ticks for rickettsiae infections as an initial step in assessing the establishment of this pathosystem in a poorly studied region of northeastern Mexico and evaluating their use as sentinels for transmission/human disease risk. We sampled owned dogs living in six disadvantaged neighborhoods of Reynosa, Northern Mexico to collect whole blood and ticks. Of 168 dogs assessed, tick infestation prevalence was 53%, comprised of exclusively *R. sanguineus* s. l. (n=2,170 ticks). Using PCR and sequencing, we identified an overall rickettsiae infection prevalence of 4.1% (n=12/292) in ticks, in which eight dogs harbored at least one infected tick. Rickettsiae infections included *Rickettsia amblyommatis* and *Rickettsia parkeri*, both of which are emerging human pathogens, as well as candidatus *Rickettsia andeanae*. This is the first documentation of pathogenic Rickettsia in *R. sanguineus* s.l. collected on dogs from northeastern Mexico. Domestic dog infestation with *Rickettsia*-infected ticks indicates ongoing transmission, thus humans are at risk for exposure and underscores the importance of public and veterinary health surveillance for these pathogens.

13

Analysis of cytokine profiles in domestic cats (*Felis catus*) infected with *Cytauxzoon felis.*

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Cytauxzoon felis is an apicomplexan parasite in the order Piroplasmida, family Theileriidae. *C. felis* is a vector-borne parasite primarily transmitted by the Lone star tick (*Amblyomma americanum*) and may also be transmitted by the American dog tick (*Dermacentor variabilis*). *C. felis* is the etiological agent of the disease cytauxzoonosis, an emerging tick-borne disease of domestic cats (*Felis catus*). Bobcats (*Lynx rufus*) serve as a natural animal reservoir for *C. felis*. *C. felis* has been historically enzootic in the South and Southeastern United States but has continuously expanded north and west in the United States with the expansion of the zoogeographic range of the Lone star tick. Cytauxzoonosis results in various pathologies in infected felines, with symptoms including fever, decreased appetite, lethargy, dehydration, dyspnea, hemolytic crisis, and icterus. Cytauxzoonosis has been associated with high mortality rates in infected domestic cats, although emerging research has shown that domestic cats can have subclinical infections, acting as reservoir hosts for the parasite. While data regarding the emergence, prevalence and transmission of *C. felis* has continued to amass, there are relatively few studies present that thoroughly analyze the immunological processes associated with feline infection. Studies that have focused on the feline immune response to cytauxzoonosis have shown there to be an upregulation of the adhesion molecule CD18 following infection, which can result in stimulation of pro-inflammatory mediators. Another study expanded upon this finding, observing increased serum concentrations of proinflammatory cytokines TNF-α and IL-1β in fatal cases of cytauxzoonosis, compared to acutely infected cases and healthy survivors of cytauxzoonosis. In this study, we analyzed the cytokine profiles, comprised of Fas, IFNγ, IL-1β, IL-2, IL-4, IL-5, IL-8, IL-10, IL-12 and RANTES, of domestic cats infected with *C. felis* and analyzed these profiles across varying clinical outcomes. We aim to expand upon the established research on how the feline immune system is modulated in response to cytauxzoonosis. This can help to elucidate further understanding of the immune processes associated with this disease while identifying potential avenues for treatment.

14

TLF3: Identification of a unique pre-beta high-density lipoprotein as a third Trypanosome Lytic Factor.

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African Trypanosomiasis is a disease caused by the African Trypanosoma family of bloodborne parasites. Humans and some non-human primates are protected against most species of trypanosomes due to an immunity complex called Trypanosome Lytic Factor (TLF). TLF is a specialized High-Density Lipoprotein

(HDL), that carries a lytic cation channel-forming protein (Apolipoprotein-L1 (APOL1)), and a ligand (Haptoglobin-related protein (HPR)), which binds to parasite receptors increasing uptake into the parasite. There are two TLF HDL complexes in blood: TLF1 (~500 kDa) and TLF2 (~1,200 kDa). How these TLFs are formed is unknown. To fully characterize all possible TLF species, we used anti-APOL1 affinity chromatography to purify all complexes containing APOL1 from human serum. Size exclusion chromatography by FPLC, using multiple columns, allowed us to further separate the complexes by size. Both TLF1 and TLF2 were isolated, as well as a third complex that is 180 kDa. Western blotting of the fractions confirmed co-elution of APOL1, HPR, and Apolipoprotein A-I, a protein found in all HDLs, suggesting this complex is a distinct HDL. Lysis assays showed this complex lyses trypanosomes. Co-immunoprecipitation confirmed that all three proteins are on the same complex. We suggest that this TLF complex, TLF3, is a pre-beta HDL, based on its size and density. We hypothesize that all three proteins are assembled together in/on the hepatocyte with minimal but sufficient lipids to generate a pre-beta HDL, TLF3. The TLF3 complex is released into the blood and matures into TLF1 by collecting cholesterol and phospholipids from peripheral tissues.

15

Cercaria emergence rates let us calculate trematode parthenita within-host dynamics.

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Inside their first intermediate host mollusc, most trematode parthenitae are impossible to observe over time. This stems from the fact that observing the parasites requires killing or at least injuring the host, as parthenitae are typically hidden within the host's opaque shell and dense tissues. Given this observational difficulty, we still have a limited understanding of the dynamics of trematode colonies. To help resolve this problem, we present a method to infer vital rates (births, growth, and deaths) of trematodes within host mollusks by combining (1) cercaria emergence data, (2) knowledge of parthenita reproductive biology, and (3) a novel application of demographic modeling to trematode colonies. If senescence of individual worms can be detected within a single colony snapshot, we show that the emergence rate of cercariae from the host can be directly mathematically related to the lifespan of senescing worms. Using species-specific estimates of average per-capita cercaria production rates and colony-specific observations of senescing individuals, we can calculate a specific death rate for each colony. This vital rate, coupled with the growth rate of the host, allows us to fully parameterize within-host dynamical models for trematode colonies with only a single, destructive observation of each colony population. As parthenita senescence in philophthalmid trematodes is particularly easy to observe and quantify, we use several species in this family to demonstrate the technique. We conclude by discussing how this approach in a general form could be applied to the infrapopulations of other host-parasite systems with closed recruitment.

16

Hybridization between human and livestock schistosomes – rampant or rare?

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Hybridization between human and animal parasites can transfer pathogenic traits between species and negatively impact human health. Knowing when and how often these events occurs is an essential step in achieving optimal outcomes within a One Health framework. The human parasitic blood fluke, *Schistosoma haematobium* can hybridize with the livestock parasite *S. bovis*. Work from independent groups using single nucleotide variants and microsatellite markers suggest that a hybridization event in the relatively distant past led to the adaptive introgression of *S. bovis* alleles into the *S. haematobium* population. Here, we expand on this work by analyzing 34.6 million genome-wide, single nucleotide

variants in 167 *S. bovis* and *S. haematobium* samples collected from 18 countries across Africa and aided with a chromosomal-scale genome assembly. We did not find evidence of recent hybridization in these samples. In addition, our results confirm the presence of an ancient introgression event that that occurred 723-15,598 (median=2,738) generations ago that was restricted to west African populations. Three introgressed, *S. bovis* loci containing 68 genes are at, or near, fixation in west African *S. haematobium* populations. Certain regions of the *S. haematobium* genome are depleted of *S. bovis* alleles indicating selection against introgression. Our results show that novel alleles have been transferred between *S. haematobium* and *S. bovis* through past adaptive introgression events.

17

The gastropod hosts of schistosomes: patterns, processes and mechanisms.

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As one of the best known groups of parasites, the digenean family Schistosomatidae can offer unique insights with respect to processes underlying diversification of parasite lineages. Our aims are to gain a more detailed overview of gastropod lineages exploited by schistosomes, to infer what processes might lie behind the patterns observed, and to suggest underlying mechanisms amenable to testing. Our own concerted search for schistosome infections among snails from multiple continents coupled with provision of sequence data for both schistosomes and infected gastropods along with examination of literature with comparable schistosome-gastropod sequence data provide the database from which our results were obtained. As far as known, all schistosome use either coenogastropod or heterobranch gastropod intermediate hosts. More basal gastropod lineages are not found infected with schistosomes. Marine, freshwater and amphibious life cycles are known. Experimental infection studies indicate relative specificity at the snail host level, yet paradoxically, the present-day record implies host switching has been pervasive, both within and between gastropod families. Schistosomes have colonized several gastropod families but are conspicuously absent from others. Schistosome host switches may be facilitated by co-infections involving immunosuppressive parasites, altered temperature regimes or other conditions stressful to hosts, hybridization among diverging schistosomes, or new ecological circumstances placing schistosomes in constant contact with new host snail species, favoring rare infectious variants. Supported by NIH grant R37AI101438.

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Physid snails as sentinels: their status 25 years later.

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Historically, the distribution of gordiid worms (Phylum Nematomorpha) was determined by observing adult worms and collecting them from aquatic systems. The paucity of collected samples suggested that nematomorphs were a rare group and only sparsely distributed. Beginning in 1997, the world of the Nematomorpha was propelled forward when it was discovered that the non-adult stages were ubiquitous in freshwater, including the cyst stage being found in physid snails. Compared to sampling for adults, the cyst stage was easily detected in numerous freshwater snails indicating hairworms were broadly distributed in the environment. Since this pivotal study was published in 2001, many new insights into nematomorph biology have been discovered. For example, by examining the folding pattern of encysted larvae, the genus can be determined for the 4 known cysts types of 22 genera (*Chordodes*, *Gordius*, *Paragordius*, and *Neochordodes*). Although sampling for snails removes some of the obstacles of sampling for adults, there have been few field studies that have examined this and as a

result, we have found few snail species that have been show to harbor hairworm cysts. In a few cases, hairworm species was determined by feeding infected snail tissue to a suitable host to culture adults in the laboratory. For example, *Paragordius* cysts have been found to grow to adult in the house cricket (*Acheta domesticus*). In the summer of 2021, I returned to some of the sites featured in the original study and collected snails from sites known to harbor hairworm cysts. We found cysts were present in many of the original sites and a few were not present where they had been previously. However, we found that cyst types matched *Chordodes* and *Paragordius*. These cysts were then fed to house crickets in the laboratory to yield adult hairworms for species determination, a step that was missing in the original pivotal study. We discuss recent hairworm studies that employ these methods and the future of nematomorph research.

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Larval trematode diversity and its correlation with aquatic invertebrate diversity and water quality over five years at three sites in Oglala Lakota County, SD.

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Parasites with complicated life cycles require multiple hosts. If these hosts are absent, then these parasites cannot complete their life cycle. Thus, a diverse assemblage of these parasites should indicate a healthy ecosystem. Although short term studies have supported this hypothesis, long term data is also required. To acquire these data, we set up 10m x 3m transects to survey three aquatic sites over five years (2015-2019), collecting aquatic snails and insects and measuring water parameters such as DO, pH, nitrate, and temperature. Two sites were on the Pine Ridge Reservation with one located near a small town (population of over 800) and the second located in a recreational park. The third was in the Lacreek National Wildlife Refuge, which served as the reference site. We dissected the snails, counting chaetogasters and, when present, identifying larval trematodes. Aquatic insects were identified to family and Shannon Diversity indices were calculated for larval trematodes, snails, and aquatic insects. We hypothesized that diversity for all taxa should be highest at the reference site in each of the five years. Interestingly, the more rural site on the reservation consistently showed the highest aquatic insect diversity for each of the five years. Because of small sample sizes, larval trematode diversity was summed over the five years before calculating diversity. The reference site had the highest larval trematode Shannon Diversity index. We found no correlation between the size of infected *Physa* sp. snails and the number of chaetogasters. We consider snail diversity and density, chaetogaster prevalence, and water parameters in the context of a long-term survey.

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Light at the end of the alimentary canal: Advancing generic diversity of elasmobranch tapeworms.

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Our understanding of cestode interrelationships has advanced in leaps and bounds with the application of molecular methods. Also, global collecting efforts have provided opportunities to expand phylogenetic analyses to include as much diversity as possible and have led to the discovery of substantial generic novelty. The aims of this study were to investigate the extent to which this applies to acetabulate cestodes that parasitize elasmobranchs (sharks, stingrays, and relatives), and to assess how much novelty remains to be formally described. Taxonomic efforts aimed at acetabulate cestodes parasitizing elasmobranchs over the last 20 years were summarized and published trees resulting from molecular phylogenetic analyses were examined from the standpoint of assessing potential generic novelty. The extent to which clades were also supported by morphological criteria and their current

taxonomic status was evaluated. A total of 44 new genera have been formally erected since 2000, of which 29 were based on morphological criteria alone, and 15 emerged from molecular analyses and were subsequently supported by morphological features. Phylogenetic frameworks led six of the 44 genera—all erected based on morphology alone—to be synonymized. Additional preliminary data suggest fewer than ten additional genera await erection. The last two decades underscore the value of iterative systematic efforts and the importance of broad taxon sampling for establishing monophyletic taxa. Generation of molecular sequence data now commonly outpaces formal characterization of the seemingly limitless spectacular morphological diversity of forms exhibited by elasmobranch-hosted cestodes.

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Sharks as dispersal platforms for remora-infecting monogenoids (Monogenoidea: Dionchidae: *Dionchus*)?: morphological and nucleotide evidence of Dionchus postoncomiracidia infecting the skin of the blacktip shark, *Carcharhinus limbatus.*

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Nearly 22 years have passed since the discovery of postoncomiracidia of *Dionchus* sp. infecting the skin of blacktip sharks, *Carcharhinus limbatus* (Carcharhiniformes: Carcharhinidae) by Bullard and colleagues. This discovery was met with skepticism by monogenoid taxonomists who were active at that time, and monogenoids are still thought of as flatworms with direct life cycles that do not use alternate hosts to facilitate larval dispersal. Based on new collections of postoncomiracidia and adults of *Dionchus* infecting the skin and gill of sharks and bony fishes, we further explore the life cycle and host specificity of *Dionchus* spp. Postoncomiracidia were sampled from the skin of blacktip sharks whereas adults of *Dionchus* were sampled from the gill of the common sharksucker (*Echeneis naucrates*), whitefin sharksucker (*Echeneis neucratoides*), and cobia, *Rachycentron canadum*. Confirming our conclusions based on morphology, the 28S sequences from the postoncomiracidia were recovered deep within a clade comprising the adult *Dionchus* sequences. No sequence matched; indicating an unexpectedly high diversity of congeners infecting these fishes. The 28S sequence of the postoncomiracidium differed from those of the adults from common sharksucker, whitefin sharksucker, and cobia by 73 bp (10%), 91 bp (12%), and 196 bp (15%). Hence, we failed to match the postoncomiracidia from the blacktip shark with an adult species infecting a bony fish. The study provides the first nucleotide sequences for Dionchidae and indicates that the postoncomiracidia and the adults from the whitefin sharksucker (a new host for a species of *Dionchus*) each comprise a new species of *Dionchus*.

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Redescription of a little studied freshwater fish blood fluke (Digenea: Aporocotylidae: *Sanguinicola*) infecting the type host (sabrefish, *Pelecus cultratus*) from the Upper Volga River, Russia, and the first phylogenetic analysis including a species of *Sanguinicola* accompanied by adult voucher specimens.

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The fish blood flukes (Digenea: Aporocotylidae Odhner, 1912) comprise ~173 species of 43 genera that infect freshwater, marine, and estuarine fishes. They are occasional pathogens of cultured fishes and the immediate ancestor to the turtle blood flukes (“Spirorchiidae”) and the distant ancestor to the mammal and bird blood flukes (Schistosomatidae). Our phylogenetic analyses routinely recover a monophyletic freshwater clade of fish blood flukes. *Sanguinicola* spp. infect 50 freshwater fishes (+1 marine) of 7 orders. Of the 6 freshwater aporocotylid genera, *Sanguinicola* is the most speciose (25 species) and fraught with incomplete species descriptions. The type species, *Sanguinicola armata* Plehn, 1905, has

not been redescribed in nearly a century. Further, no nucleotide information exists from an adult specimen of a species of *Sanguinicola*. Herein, we morphologically and genetically characterize a species of *Sanguinicola* and reconstruct a phylogeny using the large subunit rDNA (*28S*). During 2021, sabrefish, *Pelecus cultratus* (Linnaeus, 1758) Berg, 1949, and ide, *Leuciscus idus* (Linnaeus, 1758) Berg, 1949, (Cyprinidae) were collected from the Upper Volga River, Russia, and were infected with adults of *Sanguinicola volgensis* (Rašín, 1929) Mcintosh, 1934 and *S*. cf. *volgensis*, respectively. *Sanguinicola volgensis* differs from congeners by having the combination of >90 tegumental spines in a single column on each side of the body, 4 or 5 intestinal ceca, a testis with >20 paired vesicles, and ovoid eggs. *Sanguinicola* cf. *volgensis* only differs from *S*. *volgensis* by having a body that is >5 times longer than wide. Aligned sequences of the *28S* and internal transcribed spacer (*ITS2*) from these two adult flukes differed by one and two base pairs, respectively. The phylogenetic analysis recovered the new sequences sister to a sequence sourced from a cercaria presumed to be of *Sanguinicola* (as "*Sanguinicola* cf. *inermis*").

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New Species for an Old Genus.

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Posthodiplostomum Dubois, 1936 is a large and broadly distributed genus notorious for its association with diseases in their fish second intermediate hosts. In this study, we generated partial 28S rDNA and cytochrome c oxidase subunit 1 (cox1) mtDNA gene sequences of digeneans belonging to seven genera with a focus on *Posthodiplostomum*, *Ornithodiplostomum* Dubois, 1936, and *Mesoophorodiplostomum* Dubois, 1936. We also conducted a detailed morphological comparison between the three genera. Historically, these genera have caused a great deal of confusion particularly when specimens were poorly fixed or contracted. Our molecular phylogenetic analyses suggest the synonymy of *Posthodiplostomum*, *Ornithodiplostomum* and *Mesoophorodiplostomum*. Our morphological study of newly collected, well-fixed adult specimens and review of literature revealed lack of consistent differences among the three genera, thus supporting synonymy. Other researchers have also noted ambiguity between the genera and revealed variable morphology in immature specimens further complicating genus distinction. Additionally, we described four new species belonging to *Posthodiplostomum* and have established evidence for at least 13 species level lineages that do not yet have matches among morphologically identified adults. Recent phylogenetic analyses also provided more clarity to the question of the biogeographic and host origin of *Posthodiplostomum* and suggest an Old World origin and a strong history of parasitizing ardeid definitive hosts. This study was funded in part by the National Science Foundation (grants DEB-1120734 and 1852459), the National Institute of General Medical Sciences of the National Institutes of Health (IDeA grant number P20GM103442), University of North Dakota (Esther Wadsworth Hall Wheeler Award, Dissertation Research Award, Pre-PostDoc Research and Grant Writing Experience), American Society of Parasitologists (Willis A. Reid, Jr. Student Research Grant), and Annual Midwestern Conference of Parasitologists (AMCOP Student Research Grant).

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Reconsidering the identity of species belonging in *Diplomonorchis* Hopkins, 1941 from the northern Gulf of Mexico.

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Most taxonomists familiar with the Monorchiidae Odhner, 1911 accept 11 valid species of *Diplomonorchis* Hopkins, 1941. Members of this genus have 2 opposing testes in the middle 1/3 of the hindbody, a vitellarium generally concentrated in the gonadal region, and an I-shaped excretory bladder. Seven species are endemic to the western Atlantic Ocean. Knowledge of monorchiid life cycles and species accounts indicate that oculate or non-oculate cercariae of *Diplomonorchis* spp. develop in sporocysts in marine bivalves. Cercariae emerge and encyst on the incurrent siphons of bivalves or externa of snails. Sexual adults infect the digestive tracts of invertebrate-eating fish. *Diplomonorchis leiostomi* Hopkins, 1941 (the type species originally described from Beaufort, North Carolina) is the only species having a publicly available ribosomal DNA sequence (originating from Mississippi). Present taxonomic convention dictates this species ranges from North Carolina to Louisiana and southward into the Caribbean Sea. In this study we generated a new partial fragment of the 28S rDNA gene obtained from *D. leiostomi* from the type host and locality. It differed by 19 nucleotides plus an 8-nucleotide insertion when aligned over 1,259 nucleotides with the available sequence from Mississippi (GenBank accession number AY222252). The substantial difference clearly indicated they are not conspecific and prompted a reevaluation of *Diplomonorchis* spp. from the northern Gulf of Mexico. Morphological and molecular approaches revealed the presence of 3 undescribed species from coastal fishes from Mississippi, Alabama, and Florida. *Diplomonorchis leiostomi* is probably limited to the coastal Mid-Atlantic States of the United States.

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Pathology of *Huffmanela* cf. *huffmani* (Nematoda: Trichosomoididae) infections in swim bladder, peritoneum, and gonad of variable platyfish, *Xiphorus variatus* (Cyprinodontiformes: Poeciliidae) and eastern mosquitofish, *Gambusia holbrooki* (Poeciliidae) from Florida.

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Variable platyfish, *Xiphophorus variatus* (Meek, 1904) (Cyprinodontiformes: Poeciliidae) and eastern mosquitofish, *Gambusia holbrooki* Girard, 1859 (Poeciliidae) from earthen pond aquaculture systems in southern Florida were examined for parasitic infections. We observed myriad nematodes (adults and eggs) infecting the swim bladder, gonad (no egg was observed in gonad of *G. holbrooki*), and peritoneum. These nematodes resembled *Huffmanela huffmani* Moravec, 1987 (Trichosomoididae: Huffmanelinae), which infects sunfishes (Centrarchiformes: Centrarchidae) in the San Marcos River, Texas, and nucleotide sequences of *H.* cf. *huffmani* from both host species were identical to each other and nearly identical (99%) to *H. huffmani*. The lesions we observed in the infected fish were severe relative to the gross observations of lesions associated with infection by *Huffmanela* spp. in marine fishes. Assessing if the variable platyfish and eastern mosquitofish are natural hosts for *H.* cf. *huffmani* may explain severity of lesions. Pathological changes among infected variable platyfish and eastern mosquitofish were similar, evidently intensity-dependent, and comprised proliferation of the tunica externa of the swim bladder in low intensity infections in addition to inflammation, proliferation, and necrosis of tissues in the swim bladder, peritoneum, and gonad (of *X. xiphophorus*) in high intensity infections. These latter pathological changes were severe, reducing the size of the swim bladder lumen, which could reduce its efficacy. Some eggs were encapsulated by an epithelioid response. No adults were encapsulated. The present study is the first evidence that infection by a species of *Huffmanela* can cause pathological changes that could impact organ function.

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Genetic and trait variability of *Gyrinicola batrachiensis* (Nematoda: Oxyurina) across North America with notes on current taxonomic placement.

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Gyrinicola Yamaguti, 1938 includes six species of oxyurid mutualists found within the intestinal tract of numerous larval anuran species. The species include the sympatric *Gyrinicola tba* (Dinnik, 1930) and *G. chabadamsoni* Brigitte et al., 2008 in Europe, *G. chabaudi* Araujo & Artigas, 1983 in Argentina and Brazil, *G. japonica* Yamaguti, 1938 in Japan, *G. dehradunensis* Maity, Rizvi, Bursey & Chandra, 2019 in India and *G. batrachiensis* (Walton, 1929) in North America. The systematic placement and hierarchical treatment of the genus has shifted significantly since its discovery, having been considered as its own family (Gyrinicolidae), then considered as a genus of the Pharyngodonidae, then subsequently treated as a subfamily (Gyrinicolinae) under the Cosmoceridae, and finally a recent proposal suggests to resurrect Gyrinicolidae. The morphological variation of the species was analyzed in dioecious metapopulations from Oklahoma and dioecious/parthenogenetic metapopulations from Nebraska; the results of this analyses yielded significant differences among worms collected from different host species, but no differences were proposed as a diagnostic indicator of species identity. These results suggest that a single morphologically plastic species of nematode occurs in various species of sympatric anurans. Prior to this study no sequence representing *G. batrachiensis* was available, thus it was not possible to complete a comparison using genetic markers. To further examine diversity of *G. batrachiensis*, and the placement of the *Gyrinicola*, we sampled populations of these nematodes from across North America and screened them for genetic diversity using nuclear markers 28S, ITS1, 5.8S and ITS2 and performed a morphological analysis of specimens. Present phylogenies suggest that at least three clades exist among the nematodes collected across North America and that these clades, alongside *G. japonica*, form a well-supported group sister to a genetically distinct group within the Pharyngodonidae. Further representation of members Pharyngodonidae from other vertebrate classes may help clarify relations in this historical grouping.

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No place like home: Using heatmaps as tool to investigate habitat selection of metacercariae in *Pseudacris regilla.*

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The location of parasites within individual hosts is often treated as a simple categorical variable. However, many parasites can occur in multiple locations or organs and show fine-scale variation in intensity. Distributional heat maps offer a valuable tool for illustrating how infections by different parasites vary in both location and intensity within individual hosts. These visual tools offer a foundation for testing how variation among host individuals, species, coinfection status, or environmental conditions influence the spatial distribution of parasites within their hosts. Comparing and contrasting individual distributions provides detailed knowledge about how parasite distributions may be altered when habitats are co-infected. Furthermore, when plotting variance these distributions provide a window into how common an area is infected across multiple hosts. Finally, heatmaps also provide a unique view in investigating multiple parasite interactions. Such that, a heatmap for a habitat infected with one parasite taxa can then be compared to a heatmap of that same habitat infected with one or multiple different parasites. Here, we apply distributional heat maps to study infection patterns of four trematodes (*Cephalogonimus americanus* and *Alaria marcinae*, *Riberioia ondatrae* and *Echinostoma* spp.) within an amphibian host, *Pseudarcris regilla*. We found that parasite's habitat selection and therefore distribution of parasites within amphibian hosts varied both with respect to primary locations infected and for the degree of specificity / consistency. Some parasites that are generalists in habitat selection (*C. americanus* and *A. marcinae*) whereas (*R. ondatrae* and *Echinostoma* spp. seek a specialized region (e.g. organ or area) to inhabit. Plots of variance revealed that

areas with higher variance are less commonly infection (e.g. spillover locations) whereas, areas of low variance were common areas or preferred areas of infection. Finally, when examining multiple parasite taxa interactions of the three subcutaneous trematodes, highlighted one key area of species interaction, the tail reabsorption area. These overlapping areas serve as areas of interest to be further investigated to untangle mechanisms of habitat selection like, what makes that area able to support multiple infections, what resources does that habitat provide that multiple parasite desire, and/or do these coinfected areas correlate with pathology to the host.

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Avian Malaria Prevalence across important breeding grounds of northern Mexico and Texas.

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Across the Chihuahuan Desert Ecoregion (Mexico and Texas) and Edward's Plateau (Texas), birds using important and sometimes isolated breeding grounds are in decline. Understanding the disease ecology of these birds is essential to future conservation efforts supporting their recovery. The Edward's Plateau region of Texas is a semi-arid Oak-Juniper-dominated ecoregion, whereas the Chihuahuan Desert Ecoregion contains desert scrubland and high-elevation conifer woodlands. These high-elevation habitats are often important breeding grounds for birds and are called "sky-islands" due to their relative isolation. Here we present preliminary results from our analysis of these areas: (1) recording prevalence and diversity of three avian Haemosporidian parasites (*Haemoproteus*, *Leucocytozoon*, *Plasmodium*); (2) identifying previously unknown lineages of parasites; (3) analyzing host-parasite relationships. These results will be used to not only create a broad baseline of prevalence across these regions, and to infer differences between the ecoregions, but also to aid in understanding the disease ecology of birds in decline that use these critical breeding grounds.

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Is ignorance bliss? The vicissitudes of snail taxonomy for parasitologists.

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Awareness is growing that parasite evolutionary ecology is best done when grounded in accurate parasite taxonomy. Efforts to accomplish this include using DNA barcoding or integrative taxonomy to identify and voucher parasites. However, parasite evolutionary ecology should also be grounded in accurate host taxonomy. If not, patterns of co-evolution and host specificity may be misrepresented. Many parasites use or require gastropod hosts in their life cycles, but experts have long been flummoxed by the "vicissitudes and monstrosities" of snail taxonomy. To explore the diversity of *Planorbella* species in parasite evolutionary studies conducted in Manitoba, Canada we used integrative taxonomy (shell morphology, geography, gene sequencing and mitogenome sequencing). Phylogenetic analysis revealed that multiple nominal species were assigned to 3 of 5 clades, including Marsh Ramshorn *Planorbella trivolvis* and Two-Ridge Ramshorn *Helisoma anceps*, which are hosts to many parasites. These results suggested that issues with snail identification could be affecting parasite research including our own on host-parasite chemical communication. A variety of different chemicals are emitted from hosts and parasites including oxylipins, which are oxygenated metabolites of fatty acids. Oxylipins are known to function as signaling molecules and have essential physiological and functional roles. Yet, the limited taxonomic and contextual scope of our knowledge of oxylipins constrains our ability to understand their role in host-parasite interactions. We characterized oxylipins in field-collected File Ramshorn snails, *Planorbella pilsbryi* as well as lab-raised Seminole Ramshorn snails, *Planorbella duryi*. We found that snail chemical profiles of *P. pilsbryi* changed with trematode-infection status and parasite activity. For *P. duryi*, we found that ontogeny and leech-infestation affected chemical

profiles. It was essential to understand the taxonomy of our snails before exploring the chemical ecology of snail host and their interactions with parasites and predators. Our future work is aimed at testing the physiological, ecological, and behavioural roles of oxylipins in freshwater systems.

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Comparative invasion histories of two North American freshwater snails: Approaches to improving our understanding of snail-trematode invasion dynamics.

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Snails are hosts to 10,000+ species of trematodes world-wide, and are therefore, integral in our understanding of parasite lifecycles, evolution, and epidemiology. An essential first question for any parasite system is, what host(s) sustain this lifecycle? For many freshwater snails this question can be obscured by uncertain taxonomic distinctions, uneven or under-sampling across the contemporary range, and a lack of knowledge of historical ranges. To further muddy the waters, many freshwater snail species are considered invasive, and distinctions between native and non-native ranges, the timing and route of invasion are often unclear. Here we will discuss two freshwater snail species with distinct invasion histories, *Physa acuta* (=*Physella*, *Haita*) and *Radix auricularia* (=*Lymnaea*) and their contrasting roles as first intermediate hosts within their native and invasive ranges. *Physa acuta* is a globally invasive snail; originating from Eastern North America, it is now found on all continents, with the exception of Antarctica. Population Genetic data supports that *P. acuta* invasion has been a 200+ year process, with numerous independent introduction events from distinct source populations. Parasitism does not occur equally across the invasive range of *P. acuta*, where only the oldest and most genetically diverse populations seem to contribute to trematode transmission (as first intermediate hosts). The invasion history of *Radix auricularia* is less clear as both the native and presumptive invasive range have numerous morphologically and/or taxonomically similar snails (*Radix* spp., *Lymnaea* spp.). Phylogeographic data suggest that *R. auricularia* populations regularly sampled in parts of North America are genetically identical (cox1 mitochondrial gene) to populations in Europe, suggesting an invasive origin. Molecular genetic approaches to elucidating invasion history and reconciling taxonomic uncertainty will be addressed. Uncovering the invasion history of freshwater snail hosts such as *P. acuta* and *R. auricularia* has potential to inform on host-parasite invasion dynamics, and more generally the specific population-level determinants of snail-trematode compatibility.

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Paratenic host transfer and trophic transmission: a role for aquatic snails in the Gordiid (Phylum Nematomorpha) life cycle.

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Hairworms normally use aquatic insects as their paratenic hosts to bridge the gap between the aquatic environment containing the adult worms and terrestrial environments containing their definitive hosts. Within these paratenic hosts, hairworms produce long-lived cysts. Aquatic snails are also known to readily become infected with cysts both experimentally and in nature. Field studies have shown that up to 56% of snails in rivers can become infected with a mean intensity of 14 but as many as 115 cysts. In fact, aquatic snails become infected with cysts so readily and maintain cysts for so long that they have been used as indicator hosts to identify localities at which hairworms naturally cycle. Despite the commonality of this symbiotic interaction, aquatic snails have been considered a dead-end host, since it is unlikely that terrestrial insect hosts readily eat aquatic snails. I will review evidence that snails may serve several functions within the Gordiid life cycle. Since cysts are able to transfer from one

paratenic host to another, snails may represent the entry host proving Gordiid larvae a convenient place to begin life as a cyst. Cysts from snails can then transfer to predators or scavengers consuming these hosts. The transfer of cysts between paratenic hosts can achieve two things: 1) extend the life of the cyst beyond the life span of a single paratenic host, and 2) allow cysts to be filtered up trophically to insect scavengers such as midges, which have been implicated to be natural paratenic hosts. I would suggest that the transmission of Gordiid cysts to definitive hosts, therefore, works unlike the shotgun approach and much more like the pinball approach.

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Lizard *Plasmodium* Prevalence And Evolutionary History Across Sulawesi.

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Indonesia is one of the most famous biodiversity hotspots and is home to 16% of the world's reptile species. The archipelago, consisting of 17,000 islands, was formed approximately 25 million years ago when extremely high rates of plate tectonic convergence caused Australia to collide with Southeast Asia. Sulawesi is one of the largest Indonesian islands and is central to a myriad of tectonic plate movements, causing high levels of volcanic activity and land submergence into the ocean. Consequently, Sulawesi has developed a diverse endemic biota including a vast population of vertebrates and potentially their related blood parasites. However, these organisms are heavily understudied and their parasites were previously unidentified, leaving room for new discoveries. In order to better characterize these blood parasite infections, we collected blood from 913 amphibians and reptiles across five different sampling localities at different altitudes on Sulawesi. Samples were screened for parasite infection by microscopy. Positive *Plasmodium* spp. diagnoses were confirmed by Sanger sequencing. The phylogenetic relationships of the *Plasmodium* parasites were constructed using maximum likelihood in RAxML. Based on our phylogenetic tree, we hypothesize that these parasites evolved from a common ancestor in each host species (and then diverged at each locality). Parasite lineages that grouped together in our phylogenetic tree were also analyzed to determine any morphological differences. While we thus far have focused on *Plasmodium* lineages, future studies will also explore the other identified blood parasites to better characterize the vast haemoparasite biodiversity of Sulawesi.

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Disease ecology of *Trypanosoma cruzi* in the southeastern United States.

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Trypanosoma cruzi is an important human pathogen endemic throughout the Western Hemisphere. Although considered predominantly a Latin American health issue, the transmission of *T. cruzi* in North America is well documented in both sylvatic and domestic cycles. In the southeastern United States the ecology associated with the sylvatic cycle of *T. cruzi* is largely undescribed. This study examined the distribution and prevalence of *T. cruzi* in regional triatomine vector populations, as well as in sylvatic reservoir populations. Vector specimens were collected in significant numbers from four peri-domestic sites. When tested by PCR using the S-35, 36 and TCZ-1,2 primer sets the prevalence in the vectors ranged from 9 – 32%. *Triatoma sanguisuga sanguisuga* (*T. s .s*.) was the dominant vector collected in three of the sites, with a subspecies, *Triatoma sanguisuga ambigua* dominating in the fourth. Routine monitoring of one infested site found that a predictable pattern of the *T. s. s.* overwintering as 4th or 5th stage nymphs, to emerge in the spring to molt into adults. Fecal exam of live trapped specimens

found active metacyclic stage parasites present in several of the collected specimens. An as yet unidentified triatomine with unique morphology was found sharing one site with *T. s. s.* in significant numbers. Potential mammalian reservoir host specimens were trapped and tissues harvested and submitted for PCR analysis from two sites. In one site, 12 of 23 (52%) raccoons (*Procyon lotor*) tested positive. In a second site seventeen species of mammals were tested of which fourteen were PCR positive for *T. cruzi*.

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The Avian Malaria Community of Sulawesi: Islands on an Island.

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Malaria is caused by apicomplexan parasites, transmitted by dipteran vectors, and infect blood and other cells of vertebrate hosts globally. Continuous host switching events have caused these haemoparasites to radiate into possibly thousands of species found in mammals, reptiles, and birds. While many of the mammalian-infecting parasites are well studied, entire communities of sauropsid (bird, lizard) parasites are still unidentified in many regions of the world, especially tropical islands in the Southeast Pacific Ocean. The island of Sulawesi, Indonesia, has an unusually low species richness and high level of endemism compared to neighboring islands. This unique community composition creates a fantastic opportunity to investigate the evolutionary patterns of avian malaria parasites en situ. In this study, we present the first records of avian haemosporidian lineages on the island of Sulawesi. Blood samples from 73 species of birds from four mountains were screened using the MalAvi primer set and compared to lineages from the global database. Of the 91 lineages identified, only 8 were exact matches to the avian malaria database. The turnover of both parasite and host communities is so high that not one host nor parasite lineage was found on all four mountains. While this makes host-parasite comparisons difficult across localities, the isolated endemic nature of these communities allows us to examine variations in host specificity. Our goal is to determine if these changes in host specificity indicate localized host-switching. Our preliminary results suggest most malaria parasites infecting birds of Sulawesi were found in a single host species. Generalists seems to differ in host specificity depending on locality and host availability indicating isolated host-switching events, although there was no correlation between overall host diversity and parasite diversity across localities. Although each mountain community appears to exist in isolation from one another and from invasive bird populations, there is evidence of an introduced global virulent parasite species on one mountain, suggesting potential vector introduction. These results highlight the value of describing parasite lineages in previously unexplored, endemic avian communities.

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Gregarines of grasshoppers from eastern Kansas, U.S.A.

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Grasshoppers (O. Orthoptera: Infraorder Acrididea) are common inhabitants of grassy fields and other open areas with abundant vegetation. Grasshoppers in the midwestern United States usually reach peak abundance in late summer to fall, though instars and some adults may be collected earlier in the season. Around 11,000 grasshopper species are known worldwide, of which about 1,200 are known from North America. Around 115 grasshopper species have been reported from Kansas, U.S.A. Many kinds of parasites are known to infect grasshoppers including mites, dipterans, nematomorphs, nematodes, and protozoans—such as amoeba and gregarines. Gregarines (Apicomplexa) are a diverse group of protozoans that parasitize marine, freshwater, and terrestrial invertebrates. Gregarines of insects are

especially diverse. While many past studies have focused on gregarines of orthopterans, few have been on orthopterans in North America. From June to October 2021, over 400 grasshoppers were collected by hand or using a sweep net from locations in Johnson and Douglas counties in eastern Kansas, U.S.A. Specimens of 13 species of grasshoppers were collected. Grasshoppers were stored in 1-gallon plastic containers or mesh cages in the field, sorted by species, and held in separate cages overnight to collect frass. Individuals (n=380) were dissected and observed for parasitic infections using a dissecting microscope; 106 were parasitized by gregarines, 12 by nematodes, 2 by flies, and 1 by mites. Gregarine specimens were fixed on glass cover slips, stained with acid carmine, and mounted in Canada balsam on glass slides. Morphological data were gathered to identify gregarines, for which only a single species is presumed to have been recovered: *Amoebogregarina* c.f. *nigra* Kula and Clopton 1999. Gametocysts of this gregarine species were obtained from frass collected from 3 grasshopper species: the differential grasshopper (*Melanoplus differentialis*), the red-legged grasshopper (*Melanoplus femurrubrum)*, and the admirable grasshopper (*Syrbula admirabilis*). Gametocysts were washed in insect saline and preserved for molecular sequencing to confirm species identity. Molecular sequence data will be obtained from the 18s-ITS1-5.8s-ITS2-28s ribosomal gene region.

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Distribution and ecology of *Ergasilus cotti* (Kellicott 1892) from mottled sculpin and rainbow darter.

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Ergasilus cotti (Kellicott 1892) was first recognized by D. S. Kellicott as a species from populations of mottled sculpin (*Cottus bairdi*) collected in a creek near Westerville, Ohio in 1892. *Ergasilus cotti* was last observed in Ohio within the Alum Creek watershed on rainbow darter (*Etheostoma caeruleum*) in 1940. The most recent reported observation of *E. cotti* occurred during a 1969-75 survey of the fish parasite fauna of Lake Superior by Dechtiar and Lawrie. Mottled sculpin and rainbow darter are the only fish known to harbor *E. cotti*, which has developed a burrowing mode of attachment reminiscent of the gill maggot, *Salmincola*, a unique strategy among the Ergasilidae. The original *E. cotti* description by Kellicott was very brief and no type specimens remain. Little is known about the distribution, abundance, and morphology of *E. cotti*, in addition to the lack of understanding regarding the host-parasite association. Using archived museum specimens of mottled sculpin and rainbow darter, we conducted a systematic survey to determine the presence or absence of *E. cotti* from creeks primarily in Ohio, with several Pennsylvania and New York representatives. A prevalence of ~4 and ~3% was found in the respective 861 mottled sculpin and 923 rainbow darters that have been examined thus far. Infested fish were collected as early as 1922 and as recently as 2014. In total, 241 copepods have been recovered and preserved, 193 from sculpin and 48 from darters. Mean intensities of *E. cotti* infestation of sculpin and darter were ~7 (high of 37) and ~2 (high of 6), respectively. This research was conducted to develop the first detailed report of *E. cotti* since its discovery, with a focus on ecology and geographic distribution patterns for this understudied parasite. Along with expanding our knowledge of *E. cotti*, we explored the host-parasite relationship that exists between mottled sculpin and rainbow darter, two important steam species in North America.

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Taxonomic expertise is exceeded by demand for it: The fundamental necessity of taxonomy in the management and understanding of fish diseases, aquatic invasive species, and cryptic species in the Southeastern United States.

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Disease diagnostics (taxonomy of parasites and pathogens) is critical to fisheries biology and natural resource management because fishes are routinely cultured at scale and released into natural ecosystems, moved across state lines and river basins, and affected by native and non-native pathogens. The Southeastern Cooperative Fish Parasite and Disease Laboratory was established at Auburn University in 1965. Our mission is to consult on disease issues (including fish kills) and determine the taxonomic identity, life history (pathobiology), and ancestry of viruses, bacteria, fungi, protozoans, and metazoans that infect and affect aquatic invertebrates and fishes as well as those of amphibians, turtles, snakes, and birds associated with warm- and cold-water fish culture systems. We advise federal agencies, state agencies, non-profit conservation groups, small and large scale commercial fish culture operations, the hobby and public aquarium industries, veterinarians, and university researchers. We herein present several case studies highlighting the relevance of taxonomy in the region and in the fields of fisheries biology, conservation, and natural resource management. These include commercially- and recreationally-valued fishes as well as threatened and endangered fishes of conservation concern in the Southeast. The overarching outcomes of this work are that new parasite species continue to be discovered in common fishes (parasitological and disease surveys among common cultured and wild fish populations remain needed) and that paradigms and assumptions are routinely overturned. Importantly, there is a very strong need for the taxonomist who can i) field-collect hosts, ii) conduct a thorough necropsy, iii) apply taxon-specific fixation, preservation, and preparation methods to produce taxonomically-informative specimens, iv) draw, measure, photograph, and characterize (identify) species using microscopy, v) manipulate and maintain experimental hosts, vi) interface with agency personnel to translate scientific results to the public, and vii) deposit specimens in curated museums. Molecular phylogenetic approaches are important, but expertise in morphology and taxonomy presently is vastly exceeded by demand for it. Taxonomy generates the foundational knowledge required to produce management tools and strategies that protect natural resources.

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Otolith Microchemistry Analysis of Trace Elements in Relation to Parasitism in Two Fish Species in a Lentic System.

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Fisheries management often focuses on abiotic factors to evaluate health of a fish community such as habitat conditions, water temperature, and dissolved oxygen levels. Biotic factors like parasites can often be overlooked, but can have important impacts on fish communities by influencing behavior, spatial distribution, and fitness. Otoliths (fish ear stones) are calcium carbonate structures that grow throughout the life of a fish, serving as a natural time-keeping log. As the otoliths grow, they also incorporate trace elements ultimately allowing us to interpret the conditions fish experience over time. The relationship between otolith microchemistry and parasitism has received little study to date. This research seeks a connection between these areas of study to provide a more comprehensive understanding of fish health in a lentic system. In this study, we collected 32 *Lepomis macrochirus* (Bluegill) and 31 *Pomoxis nigromaculatus* (Black Crappie) from a private lake near Dalton, PA. Fish were dissected, major internal organs examined, and all parasites categorized and quantified. Otoliths from each fish were processed and core sections were run through LA-ICPMS to determine annual microchemistry. The trace element microchemistry results were compared to abundance of all parasites. There was a positive correlation with parasite abundance and concentrations of otolith manganese relative to calcium in Bluegills. The Mn:Ca ratio is indicative of hypoxia and the trend persisted when Mn concentrations were corrected for fish growth. Black Crappie did not show any conclusive results with trends in hypoxia and parasitism. Crappie did possess higher levels of strontium than Bluegill, which may be indicative of differences in habitat use and a possible explanation for the variation in Mn:Ca levels observed between the two species. Another possible explanation for the

differences in Mn:Ca levels between species could be the presence of the trematode parasite *Posthodiplostomum minimum*, which was far more abundant than any other parasite species and may be associated with the trend observed with hypoxic conditions. More heavily parasitized fish may be behaviorally impacted to not swim away from area of low oxygen, or fish subjected to hypoxic conditions may be more susceptible to parasite infections.

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Parasitological survey of silver carp, *Hypophthalmichthys molitrix* (Valenciennes, 1844) (Cypriniformes: Cyprinidae) reveals the first record of an ectoparasite, *Dactylogyrus* cf. *skrjabini* (Monogenoidea: Dactylogyridae) from this host in North America.

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The parasites of exotic invasive carps in North America (silver carp, *Hypophthalmichthys molitrix*; bighead carp, *Hypophthalmichthys nobilis*; black carp, *Mylopharyngodon piceus*; and grass carp, *Ctenopharyngodon idella*) are a concern to parasitologists and natural resource managers. Yet, no ectoparasite has been reported from silver carp in North America. During June and December of 2021, a parasitological survey of silver carp from the Tennessee River Basin resulted in the discovery of numerous monogenoid specimens infecting the gill. These specimens were heat-killed and routinely stained for morphology or placed directly into 95% EtOH for DNA extraction and sequencing of the large subunit ribosomal DNA (28S). We herein morphologically diagnose these monogenoids, compare them with published descriptions, and conduct a 28S phylogenetic analysis. The specimens were identified as *Dactylogyrus* cf. *skrjabini* based on the morphometrics of the dorsal anchor (point length; length to notch; inner root length; outer root length; total length), the fine anatomy of the penis and accessory piece (together comprising the male copulatory organ), and the uniquely large 5th hook pair. They differed from the original description of *Dactylogyrus skrjabini* Achmerov, 1954 (type locality Amur River, Russia) by having a complex distal portion of the accessory piece, by the fine anatomy of the dorsal anchors, by the anatomy of the dorsal and ventral bars, and by the total body length. The 28S sequences (2 sequences of 763 bp aligned length) were identical to those ascribed to *D. skrjabini* from the Watarase River, Japan, by Nitta and Nagasawa in 2019. The present study is the first report of an ectoparasite from silver carp in North America, the first nucleotide information for a silver carp ectoparasite in North America, and the first record of this monogenoid lineage in North America. A list of symbionts of silver carp worldwide is provided herein as a means of estimating the total number of potentially co-invasive microbes, viruses, protozoans, and metazoans that infect silver carp in North America.

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Untangling the systematics of the Diplostomidae.

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The Diplostomidae is a diverse family of digeneans distributed worldwide. Members of this family most often parasitize birds and mammals as adults. As larvae, diplostomids utilize a wide range of intermediate hosts including fish, amphibians, reptiles, and mammals. In many cases, larval diplostomids are known to cause disease in their intermediate hosts. Several systems of the Diplostomidae have been proposed in the past based solely on adult and larval morphology. The most recent system of the group proposed in the Keys to the Trematoda included four subfamilies and 41 genera, however, subsequent molecular phylogenetic studies have introduced minor changes in that system. We generated ribosomal and mitochondrial DNA sequences from four subfamilies, 22 genera, and 84 species of diplostomids to

re-evaluate the systematics of the Diplostomidae and validity of its constituent taxa. Molecular phylogenetic analyses based on ribosomal DNA sequences demonstrated the extreme non-monophyly of the sub-families as well as some genera. Our phylogenies permitted the reassessment of taxonomic value of adult and larval morphological characteristics and definitive host groups to distinguish between diplostomid subfamilies and genera. In summary, our molecular and morphological data provided support for substantial systematic changes to the Diplostomidae including the abandonment of the currently accepted subfamilies. Our study has also resulted in the restoration of *Parallelorchis* and synonymization of the genera: (i) *Ornithodiplostomum* and *Mesoophorodiplostomum* with *Posthodiplostomum*, (ii) *Didelphodiplostomum* with *Tylodelphys*, (iii) *Pharyngostomoides* with *Alaria*, and (iv) *Fibricola* with *Neodiplostomum*. Several new diplostomids have been described including a new genus from crocodilians in Africa and nine new species from reptiles and birds in North America, South America and Africa. Considering the extensive systematic changes to the Diplostomidae, we have provided a new key for diplostomid genera. This study was funded in part by the National Science Foundation (grant DEB-1120734), University of North Dakota (Esther Wadsworth Hall Wheeler Award, Dissertation Research Award, Pre-PostDoc Research and Grant Writing Experience), American Society of Parasitologists (Willis A. Reid, Jr. Student Research Grant), and Annual Midwestern Conference of Parasitologists (AMCOP Student Research Grant).

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Taxonomic revision of the genus *Megistopoda* Macquart, 1852 (Diptera: Streblidae) and preliminary results of their species delimitation.

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Bat flies (Diptera: Streblidae and Nycteribiidae) are obligate, blood-feeding ectoparasites of bats, parasitizing only bats. Bat fly species belonging to the genus *Megistopoda* are characterized by presenting the femur III longer, thorax shieldlike, and stenopterous wings. *Megistopoda* species are therefore unable to fly and their ability to move among host individuals is restricted and this lack of flight can lead to strong host associations. The genus *Megistopoda* is composed of three described species *M. aranea*, *M. proxima* and *M. theodori*, each of which has been found to be associated with host species belonging to the New World leaf-nosed bats (Chiroptera: Phyllostomidae) genera *Artibeus* or *Sturnira*. With only three widely distributed species, *Megistopoda* is an understudied genus and species delimitation has not been rigorously assessed. Most of the used characters to identify *Megistopoda* species are ambiguous and intraspecific variation is usually not considered. In this talk, I will present the results obtained during my master's studies, where we analyzed morphological characters and a total of 12 body measures of 852 *Megistopoda* individuals (obtained from museum collections and recent fieldwork) from across their geographic range. We identified nine putative species, six new to science, but describing diagnostic characters. Two analyses (ANOVA and PCA) were performed to recognize significant differences among the quantitative characters. Thorax chaetotaxy, the femur III length, and the wing measures were the most informative to recognize morphospecies. Future research will include phylogenetic analyses using morphological and molecular data to determine relationships, host associations, and geographic distributions among *Megistopoda* species.

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Anatomical Variability in the Acanthocephala (# 1 of 2 parts).

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Unique and unusual features in the many species of acanthocephalans described and/or studied by Amin from fish, amphibians, reptiles, birds, and mammals, in various parts of the world including South America, Vietnam, Japan, the United States, the Middle East, and North and East Africa, are described. The presentation is in 2 parts. (1) An introductory section dealing with the classification, general morphology, ecology, and life cycles of the Acanthocephala. (2) Unusual anatomical features of taxonomic or of questionable taxonomic importance addressing variations in the proboscis, proboscis hooks, male and female reproductive organs, and lemnisci. Newly described structures including (a) Para-receptacle structure (PRS) and hoods in certain species as well as a new order of Acanthocephala from Vietnamese birds, are also featured.

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Structural-Functional Relationships and Curiosities in the Acanthocephala (# 2 of 2 parts).

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This treatment of variability in the Acanthocephala is in 3 parts (1) Structural and functional relationships explaining the relationship between the metamorphosis of the giant nuclei in Eoacanthocephala and worm reproductive cycle. (2) Host-parasite relationships elucidating the relationships between worm anatomy and biology during worm growth. (3) Curiosities in reviews and revisions highlighting taxonomically based zoo-geographical patterns and trends in the genera *Neoechinorhynchus*, *Polymorphus*, and *Pallisentis*. A comprehensive treatment of the acanthocephalans of South America and those marine forms off the Eastern United States is also included here.

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A clash of clades: Conflict in phylogenetic signal between scolex morphology and proglottid anatomy.

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This work aims to expand the understanding of the “tetraphyllidean” group Clade 4 as part of an effort to resolve the non-monophyletic order “Tetraphyllidea.” In addition, newfound diversity within Clade 4 proves to be an excellent system for investigating the evolutionary intrigue surrounding the phylogenetic signal of proglottid anatomy versus scolex morphology. Specimens were prepared for light microscopy and scanning electron microscopy. Sequence data were generated for multiple orthogroups for 15 members of the clade as part of a larger project. The phylogenetic relationships for Clade 4 were extracted from an ASTRAL tree of the larger analysis. Examination of material from previous global collections of batoids yielded cestode specimens from 13 species in the elasmobranch families Dasyatidae, Glaucostegidae, Myliobatidae, Pristidae, and Rhinidae. Morphological and phylogenetic analyses revealed 15 undescribed species. These taxa grouped robustly with representatives of the genus *Pithophorus* (Southwell 1925) included in the phylogenetic analysis. Morphology and tree topology suggest three potential subclades within Clade 4. When the conflicting proglottid anatomies and scolex morphologies seen in these specimens were mapped onto the tree, proglottid anatomy was congruent with the topology. The monophyly and morphological diversity of Clade 4 suggest it is a candidate for establishment as a new order. However, further investigation into additional host species is required for a more comprehensive understanding of the clade. Proglottid anatomy, rather than scolex morphology, was found to reflect the phylogenetic relationships of this group.

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Morphological and molecular characterization of adult hairworms (Phylum Nematomorpha) from Iceland and the Faroe Islands and documentation of their non-adult stages and hosts.

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No species of freshwater Nematomorpha have been described from Iceland, but they have been identified anecdotally. Recent surveys in Iceland using freshwater gastropods as biodiversity indicators resulted in the collection of adult free-living hairworms and their non-adult stages including cysts in snail paratenic hosts and juvenile worms in ground beetle definitive hosts. Additionally, specimens acquired from the Icelandic Institute of Natural History indicate nematomorphs are common in Iceland. A single specimen from the Faroe Islands National Museum represents a new species record. Our morphological and molecular characterization indicated all the samples belong to the species *Gordionus wolterstorffii*, a common nematomorph found throughout Europe. Also, we provide the first descriptions of the cyst stage for the genus *Gordionus*. Molecular phylogenetic analysis based on 10 species of *Gordionus* and one species of the closely related genus *Parachordodes* indicates that *Gordionus* is not monophyletic. Combining our morphological and phylogenetic investigations, we discuss the lack of clarity in diagnostic morphological characters and the need for additional global collections to clarify the taxonomy of *Gordionus*.

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Chemical cues drive density dependent prophylaxis in freshwater snails.

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Despite the benefits of animal aggregation, this behaviour may also lead to higher risks of parasite infection as group density increases. Investment in immunity is moderated by some species relative to the risk of infection (group density), which is also known as density-dependent prophylaxis (DDP). Yet, although DDP is documented in many taxa, the mechanisms driving DDP remain poorly understood. Freshwater snails serve as required hosts for many parasites as well as forming large aggregations and experiencing fluctuations in density. Additionally, chemical cues are used by snails to aggregate. To investigate if freshwater snails exhibited DDP and investigate the role that chemical signaling compounds may play as a mechanism for this phenomenon, we set up a series of four experiments on the freshwater snail *Stagnicola elodes*, which is a common host for many trematode parasite species. We first tested if DDP in snails was present in lab conditions (control vs snail-conditioned water), and if differences in exposure to chemical cues affected snail immune function. We then characterized the fatty acids in snail-conditioned water to determine what signaling molecule precursors were present. Third, we characterized the chemical cue group, oxylipins, released by infected and uninfected snails. Finally, we exposed snails to specific oxylipins to test their ability to induce an immune response. In our first experiment, snails exposed to water with higher densities of snails and those that were raised in snail-conditioned water had higher haemocyte counts. Our lipid analysis demonstrated that fatty acid molecules that are also oxylipin precursors were detectable in snail-conditioned water. Additionally, trematode-infected snails emitted 50 oxylipins in higher amounts, with 24 of these oxylipins only detected in this group. Lastly, naïve snails that were exposed to oxylipins that were higher in infected snails induced higher immune responses compared to sham-exposed snails. Together, our experiments provide evidence that not only do snails exhibit DDP, but the changes in oxylipins emitted by infected hosts may be one of the molecular mechanisms driving this phenomenon.

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Process Development of Sj-p80: A Low-Cost Transmission-Blocking Veterinary Vaccine for Asiatic Schistosomiasis.

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Asiatic schistosomiasis caused by *Schistosoma japonicum* is a neglected tropical disease resulting in significant morbidity to both humans and animals - particularly bovines - in endemic areas. Infection with this parasite leads to less healthy herds, causing problems in communities which rely on bovines for farming, milk and meat production. Additionally, excretion of parasite eggs in feces perpetuates the life cycle and can lead to human infection. We endeavored to develop a minimally purified, inexpensive, and effective vaccine based on the 80 kDa large subunit of the calcium activated neutral protease (calpain) from *S. japonicum* (Sj-p80). Here we describe the production of veterinary vaccine-grade Sj-p80 at four levels of purity and demonstrate in a pilot study that minimally purified antigen provides protection against infection in mice when paired with a low-cost veterinary adjuvant, Montanide™ ISA61 VG. Preliminary data demonstrate that the vaccine is immunogenic with robust antibody titers following immunization, and vaccination resulted in a reduction of parasite eggs being deposited in the liver (23.4–51.4%) and intestines (1.9–55.1%) depending on antigen purity as well as reducing the ability of these eggs to hatch into miracidia by up to 31.6%. We therefore present Sj-p80 as a candidate vaccine antigen for Asiatic schistosomiasis which is now primed for continued development and testing in bovines in endemic areas. A successful bovine vaccine could play a major role in reducing pathogen transmission to humans by interrupting the parasitic life cycle and improving quality of life for people living in endemic countries.

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Modulation of thioester-containing proteins (TEPs) upon immune stress in the *Biomphalaria glabrata* embryonic (Bge) cell line.

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Thioester-containing proteins (TEPs) are a diverse family of proteins characterized by the presence of specific domains used to bind and target foreign molecules. TEPs have been found to serve significant defensive roles in many invertebrates including *Biomphalaria glabrata* snails. These fresh water snails serve as one of the main intermediate hosts for the human parasite *Schistosoma mansoni*. In this study, we utilized the *B. glabrata* embryonic (Bge) cell line as an *in vitro* model to better understand snail host-schistosome interactions and to define the potential role of TEPs in defense against specific pathogens. For this purpose, we tested the modulation of TEP genes in Bge cells in response to four types of microbial products (lipopolysaccharide, peptidoglycan, beta-glucan, and *S. mansoni* larval transformation products or LTPs). Gene expression for TEPs and several transcription factors associated with immune pathways including dorsal-related immunity factor (Rel/DIF), Relish, signal transducer and activator of transcription (STAT), and cAMP response element-binding protein (CREB) was tested after 2-, 4-, and 12-hr post-exposure to the microbial stress using real time quantitative PCR. Results showed differential constitutive expression of the various TEPs in Bge cells, with A2M-1 and C3-1 having the highest level of expression, while C3-2 and TEP-1 had the lowest. Furthermore, preliminary time-exposure results showed that TEP-1 was significantly up-regulated 4-hr post-exposure to peptidoglycan and that a trend of down regulation was observed on transcription factors Rel/DIF, Relish, CREB, STAT regardless of the immune stress. These studies aim to characterize the specificity of TEPs and their associated signaling pathways in Bge cells, which can be further used as an important resource to better understand the humoral immune components of *B. glabrata* snails.

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Host preference of *Phasmarhabditis californica* on three pest slug species.

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Phasmarhabditis (Family Rhabditidae) is a genus of parasitic nematodes that infect terrestrial slugs. Among them, *Phasmarhabditis hermaphrodita* has been well studied and is currently commercially available as a biocontrol product (Nemaslug®). In Canada, the use of *P. hermaphrodita* has not been possible as there are no records of this nematode in the region. However, the recent isolation of a new strain of *Phasmarhabditis californica* from Alberta, offers opportunities to study this nematode as a potential bio-control agent in Canada. I evaluated the host preference of this nematode against three slug species namely, *Deroceras reticulatum, Arion fasciatus* and *Arion rufus*. Chemotaxis- choice test experiments were performed in 9 cm petri dishes. Foot mucus (0.01g) were swabbed from select adult slug species and tested against a control (distilled water) or the foot mucus of another slug species. Fifty dauer larvae of *P. californica* were placed in the middle of each agar plate and incubated at 16°C in the dark for 24 hr. The procedure was repeated 20 times. The number of nematodes found near each cue was counted and the attraction index (AI) for each host species was calculated. The AI values suggest that *P. californica* prefers both *D. reticulatum* and *A. fasciatus* cues over the control. However, when compared with a control, there was no significant difference of the attraction indices between *D. reticulatum* (AI=0.279) and *A. fasciatus* (AI=0.406), suggesting equal attraction to both host species. In addition, two choice tests were performed between *D. reticulatum* against *A. fasciatus* and *D. reticulatum* against *A. rufus*. In both cases, *P. californica* prefers *D. reticulatum* over the two *Arion* species tested. Up to date, the only nematode molluscicide product, the Nemaslug®, is not available for many countries in the world including Canada. Therefore, in support of the potential development of a biocontrol product in the future, this study establishes the baseline knowledge of the novel Canadian strain of *P. californica*.

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Minimal definitive host presence is sufficient to sustain avian schistosome populations.

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Swimmer's itch (cercarial dermatitis) is no small problem in Northern Michigan, where the avian schistosome *Trichobilharzia stagnicolae* has historically been thought of as the main causative agent of swimmer's itch. The definitive host for *T. stagnicolae* is the common merganser (*Mergus merganser*), which has been targeted for relocation from numerous inland lakes in Northern Michigan as part of efforts to control swimmer's itch by severing the life cycle. With skepticism that *T. stagnicolae* was the sole avian schistosome contributing to swimmer's itch in the region, we sought to measure the effectiveness of this trap and relocate control method in a 2-year study. We assessed three avian schistosome species on four lakes with varying levels of merganser control efforts using quantitative polymerase chain reaction (qPCR). Weekly water samples were collected and initially screened using a pan-schistosoma qPCR assay. Positive samples were then secondarily assessed using species-specific qPCR assays for three prominent avian schistosomes known to be present in Northern Michigan; *T. stagnicolae*, *T. physellae* and a newly discovered swimmer's itch-causing parasite that cycles through *Planorbella trivolvis* snails and the Canada Goose (*Branta canadensis*). Our data suggest that despite their geographical proximity to each other, each study lake differed with respect to the profile of swimmer's itch-causing parasites. That *T. stagnicolae* remained the dominant avian schistosome at the lake at which merganser relocations had been occurring for the three years prior to our study indicates that definitive host relocation was not a successful approach for controlling this parasite for this lake. On the two lakes where no control efforts took place, the novel avian schistosome species was the dominant parasite, which would have rendered merganser relocation irrelevant with respect to swimmer's itch control. We hypothesize that the lack of effect on avian schistosome populations by

these control efforts is presumably due to the variety of swimmer's itch parasite species present at the study lakes and the contribution of migratory and non-resident mergansers.

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Parasite communities of freshwater mussels of Texas.

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The decline in populations of 70% of freshwater mussels is a global conservation concern. In Texas alone, 15 out of ~52 species have been recently listed. Parasitism rates are not well characterized, although some parasites such as trematode parthenitae likely cause castration and affect mussel fitness. This research aims to investigate the parasite communities of mussel species, emphasizing trematode parthenitae and factors affecting infection. Collections occurred on San Saba River from April to November 2021 and Sabine River in August 2021. Mussels were transported to the lab and kept in aquaria until dissection. Helminth and mite parasites were counted and collected. Generalized Linear Models were used to identify factors (collection date, collection site, host species, host weight, and host length) affecting prevalence and abundance of each parasite. Bucephalid sporocysts were found in *Cyclonaias petrina* (8/15), *Cyclonaias pustulosa* (2/11), *Leptodea fragilis* (1/1), and *Tritogonia verrucosa* (2/31), while *C. pustulosa* (1/11) and *T. verrucosa* (2/31) were infected with gorgoderid sporocysts. Gorgoderid metacercariae were found in *C. petrina* (3/15), *C. pustulosa* (6/11), *Lampsilis teres* (1/1), *T. verrucosa* (6/31), and *Truncilla truncata* (1/1). An unidentified metacercaria was found in *C. pustulosa* (2/11) and *T. verrucosa* (2/31). No factors tested affected infection patterns of either type of sporocyst or metacercariae. *Aspidogaster* sp. was observed in all mussel species except *La. bracteata* and *Obliquaria reflexa*, and abundance varied among collection sites. *Cotylapsis* sp. was found in all mussel species except *C. pustulosa*, *La. bracteata*, and *Le. fragilis*, and abundance increased with mussel weight. Unionicolid mites infected all mussel species; however, abundance decreased with mussel weight. Therefore, mites may be negatively affecting the body condition of mussels. Of the two imperiled species, *La. bracteata* and *C. petrina,* only *C. petrina* contained gonad-infesting trematodes at a high prevalence which may negatively impact population persistence.

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Latitudinal gradients in parasite diversity of the striped shore crab, *Pachygrapsus crassipes*, throughout its two coastal habitats.

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The striped shore crab, *Pachygrapsus crassipes*, is highly unusual as it is purported to regularly use two very distinct types of coastal habitats throughout its range. In low-energy estuarine habitats, *P. crassipes* lives on mud, frequently occupying high intertidal burrows in the banks of channels and vegetated marsh. In contrast, in the high-energy rocky intertidal zone, *P. crassipes* lives on rock, inhabiting high and mid-intertidal crevices and tidepools. The crab's common use of two distinct habitats throughout its range provides a striking opportunity to examine latitudinal variation in parasite diversity and load while simultaneously examining the influence of habitat on parasitism. In the summers of 2018 and 2019, we quantified parasitism by animal and several protozoan parasites in 327 *P. crassipes* crabs collected from 13 estuarine and 23 rocky intertidal localities throughout its North American Pacific Coast geographic range from Ecola State Park, Oregon (45°55'10.0"N; 123°58'25.6"W) to Bahia Magdalena, Baja California Sur, Mexico (24°47'51.8"N 112°06'56.1"W). We reveal that parasite diversity was approximately two-fold higher in estuary versus rocky intertidal habitat. This finding is consistent with the hypothesis that some biotic interactions are more intense in lower flow/less turbulent environments. We further

demonstrate that parasite diversity followed the general latitudinal diversity gradient in the rocky intertidal habitat, while, in estuaries, parasite diversity peaked near the host's range center. Interestingly, when diversity is broken up by functional parasitic consumer strategies—species diversity within all parasitic groups increased towards the south—with the exception of trophically transmitted parasites in the estuary, which peaked near the range center. Furthermore, the general increase in diversity at southern latitudes was largely driven by the accumulation of trophically transmitted parasite species. This finding is consistent with the general expectation that trophic interactions are more intense in the tropics. Hence, our study provides a novel documentation of spatial patterns of parasitism—expressed with different currencies and diversity metrics—throughout the entire geographic range of a crab species that inhabits two distinct coastal habitats.

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Telling Science Stories through Comics.

Caroline Hu
Harvard University, MA, USA

Caroline Hu is a staff scientist at Harvard University and comics artist. In this talk, she will introduce the comics medium and how it can make scientific concepts more accessible. Furthermore, she will discuss how to find and construct story structures from scientific papers, as well as everyday life as a scientist.

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Aesthetics and Abstraction in Making Parasite Art.

Mona Luo

Parasites present a fascinating subject for artistic interpretation due to their complex relations with other organisms. Between indirect life cycles, host pathology, and unique morphology, the question of what to unpack and how can become overwhelming, especially for audiences unfamiliar with the subject. Through a presentation of various art projects with different target audiences, we can examine the value of aesthetics and abstraction in depicting certain aspects of the parasitic lifestyle. Among these projects are traditional depictions of lifecycle diagrams, parasite Valentine's cards, and fine arts approaches to the world of parasites. A picture may be worth a thousand words, but often even that doesn't feel like enough. Therefore, it is imperative to find the appropriate visual language that is both descriptive and captivating.

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Finding a Niche: How Symbiosis Helped Me Find My Place in The World Of Science Communication (SciCom).

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The COVID pandemic has provided us with a recent example of the importance of educating the general public about science. While scientists are a logical choice as spokespeople for science, the skills needed to clearly communicate information to a general public are often quite different from the skills we acquire during our training as scientists. In this session, I will talk about how I became interested in SciCom, how I've acquired skills for SciCom, and my experiences with podcasting, public speaking, and writing books for a general audience. I will also talk about how collaborations with other scientists and with artists have helped me communicate science more effectively.

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A comparative study of body lice and bed bugs reveals factors potentially involved in differential vector competence for the relapsing fever spirochete *Borrelia recurrentis.*

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While bed bugs (*Cimex lectularius* L.) are not established vectors of any human pathogens, a recent study reported that they may be competent vectors of *Borrelia recurrentis*. However, many aspects of infection and transmission remain unclear in this possible secondary vector. Here, we carried out several quantitative laboratory studies to gain a better understanding of the host suitability of bed bugs relative to the established body louse vector as well as the factors that may affect the ability of bed bugs to transmit the pathogen. We fed bed bugs *B. recurrentis* and estimated the level and duration of infection in the hemolymph using live imaging. We performed qPCR to examine whole body spirochete levels and the occurrence of vertical transmission to progeny. We also developed an assay to compare the amount of force required to release infectious hemolymph from recently engorged bed bugs and body lice. Lastly, we analyzed humoral antibacterial activity in the hemolymph, hemolymph pH, and hemocyte activity in both insect species. Our results confirm that within 24 hours of ingestion *B. recurrentis* can penetrate the midgut epithelium of bed bugs and enter the hemolymph, overcoming a major host barrier, as in body lice. Once in the hemolymph, spirochetes remain visible for at least four days. Moreover, we show that bed bugs are more physically susceptible to crushing than body lice, suggesting that crushing is a feasible route for natural dissemination of *B. recurrentis* from the hemolymph of bed bugs, as for body lice. Nonetheless, our data also indicate that bed bugs are suboptimal hosts for *B. recurrentis*, as the bacterium does not appear to proliferate to high levels or stably colonize the hemolymph and exhibits pleomorphism in this environment. In particular, our data suggest that hemolymph pH and unique cellular immune responses, rather than humoral effectors, may be involved in limiting spirochete survival in bed bugs. Notably, we document the formation of extracellular DNA traps by bed bug hemocytes for the first time. For these reasons, while bed bugs may be capable of limited transmission given their ecology, vector competence is probably minimal relative to body lice.

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Parasitic mites induce non-consumptive effects in cactophilic flies.

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University of Alberta, Edmonton, Canada

When predator-prey interactions end in the predator eating a prey, this can decrease the prey population size. However, the mere presence of predators can have non-consumptive effects on the prey. These effects are known cumulatively as the 'ecology of fear' and can include changes in prey behavior, appearance, and body functions. The ecology of fear can be applied to parasites as well: flies (*Drosophila nigrospiracula*) exposed to parasites (*Macrocheles subbadius*), without direct contact or infection, suffered shorter lifespan and lower fertility, but why those decreases occurred is unclear. We explored whether parasite avoidance behaviors such as increased grooming or vigilance trade off with feeding in the fly-mite system. When exposed to mites, flies increase their defensive grooming behavior at the expense of feeding, which may then have impacts on their fitness. I also investigated how previous exposure to parasites (prior to sexual maturity) impacts parasite avoidance behaviors due to learning or habituation. I conducted 2x2 factorial experiments, where previous exposure and current exposure differed. Previous exposure consisted of exposing newly emerged flies to mites for 5 days. Scans to assess behavior were performed every minute for an hour on 8-day-old unmated females. GLMs and negative binomial regression analyses showed that mite presence increased grooming at the expense of feeding. Preliminary data shows that previously exposed flies exhibited a stronger response

than naive flies. Parasites have a potentially larger impact on host populations than previously documented.

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Synthesis of reactive oxygen species provides protection to bacterial infection in the gut of cat fleas (*Ctenocephalides felis*).

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Fleas (Order Siphonaptera) are opportunistic blood feeders that parasitize a wide variety of mammals and birds. They are also competent vectors of numerous bacterial pathogens that cause severe human diseases (e.g., murine typhus, flea-borne spotted fever, cat scratch disease, and plague). Because they acquire infectious pathogens while blood feeding, the immune response in the flea gut is thought to be the first line of defense against invading microbes. While immune responses have been well documented in other disease vectors, few studies have identified the immune mechanisms that effectively resist or limit infection in the flea. In other hematophagous insects, the synthesis of reactive oxygen species (ROS) is the immediate immune defense mechanism against foreign microbes. To investigate the role of ROS in flea gut immunity, cat fleas (*Ctenocephalides felis*) were orally infected with a well-known insect bacterial pathogen, *Serratia marcescens*. Specifically, fleas were treated with an antioxidant to reduce the amount of microbicidal ROS before infection, and subsequent *S. marcescens* infection loads were measured. Additionally, we measured hydrogen peroxide (ROS) levels, and the relative quantity of mRNA for select genes associated with DUOX, a surface protein of epithelial cells responsible for ROS production. Four experimental groups were examined: (1) *S. marcescens*-infected fleas; (2) fleas fed an antioxidant; (3) fleas fed an antioxidant and then infected with *S. marcescens*; and (4) fleas fed on untreated blood (control). Overall, our data shows that ROS levels in the flea gut increase in response to bacterial infection, and ultimately decrease *S. marcescens* loads through their microbicidal activity. Moreover, transcriptional profiles show differential expression of select genes in the DUOX pathway following bacterial challenge. Given these results, this study provides evidence that ROS is a key mechanism for early gut defense in cat fleas.

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Effects of Photosensitive Insecticides (PSIs) on life history traits and population survival of *Anopheles gambiae* mosquitoes.

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Classical insecticides are applied ubiquitously across the globe to minimize the transmission of insect-borne disease, yet their application has deleterious effects on the surrounding environment. A promising class of insecticide, photosensitive insecticides (PSIs), is an environmentally sustainable alternative to classical insecticides, yet the long-term consequence of their application on insect populations remains unclear. Here, we assessed the toxicity of two potential PSIs, Methylene Blue and Rose Bengal, on the *Anopheles gambiae* mosquito. Both Methylene Blue and Rose Bengal demonstrated larvicidal activity, achieving 100% mortality. PSI toxicity increased with food abundance yet was ineffective against the pupal life stage of the mosquito, indicating an ingestion dependent mechanism of toxicity. Currently, we are investigating the long-term consequences of PSI exposure on various life history traits. After larvae are exposed to a sub-lethal concentration of a PSI, treatment with Methylene Blue – but not Rose Bengal – accelerates the rate of pupation, but neither PSI appears to affect longevity, eclosion rate, nor pupal mortality relative to untreated larvae. Further work investigating life history traits following PSI treatment will further enhance our understanding of the long-term consequence of PSI application towards mosquito populations.

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The miRNA profiles of a specialist, *Rhipicephalus (Boophilus) microplus*, and generalist, *Ixodes scapularis*, tick during feeding.

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Ticks are important vectors of pathogens that can affect livestock, domestic animals, wildlife, and humans. The cattle fever tick, *Rhipicephalus (Boophilus) microplus*, is a one-host tick that feeds on ruminants, like cows, nilgai, and deer. The black legged tick, *Ixodes scapularis*, is a three-host tick that can feed on small and large animals and humans. During feeding, ticks release extracellular vesicles (EVs) via their saliva. EVs are essential for the transportation of intracellular cargo, such as microRNAs (miRNAs). miRNAs are short, ~18-22nt, non-coding RNA that can alter the host's gene expression at the tick-host interface. The focus of this study was to compare the EV and salivary gland miRNA profiles between a specialist and generalist tick during 3 days of feeding. We hypothesize there will be a greater number of unique miRNAs found in the saliva of *R. microplus*, due to the co-evolution with their ruminant host. In contrast, we hypothesize that *I. scapularis* will have a greater number of conserved miRNAs, due to their ability to feed on multiple hosts. This comparison will provide us with a clue of how salivary miRNAs profiles adapt during specialization of an arthropod.

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Transglutaminase-based modulation of the physiological interaction between the immune and circulatory systems of mosquitoes.

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The immune and circulatory systems of mosquitoes are functionally integrated. An infection induces the aggregation of immune cells called hemocytes on the surface of the heart, where they phagocytose and kill pathogens in areas of high hemolymph flow. In a recent RNAseq study on the mosquito *Anopheles gambiae*, we uncovered that mosquito transglutaminases are preferentially expressed in the heart-associated hemocytes, called periostial hemocytes, relative to the circulating hemocytes or the entire abdomen. In this presentation, we will discuss follow-up experiments showing how transglutaminases are involved in modulating heart-associated immune responses and circulatory physiology. Specifically, we found that TGase3 plays a negative role in (i) periostial hemocyte aggregation during the early stages of infection and (ii) the sequestration of melanin by periostial hemocytes during the later stages of infection. Moreover, we will present the results from ongoing experiments assessing the role that transglutaminases play on heart contraction dynamics. Overall, the data demonstrate that transglutaminases modulate the physiological interaction between the immune and circulatory systems of mosquitoes

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Patterns of gene expression in wood ants infected with larvae of the iconic manipulator *Dicrocoelium dendriticum.*

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Wood ants infected with larvae of the lancet liver fluke, *Dicrocoelium dendriticum*, leave their nests during the cool hours of the day, ascend an herbaceous plant, and then attach themselves to a flower petal with their mandibles. Infected ants remain attached to the flower petal overnight, detach the next morning when temperatures rise, and return to their nest. They repeat this bizarre attach/detach

sequence for the rest of the summer. Uninfected ants from the same nest have not been observed to engage in these odd behaviors. During the manipulation, ants do not forage, do not defend themselves from predators, and do not perform typical worker duties for their queens. We seek to understand the mechanisms that underlie this complex manipulation of host behavior. Using a transcriptomic approach, we compared the gene expression pattern of brains from infected and uninfected *Formica aserva* collected from a site of liver fluke emergence in southern Alberta, Canada. With a lab set-up, we recreated the manipulation cycle to mimic pre-attached, attached, and post-attached stages, and sampled infected and uninfected ant brains from each stage for differential gene expression analysis. We found a total of 3295 genes that were differentially expressed between infected and uninfected ants, including those involved in environmental sensing (odorant, vision, gustatory), circadian rhythm, immune response, muscle contraction, the production of biogenic monoamines, and certain hormones. We found genes involved in odorant and vision were downregulated in attached infected ants. Vision genes were upregulated in post-attached infected ants compared to uninfected controls. We also found muscle genes were upregulated in infected ants during the pre-attached stage and then downregulated at the post-attached stage. Genes involved in serotonin synthesis were also downregulated during the post-attached stages in infected ants. These results suggest that the regulation of biogenic monoamines (e.g., serotonin) in the brains of infected ants plays a role in this complex manipulation of host behavior. Overall, this study helps us better understand how *D. dendriticum* manipulates their ant host behavior.

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Ivermectin formulation and body location affect *Anopheles stephensi* feeding rate, survival, and reproduction when fed on treated cattle.

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Ivermectin is the most widely used endectocide in the world. It is available in several different formulations and is effective on both internal and external parasites. To test how ivermectin distributes in the body and the formulations' effect on drug effectiveness, calves were treated with either a topical or injectable form of ivermectin. *Anopheles stephensi* mosquitoes were fed on different body locations on calves, and mortality, blood meal digestion, and ovarian development were recorded for 2-, 5-, 9-, 14-, and 23 days post treatment. Blood was also drawn from treated calves at these time points and the sera tested for ivermectin concentration. Injectable and topical ivermectin both reduced mosquito survival until day 14 post treatment, no matter where they fed on the body. Mosquitoes fed on topically treated calves near the site of application experienced a reduction in survival on day 23 post treatment. Mosquitoes fed on calves injected with ivermectin experienced a delay in blood meal digestion and ovarian development until day 14 post treatment. Mosquitoes fed on calves treated with topical ivermectin experienced delays in blood meal digestion and ovarian development at day 23 post treatment. Ivermectin concentration decreased in the sera over the course of the experiment, even though mosquitoes feeding on topically treated calves still experienced significant mortality at day 23 post treatment near the application site. While both formulations reduced survival and fecundity, topically applied ivermectin had longer residual efficacy compared to injectable ivermectin. Therefore, topical ivermectin would be the optimal choice when implementing ivermectin-based vector control.

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Characterization of flatfish gut microbial communities, parasitic infection levels, and health indices across a gradient of wastewater effluent exposure in Santa Monica Bay.

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Flatfish live in contaminated marine sediments where pollutants like heavy metals and chlorinated hydrocarbons accumulate near wastewater discharge sites. Parasitic infection can influence how fish respond to pollution by increasing or decreasing the susceptibility of hosts to the effects of wastewater pollutants. The fish gut microbial community composition can serve as a useful additional measure to standard physiological stress markers. Gut microbes play a pivotal role in host health by regulating homeostasis, immunity, metabolism, and susceptibility to environmental contaminants. The gut microbiome may be influenced by parasitic infection and pollutant exposure. The Hyperion Water Reclamation Plant in Santa Monica Bay (SMB) is the largest wastewater treatment plant in the western United States, and has historically contributed millions of gallons of domestic, commercial, and industrial treated effluent daily into the bay. Pacific sanddabs, *Citharichthys sordidus*, were collected from Santa Monica Bay and analyzed for parasites, gut microbiota, and fish health indices. Fish gut bacterial and archaeal composition were characterized using 16S ribosomal RNA gene sequencing, fish were dissected and intestinal parasite and ectoparasite taxa were counted, and body indices (liver somatic index and body condition factor [weight to length ratio]) were recorded. With 100% of fish infected with tapeworms at wide-ranging intensities, I hypothesized that there would be significant changes in gut microbial community composition along a pollution gradient and among fish with different parasite loads. Several bacterial genera had greater relative abundance in sites near the Hyperion wastewater outfall pipe, particularly *Peptoclostridium*, a pathogen that is associated with wastewater sludge. Similarly, distance from the outfall had significant effects on bacterial community composition. Parasite load did not appear to effect gut microbial community composition, however, there were specific bacterial genera that were associated with higher parasite loads. Identifying these sensitive indicators of trace pollutant exposure can be useful for detecting early signals of population and ecosystem-level responses in coastal marine environments.

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Taxonomic and trait-based approaches in the assessment of flounder metazoan parasite communities as indicators of chemical pollution in the Gulf of Mexico.

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Metazoan parasite communities are good bioindicators of chemical pollution in marine environments. However, a problem faced during the study of these communities has been that with the increase in geographical distance between sampling sites, their taxonomic species composition and their relative abundance change. In contrast, the functional traits of the species (e.g., transmission, feeding mode, life stage) do not change, apparently because distant sites with similar characteristics (e.g., nutrient levels, bathymetry, pH, etc.) may have similar selection forces for the species forming those communities. Thus, we aimed to compare the performance of the taxonomic and functional trait-based approaches as bioindicators of chemical pollution along the continental shelf of the Mexican part of the Gulf of Mexico. Parasite data were obtained from 152 *Syacium gunteri* and 483 *Syacium papillosum* from 38 and 55 sites, respectively, sampled during 17 oceanographic cruises. At each site, environmental variables were measured, including hydrocarbons, heavy metals, and physicochemical variables from water and sediments. The data were divided into three regions: Tamaulipas-Veracruz, Tabasco-Campeche and Yucatan shelf. In addition to traditional taxonomy, the trait-based approach community-weighted means (CWM) was performed. For analysis, we used PERMANOVA with regions and hosts as factors, SIMPER and BIOENV. Sixty-five metazoan parasite species were identified for the three regions, and five traits were used: body tegument, transmission, feeding mode, life stage and attachment organs. Significant spatial parasite community variability was detected by PERMANOVA using the taxonomic and CWM trait-based approaches for all regions, hosts, and the interaction of both factors. The exception

was the Yucatan shelf where no differences between hosts were found. The SIMPER analysis for regions and hosts showed the same group of frequent and abundant parasite species but in very different numbers. Finally, the BIOENV analysis showed that the environmental variable explaining most of the variability among regions were polyaromatic hydrocarbons. Thus, our results showed that species and functional groups produced similar results. However, using functional groups, the time and financial resources were minimal compared with those used for taxonomy. Thus, functional groups are the best choice for saving time and money in environmental studies.

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Habitat fragmentation influences amphibian skin microbiome composition, helminth parasitism, and disease status in the Brazilian Atlantic Forest.

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Habitat destruction is one of the greatest modern threats to wildlife, particularly in biodiversity hotspots like the Brazilian Atlantic Forest. In heterogeneous landscape, habitat fragments are frequently left in areas that are less desirable for farming, allowing for persistence of certain wildlife populations. However, these populations are now faced with the stressors of reduced genetic diversity due to reduced population sizes, increases in disease due to increased population densities, and an overall reduction in complex community interactions due to community simplification. For this study, we collected samples from Blacksmith Tree Frogs (*Boana faber*) across 3 sites in continuous forest and 3 forest fragments to see the effects of habitat fragmentation on microbiome composition, helminth parasite diversity, and disease status. We aim to discover how helminth infection may be priming the immune system against further pathogen infection or alternatively overloading the immune system allowing for high pathogen loads. We also aim to find out what role the skin and gut microbiome play in this complex dynamic.

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Avian hosts and landscape drive parasite prevalence in the Caucasus Mountains.

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Avian haemosporidia are blood parasites that negatively impact bird populations across the globe. Although these parasites are of great concern for avian conservation, there is currently little understanding of how a variable landscape influences prevalence rates of avian haemosporidia. With this in mind, we explored the interactions between three avian host species (*Phyloscopus nitidus*, *Phyloscopus lorenzii*, and *Phyloscopus collybita*), haemosporidian parasites, and the landscape in an undersampled region (The Caucasus mountains). We hypothesized that avian haemosporidian prevalence would be driven by avian host in conjunction with landscape and environmental variables (e.g., elevation, vegetation, precipitation, and temperature indices). We found a combined overall infection prevalence of 16.5% , where *P. nitidus* had the highest infection prevalence of 29.9%, followed by *P. collybita* with 20%, and *P. lorenzii* with just 5.9%. Of the haemosporidian genera, *Haemoproteus* was the most common lineage, followed by *Plasmodium*, then by *Leucocytozoon*, and this was consistent across avian host species. Of the 10 parasite lineages identified in this study, 9 were found to be novel. Linear regression models identified that avian host, vegetation and precipitation indices were most important for predicting parasite prevalence. These findings indicate that haemosporidian prevalence is driven by both avian host and the landscape as well as highlight the importance of sampling understudied regions.

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Genetic mapping of an adaptive parasite trait: larval release time in schistosomes.

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To maximize their transmission, parasites may synchronize release of infective stages to coincide with activity patterns of their hosts. Rhythmicity of parasite behaviors is well documented but little is known about the underlying molecular mechanisms. Schistosome blood flukes show specific behavior when infecting humans: the shedding of infective cercaria larvae from the intermediate snail host is synchronized with daily water activities of humans. We staged two-independent three-generation crosses between two *Schistosoma mansoni* populations showing either day cercarial shedding around 12:00 or night shedding around 20:00. Number of cercariae shed by individual snails was counted each hour for 24 hours. To test the robustness of the phenotype, some snails were repeatedly shed for several days. While 46 F1s showed a main shedding peak around 14:00 with a minor shedding peak around 20:00, 205 F2s showed a shedding peak in-between the parental shedding peaks (from 12:00 to 20:00) with 30% showing a peak at night (after 18:00). Using the proportion of cercariae shed at night, the phenotype showed a robust replication with a correlation of 70% between two sampling days. We genotyped the parents using whole genome sequencing, and the F1s and 133 F2s using exome sequencing. We performed a quantitative trait locus (QTL) analysis to identify the region of the genome controlling the shedding time using the proportion of cercariae shed a night as phenotype. We identified 2 major QTLs on chromosome 1 (LOD = 6.51) and 6 (LOD = 6.61) and a minor QTL on chromosome 5 (LOD = 4.71). The three QTL act additively to explain 21% of the phenotypic variation. Alleles on chromosomes 1 and 6 are co-dominant while alleles on chromosome 5 are recessive. We identified 140, 64, 28 candidate genes that are expressed at the stage of interest (sporocyst or cercariae) on chromosomes 1, 6 and 5, respectively. Some of these are associated with relevant functions for the trait such as cell adhesion/migration, signal transduction, light perception (rhodopsin-like receptor, melanin synthesis). Our future work will aim to identify the genetic and molecular basis of this transmission related trait.

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Prospecting for zoonotic pathogens in museum specimens using targeted DNA enrichment.

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There over 60 zoonoses linked to small mammals, including diseases caused by viruses, bacteria, fungi, helminths, and protozoans. Some of the most devastating pathogens in human history resulted from zoonotic transmission. Examples include Ebola, bubonic plague, HIV and the ongoing SARS-CoV-2 pandemic. Our goal is to maximize the value of museum collections for pathogen-based research. We are developing a high-throughput assay based on targeted, nucleic acid capture using oligo probes which provides an extremely effective approach to identify small amounts of DNA target amidst a sea of background contamination. We are utilizing this approach to capture DNA from a diverse group of human pathogens from museum-archived mammal specimens. Our oligo probe set comprises 39,916, 80bp RNA probes targeting 28 pathogen groups, including bacteria, helminths, fungi, kinetoplastids, and

protozoans. Control experiments with 6 pathogen species indicated ≥ 12,800-fold enrichment of the target pathogen loci and a preliminary application to South African, South American, and Texan mammalian museum specimens identified several pathogens groups including; *Bartonella*, *Litomosoides*, *Campylobacter* and *Pasteurella* species. These probes are highly customizable to target multiple pathogen groups and our approach demonstrates the utility of a single assay for the detection of pathogens from different host species.

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Making sense of sensory behaviors in vector-borne helminths.

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Many parasitic nematodes perform dramatic, patterned migrations that are necessary for mating and reproduction, infection, transmission, and often cause disease pathology. Vector-borne parasites like filarial nematodes engage in particularly complex journeys, during which they must carefully regulate sensory signaling programs to reliably locate discrete host niches at specific developmental time points. The molecular pathways that underpin these behaviors are beginning to be uncovered. Using a diverse set of computational and molecular tools, we identified and annotated thousands of nematode chemosensory receptors and their downstream signaling partners. The core structure of filarial parasite sensory pathways is conserved among nematodes, but the sentinel cue receptors are diverged in accordance with different environmental contexts (i.e., free-living, vector-borne, or host-contained). To enable potential genome-wide analyses of sensory behaviors and substantially augment the collection of known sensory cues, we unveil a novel, reconfigurable microfluidics platform that will enhance the throughput of sensory behavioral assays and is adaptable to nematodes and flatworms, both free-living and parasitic. These data and technologies lay the foundation for a rich future of investigations into helminth sensory processes.

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Preliminary validation of a probe-based qPCR for detection of zoonotic *Onchocerca lupi* in clinical samples of companion animals.

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Onchocerca lupi is a zoonotic filarial nematode that infects wild and domestic canids in southwestern North America and the Old World. In dogs and cats, this nematode is associated with ocular disease, termed ocular onchocerciasis. Conventional PCR (cPCR) is often used to detect *O. lupi* DNA in suspected clinical cases, but alternatively, real-time PCR (qPCR) allows for more rapid results compared to cPCR. To test this hypothesis, 64 clinical samples of dogs (n=60) and cats (n=4) presenting with suspected to be ocular onchocerciasis were submitted by veterinary ophthalmologists or pathologists. The majority of samples were collected from New Mexico. Of these samples, 46 were tissues removed from subconjunctival nodules, 16 were nematode fragments removed from periocular tissues, and two were formalin-fixed paraffin-embedded (FFPE) tissues collected for histopathology. Genomic DNA was extracted using commercial kits, subjected to cPCR followed by Sanger sequencing, and a novel probe-based qPCR protocol. Both PCRs targeted a partial region of the cytochrome oxidase c subunit 1 (*cox1*) of the mitochondrial DNA. As an initial step, we determined the detection limit of the qPCR using 10-fold serial dilutions (1:10 to 1:1,000,000) of a DNA of a morphologically-confirmed adult nematode, generating a standard curve (R^2=0.99). The qPCR's detection threshold line is 0.00377 ng/µL. To further

confirm the specificity of the primers and probe, DNA samples belonging to five different *Onchocerca* isolates of wild North American ungulates were tested, none of which were detected via qPCR. Of the tissue samples, 23 (50%) tested *O. lupi*-positive by cPCR and 22 (48%) tested positive by qPCR. All 16 nematode samples tested *O. lupi*-positive in both cPCR and qPCR. Three tissue samples that produced bands in the cPCR, had sequences matching the canine heartworm, *Dirofilaria immitis*, all of which tested negative in the qPCR. One FFPE sample tested positive in both assays. This novel probe-based qPCR assay was proven sensitive and specific for detection of *O. lupi* in host tissues and nematode specimens, allowing for expedited results when compared to the cPCR, which may positively impact clinical management of infected companion animals.

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A Survey of Pet Caretakers on the Use and Perceptions Regarding Heartworm Prophylaxis for Prevention of Canine Heartworm Disease.

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Canine heartworm disease (CHWD) is caused by infection with the nematode parasite *Dirofilaria immitis* transmitted through the bite of a mosquito carrying the infective stage larva. The disease is insidious in its onset and 100% preventable with the use of highly effective pharmaceutical compounds that target the migrating larval stage acquired from the mosquito. However, use of CHW prophylaxis among pet dog owners is not universally accepted and viewed with skepticism. Previous research conducted in the Cumberland Gap Region (CGR) indicated approximately 40% of dog owning individuals do not make use of prophylactic products. In this study, we surveyed pet dog owners across the United States from October-February to determine reasons for the use or non-use of canine heartworm prophylaxis to prevent CHWD. Results of 312 responses were analyzed from 31 states in the Northeast, Mid-Atlantic, Southeast, Southwest, Mid-West, and Northwest regions of the United States (US), including Puerto Rico (PR). Pet dog owners in the US chose not to give their pets CHW prophylaxis for economic reasons (45%), environmental factors (20%), low perceived risk of CHWD (10%), or subscribe to beliefs associated with a holistic approach to prevention (7.5%). These results allow veterinary professionals to address the educational techniques of heartworm prophylaxis and disease to increase their use and gain better rapport with patients.

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Texas panhandle Coyotes: a Survey of parasites, with a focus on those of Zoonotic importance.

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Coyotes, *Canis latrans*, are native canids to the American plains and deserts, whose range, habitat, and populations have expanded over the past few decades. While fulfilling an important ecological niche, populations have had more negative encounters with humans, domestic animals, and local wildlife. Coyotes are also an important reservoir of zootherionotic and anthropozoonotic pathogens, such as *Dirofilaria immit*is, *Onchocerca lupi*, *Taenia* spp., and *Alaria* spp., to name a few. Their populations have not been studied in the unique ecological niche of the Texas Panhandle, and the threats they may pose to ranching, farming, society, and our domestic animals have not been studied either in this area. We have evaluated 50 coyote carcasses to date for potential parasites of veterinary importance. Carcasses were obtained from the 26-county region defining the Texas panhandle. Complete necropsies were performed, and eyes, respiratory tract, gastrointestinal tract, urogenital tract, muscles, and thoracic and abdominal cavities were explored for potential parasites. Gross specimens were collected for identification, as well as fecal samples for processing. One adult coyote was positive at necropsy for *Dirofilaria immitis.* In regard to fecal testing, five samples were positive for *Ancylostoma caninum*, two

positive for *Toxascaris leonina*, one positive for *Alaria* spp., and one positive for *Cystoisospora canis*. While numbers are low, potentially due to the current and chronic drought conditions in the region where animals were sourced, or population density, these animals are still acting as reservoirs of parasites of veterinary importance in the region, which may increase the risk of transmission to humans and their animals.

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Survey of invasive wild-caught Asian tiger prawn, *Penaeus monodon* (Fabricius, 1798) from the Gulf of Mexico and northwestern Atlantic Ocean for WSSV (White Spot Syndrome Virus), IHHNV (Infectious Hypodermal and Hematopoietic Necrosis Virus), and Taura Syndrome Virus (TSV).

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We screened the gill and somatic muscle of 152 wild-caught tiger prawn, *Penaeus monodon* for white spot syndrome virus (WSSV), infectious hypodermal and hematopoietic necrosis virus (IHHNV), and taura virus using molecular methods (PCR and qPCR) and transmission electron microscopy (TEM). The sampled tiger prawn comprised one freshly-sampled individual from the Mississippi Sound during 2020, 54 tiger prawn from the northern Gulf of Mexico off Mississippi, Alabama, and Florida during 2014 through 2016 and archived (frozen) in the Hill Laboratory, 76 tiger prawn from the northwestern Atlantic Ocean off North Carolina, South Carolina, Georgia, and Florida during 2014 through 2020 and archived (frozen) by the South Carolina Department of Natural Resources Marine Resources Research Institute, and 21 tiger prawn from 1988, 2011 through 2013, and 2016 and archived (all EtOH-preserved except 2 that were initially fixed in 10% neutral buffered formalin [nbf]) in the collection of the Florida Fish and Wildlife Conservation Commission's Fish and Wildlife Research Institute. Molecular viral detection relied upon qPCR with TaqMan chemistry (for WSSV), conventional PCR (IHHNV), as well as rt-PCR (TSV). TEM was performed on viral extracts of WSSV-positive gill. Viral isolation for TEM was performed through gill homogenization in 0.1 M phosphate buffer and isolated in a double cushion sucrose gradient; phosphotungstic acid and uranyl acetate were used as negative stains. A total of 18 tiger prawn were positive for WSSV by qPCR, one was positive for IHHNV by conventional PCR, and none was positive for TSV. TEM confirmed WSSV infection in PCR-positive gill samples using phosphotungstic acid or uranyl acetate for negative staining. This is the first report of a WSSV or IHHNV infection in a wild-caught tiger prawn from the Gulf of Mexico or northwestern Atlantic Ocean. In addition, IHHNV previously had not been reported from any host from the northwestern Atlantic Ocean.

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Don't mess with Texas Ticks: Ticks and their pathogens in the Texas Panhandle.

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Ticks are obligate blood feeders that transmit the most diverse array of protozoan, bacterial, and viral pathogenic agents of zoonotic importance. Over the past four decades, there has been an increase in emergence of tick-borne diseases (TBDs) in the United States. Diagnosis of TBDs continue to rise in West Texas and the Texas panhandle, a region perceived as non-endemic to tick-borne illness. However, there are limited reports of tick surveys and molecular epidemiology of TBDs for different species found in these areas. This study was designed to both identify tick species and utilize molecular screening of these ticks for 10 pathogens collected from 11 counties within the Texas Panhandle in the environment and on horses, dogs, and cats. Our objectives were to identify the species of ticks present in the Texas

panhandle region and to detect and identify the pathogens carried by each tick species. 313 ticks of varying species were collected from animal hosts (n=295), by dragging (n=8) or using dry ice traps (n=10) in 11 panhandle counties. Ticks were identified as five species of hard ticks (*Ixodes scapularis*, *Rhipicephalus sanguineus*, *Amblyomma americanum*, *Amblyomma maculatum,* and *Dermacentor variabilis*) and one species of soft tick (*Otobius megnini*). All ticks were screened using a quantitative qPCR method to identify tick-borne pathogens. 29.1% of the hard ticks were positive for at least one pathogen and 9.5% were positive for multiple pathogens. 2.6% of the soft ticks tested positive for *Babesia* spp. The results of our study contribute to the lacking information on ticks and tick-borne diseases in the Texas panhandle.

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High prevalence of canine heartworm, *Dirofilaria immitis*, in dogs from low- and middle-income communities in South Texas, U.S.A., with evidence of *Aedes aegypti* mosquitoes contributing to transmission.

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The canine heartworm, *Dirofilaria immitis*, a filarioid nematode of dogs and other carnivores is widespread in the United States and the world. Dozens of Culicidae mosquitoes serve as intermediate hosts of *D. immitis*, but their contribution to transmission varies according to factors like host feeding patterns, geographic locations, and climatic conditions. The yellow fever mosquito, *Aedes aegypti,* is a competent vector of *D. immitis* but is often dismissed as an epidemically relevant vector given its anthropophilic feeding behavior. A recent study documented populations of *Ae. aegypti* in South Texas, United States, which fed more frequently on dogs than on humans suggesting their potential involvement in canine heartworm transmission. Here we assess the prevalence of *D. immitis* in dogs and in *Ae. aegypti* in 12 communities in the Lower Rio Grande Valley in South Texas along the U.S.A.-Mexico border from 2016-2019. We tested canine serum samples for *D. immitis* by DiroCHEK Heartworm Antigen Test Kit pre- and post-immune complex dissociations (ICD) by heat-treatment and blood using high-resolution melt (HRM) and a quantitative probe-based PCR. *Aedes aegypti* heads, abdomens, and pools were tested using conventional PCR plus Sanger sequencing and HRM qPCR. Detection of canine infections varied based on diagnostic modality, with 81 (40.5%, n = 200) positive based on post-ICD DiroCHEK; one (0.007%) based on HRM qPCR; and 30 (20.3%, n = 148) based on probe-based qPCR. Overall prevalence in dogs was 42.5% (85/200) when all testing modalities were included. In *Ae. aegypti* abdomens, 20 (21.7%) that fed on dogs and 5 (5.4%) individuals that were previously determined to have fed on other vertebrate species were positive based on conventional PCR followed by confirmation with Sanger sequencing. In *Ae. aegypti* heads, one (1.1%) was positive based on conventional PCR plus Sanger sequencing and three (3.6%) were positive based on HRM qPCR. No *D. immitis* DNA was found in the 208 pools of whole bodied gravid *Ae. aegypti* females (358). Our study highlights a high prevalence of heartworm infection in dogs in South Texas and provides evidence that *Ae. aegypti* could be contributing to heartworm transmission in canine populations in this region.

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Triatomines in kennel environments: Collections by a trained dog, infection with *Trypanosoma cruzi*, and blood feeding hosts.

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Chagas disease is a neglected tropical disease endemic to Latin America and the southern United States. Caused by the protozoan parasite *Trypanosoma cruzi*, Chagas disease manifests as cardiac damage in infected mammals, ranging from chronic disease to sudden death. Triatomine insects, called 'kissing bugs,' are the insect vectors for *T. cruzi*. Identifying ecological interactions between triatomines, *T. cruzi* strains, and mammal hosts is necessary to understand parasite transmission dynamics and effectively intervene to protect animal and human health. In this study, we collected triatomines from 10 multi-dog kennels across four Texas ecoregions over a one-year period (2018-2019). We tested a subset of triatomines from each kennel to determine their *T. cruzi* infection status and identify the primary blood meal hosts. We hypothesized that *T. cruzi* infection prevalence would be equal across kennels, and dogs would serve as a primary blood meal host. Through manual trapping efforts, kennel staff collections, and with the help of a trained triatomine scent detection dog, we collected over 540 triatomines of four species: *Triatoma gerstaeckeri* (n=519), *Paratriatoma lecticularia* (n=15), *T. sanguisuga* (n=6), and *T. indictiva* (n=2). The number of triatomines collected from each kennel ranged from three to 240 bugs. Importantly, the trained dog collected 30 triatomines, including nymphs, from areas where kennel owners had been unable to locate the vectors. Using qPCR, we found a *T. cruzi* infection prevalence of 50% (80/159) with no significant predictors of the level of infection based on kennel, triatomine species, year of sampling, or geographic location based on ecoregion. Insects were infected with two *T. cruzi* discrete typing units: TcI (65%), TcIV (22%), or a mixed TcI/TcIV infection (13%). We determined the blood meal hosts of 39/103 triatomines using PCR and Sanger sequencing. We found 34 triatomines (87%) fed on a canine, and one triatomine each fed on a cat, raccoon, black rat snake, chicken, or pig. Infected triatomine populations are regularly interacting with dogs in these kennel environments, and dogs are serving as an important host for maintaining and possibly infecting triatomines, indicating dogs may be an apt target for future *T. cruzi* intervention efforts.

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Phenology and environmental predictors of dispersal activity of adult *Triatoma sanguisuga* – vector of the Chagas parasite - in Central Texas.

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Chagas disease is a neglected, zoonotic disease caused by the protozoan *Trypanosoma cruzi* and is the leading cause of parasitic heart disease across the Americas. The parasite is transmitted by blood-feeding triatomine insects (kissing bugs) which are endemic across South and Central America, Mexico, and the southern US. In Texas, there is increasing awareness for local transmission to humans and dogs, but the seasonal activity and climatological predictors of the insects remain poorly understood. Our objective was to characterize the phenology, abundance, and selected environmental predictors of dispersal activity of *Triatoma sanguisuga* - the eastern bloodsucking conenose – which is the most epidemiologically important triatomine of the eastern US. From June- November 2020, we conducted active, manual timed searches for triatomines every other night around a building with outdoor lights in Brazos County, TX, with a history of triatomine occurrence and infestation. Each of 78 search sessions lasted two hours, with weather conditions and insect collections tallied every 20 minutes. Specimens were morphologically identified to species and sex. To determine environmental predictors of activity we used negative binomial regression with total triatomines seen per night as the outcome and weather conditions as the explanatory variables. With a total of 185.5 person hours, we found 176 kissing bugs

(1.05 triatomines/person hour):104 females; 65 males; 7 unknown sex; all *T. sanguisuga* adults. The earliest and latest triatomine encounters were June 4th and October 23rd, respectively. The peak of activity was the first week of August with 2.7 triatomines/person hour. Windspeed ranged from 0 to 32 km/h and increased speed was associated with a decrease in the expected log-counts of triatomines, while temperature (range 8-33 C°) and humidity (32%-99%) increases were associated with increases in triatomine findings. Given ongoing and future changes in the climate, understanding how climate impacts vector behavior is critical for public health protection measures.

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The impact of schistosome infection on *Biomphalaria glabrata* host snail microbiome.

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The microbiome of vectors can be a key determinant in their ability to transmit pathogens. For instance, gut microbiome impacts malaria and leishmania transmission by mosquitos and sandflies, respectively. We aim to explore the role of *Biomphalaria glabrata* snail microbiome in schistosome transmission. Snail hosts vary in their susceptibility to schistosome infections, and the complex mechanisms behind this are not fully understood. We have previously showed that the snail hemolymph (blood) contains a diverse microbiome. As the developing schistosome parasites are in close contact with the host hemolymph, and its microbiome, we hypothesize that schistosome infections can alter the snail microbiome composition and abundance over the course of infection.
We generated two cohorts: one cohort of 96 uninfected snails and one cohort of 96 snails exposed to *Schistosoma mansoni* parasites. During the prepatent (4 weeks) and patent (2 weeks) periods, we sampled hemolymph and hepatopancreas from 6 snails of each cohort weekly. We quantified the bacterial density (16S) in each collected sample, as well as the parasite burden (ratio of single copy genes of parasite and snail) in snails tissues using qPCR. We are currently characterizing the microbiome of each sample by sequencing the 16S rDNA V4 region using MiSeq platform. We will compare microbiome profiles within and between snail tissues using alpha- and beta-diversity. To reveal temporal trends in microbiome change, we will apply statistical methods such as MITRE or Dirichlet autoregressive model.
This time-series microbiome data allows us to evaluate i) the stability of hemolymph and tissue microbiome using the uninfected snail cohort, ii) the impact of parasitic infection on microbial composition and density using the *S. mansoni* exposed snail cohort, and iii) to identify potential associations between bacterial taxa, parasitic infection status and parasite development. As snail vector plays a critical role in the transmission of schistosomiasis, it is crucial to explore interactions between snail, its microbiome, and schistosome parasites. Understanding these links may reveal novel methods for schistosomiasis vector control, as well as developing an exciting molluscan model for microbiome research.

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Picky snail hosts and resistant parasites: host specificity of acanthocephalans in ostracod and snail hosts.

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It is assumed that most species of turtle acanthocephalans in the genus *Neoechinorhynchus* infect ostracods as intermediate hosts and turtles as definitive hosts in their life cycles. Intriguingly, *Neoechinorhynchus emydis* is the only turtle acanthocephalan species that has also been reported in

snail paratenic hosts. However, it is currently unclear how snails become infected with *N. emydis* and if other turtle acanthocephalan species can infect snails. To better understand these life cycles, we first exposed two species of ostracods (*Physocypria* sp. and *Cypridopsis* sp.) and the freshwater snail (*Planorbella* cf. *P. trivolvis*) to eggs of four species of turtle acanthocephalans (*N. chrysemydis, N. emydis, N. emyditoides*, and *N. pseudemydis*) in the laboratory. Although eggs of all four species of acanthocephalans hatched in both species of ostracods, development to the infective stage only occurred in *Physocypria* sp. ostracods. In contrast, eggs of the four species of acanthocephalans never developed in snails, strongly suggesting that snails become infected with *N. emydis* by ingesting infected ostracods. Second, we exposed infected *Physocypria* sp. ostracods with all four acanthocephalan species to snails in the laboratory. Only *N. emydis* was able to infect snail hosts by ingesting ostracods, congruent with our field observations. Additionally, proboscis hooks of the other three acanthocephalan species (*N. chrysemydis, N. emyditoides, N. pseudemydis*) were found in snail feces, indicating that they were digested by snails, and snails were incapable of serving as hosts for these three acanthocephalan species. Overall, these laboratory experiments suggest that *N. emydis* uses ostracods, snails, and turtles in its life cycle, whereas other turtle acanthocephalans only use ostracod and turtle hosts.

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Does an oral route of infection exist for *Cyrtosomum penneri* (Nematoda: Atractidae) in Florida lizards?

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Nematodes of the cosmopolitan family Atractidae produce juveniles that develop to the third stage in utero, i.e., autoinfection. *Cyrtosomum penneri* have been experimentally and naturally demonstrated to be transmitted through copulation in lizard hosts. While interspecific mating is known to occur in wild lizards, which could facilitate transmission between lizard species, it is unclear if an alternative route of transmission exists. A previous study attempted to infect lizards by orally pipetting worms in insect saline, which did not result in infections. Yet, an oral route of infection for atractids has been suggested by numerous authors. This study aims to explore the possibility of oral transmission of *C. penneri* in three species of lizards: *Anolis sagrei*, *Leiocephalus carinatus*, and *Agama agama*. The latter two lizards are known to prey upon smaller lizards, such as *A. sagrei*. Lizards were captured, dewormed, and experimentally exposed to *C. penneri* through (1) coprophagy – worms in feces pipetted into mouth, (2) predation – worms in tissue fed to a lizard, and (3) venereally – pipetted into the cloaca. All lizards were dissected and fully explored for live worms 5-7 days post exposure. The results of the investigation will be discussed at the meeting.

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Description, redescription, and life cycles of four philophthalmids (Trematoda: Digenea) from the California horn snail, Cerithideopsis californica (Gastropoda: Potamididae).

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We describe the colony demographics, parthenitae, cercariae, metacercariae, and adults of *Cloacitrema michiganensis* McIntosh 1938, *Cloacitrema kurisi* n. sp., *Parorchis catoptrophori* Dronen & Blend 2008, and *Parorchis laffertyi* n. sp. using molecular-genetic analysis and experimental infections. All four species infect the California horn snail, *Cerithideopsis californica*, as a first intermediate host. *Cloacitrema kurisi* n. sp. and *Parorchis laffertyi* n. sp. are pseudo-cryptic species that have been operationally unrecognized in the California horn snail trematode guild. We document a developmental time series for the metacercariae of all four species. To obtain adults, we experimentally infected final

host chickens (*Gallus domesticus*) and ducks (*Anas platyrhynchos domesticus*). CO1 and 28S phylogenetic analyses confirmed the presence of two separate cryptic species complexes. *Cloacitrema kurisi* n. sp. likely contaminated the first description of *C. michiganensis* originating from that snail host, so we provide an amended description of *C. michiganensis* in the California horn snail. *Parorchis catoptrophori* was previously misidentified as *Parorchis acanthus*, thus our data provides a new geographic record for the species and new descriptions of the parthenita, cercaria, and metacercaria. Adults of the four species can be distinguished from congeners by the following combination of traits: *Cloacitrema michiganensis* by their intra-cecal, pretesticular uterus; small pharynx; and large, equatorial ventral sucker; *Cloacitrema kurisi* n. sp. by their extra-cecal, post-testicular uterus; dextral ovary; large pharynx; complete absence of an esophagus; and small, equatorial ventral sucker; *Parorchis catoptrophori* (as indicated in the original description) can by their bipartite pharynx, possession of a greater number of collar spines (~80 vs. ~60 in most other species), large pharynx relative to the oral sucker, presence of esophageal diverticuli, and deeply lobed testes; *Parorchis laffertyi* n. sp. by the large, bipartite pharynx and esophageal diverticuli. This work highlights the utility of sound descriptive/life-cycle work including larval trematodes, even for relatively well-characterized and well-studied trematode guilds.

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Prevalence of Soil-Transmitted Helminth Infections Among Children in Selected Barangays of Koronadal City.

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Infections with soil-transmitted helminths (STHs) are the most common parasitic infections among children worldwide, particularly in poor areas. This is also true in the Philippines, where the prevalence of the disease among school-aged children was reported to be as high as 67 % in 2001. Barangay Zone I & Barangay Zone III belong to urban areas while Barangay Mabini and Rotonda belong to semi-rural areas. The study involves the examination of 20 children; 10 male and 10 female, ages 10 years and below. This study was conducted to find out the prevalence of soil-transmitted helminth infections in selected barangays of Koronadal City. Survey pertaining to the practices of children on each site through house-to-house visit and by distributing survey forms. Stools were examined with direct fecal smear under light compound microscope and inverted microscope. Presence of soil-transmitted helminths were observed, recorded and documented as result. Barangay Zone I and Rotonda were not infected with STHs. While in Barangay Zone III, 20% of the respondents were infected and in Barangay Mabini had 5% . When it comes to sexes, STHs is more prevalent in males compared to females. The practices of the children greatly affect the prevalence of STHs on each site. This study also presented that STHs helminths are more prevalent in urban areas compared to semi-rural areas.

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Using HepG2 cells as a hepatocyte model to study APOL1 secretion onto TLF complexes.

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Trypanosome Lytic Factor (TLF) is an innate immunity high density lipoprotein (HDL) complex present in plasma of humans and higher order primates. The three main players of TLF complexes are Apolipoprotein A1 (APOA1, structural protein), Apolipoprotein L1 (APOL1, cation-channel forming protein), and Haptoglobin Related Protein bound to Hemoglobin (HPR-Hb, ligand). Of the three, APOL1 is a necessary and sufficient factor for the lysis of African trypanosomes. APOL1 is an interferon

inducible gene. Although expressed in many cells, APOL1 in plasma is predominantly secreted from the liver. The mechanism of secretion of APOL1 and its assembly into TLF complex is not yet understood. Here we used liver hepatocellular carcinoma cells (HepG2) cells to study the secretion of APOL1 and its assembly into the TLF complex. Our results show that APOL1 is produced and secreted by HepG2 cells. Upon induction with gamma interferon, the intracellular APOL1 production increases (90% to 99.8%). However, the secretion of the protein into the media decreases upon induction with interferon (10% to 0.2%). Size exclusion chromatography shows that secreted APOL1 is distributed among complexes of various sizes, from 63.5 kDa to 711.7 kDa and coelute together with APOA1, the structural component of HDL. Whether the two proteins are in the same complex is yet to be studied. Our results show that HepG2 cells can be used to study the secretion of APOL1 and assembly of TLF complexes (500kDa). In the future we intend to investigate the composition and trypanolytic activity of the secreted APOL1 containing complexes.

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Host community diversity and parasite host range help shape parasite gene flow in complex rivers.

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Host-parasite coevolution is fundamentally shaped by differences between host and parasite in gene flow, population size, and generation time, all of which vary across spatially heterogeneous landscapes. In this complex geographic mosaic, variation in host community composition is one factor that may affect parasite evolutionary potential, but its importance should differ between parasites with different host ranges. Here, we tested how host fish community composition and parasite-host specificity together shape the distribution of parasite genetic diversity across the complex river networks and waterfalls of Trinidad's Northern Range Mountains. We conducted a co-structure analysis between two species of monogenean parasite that differ in their host specificity and their guppy host, *Poecilia reticulata*. We found that the generalist parasite *Gyrodactylus bullatarudis* dominated infections on guppies in the more species diverse lower course fish communities and exhibited higher gene flow 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 gene flow among populations that more closely mirrored that of its guppy host. Our results highlight the importance of a community- and landscape-scale approach to studies of coevolution.

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Surveillance for *Echinococcus multilocularis*, an emerging zoonotic parasite in wild canids in New York State.

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Echinococcus multilocularis is the etiologic agent for alveolar echinococcosis in humans, a potentially fatal zoonotic disease caused by infection with the larval stage of the cestode parasite. This parasite has been discovered in novel areas outside its perceived range throughout the last decade. In Canada, there has been a concerning trend of range expansion and increased prevalence in wildlife. In the northeastern United States, *E. multilocularis* was discovered for the first time in 2018, in northern New York State. As a result, we initiated a disease surveillance study of a definitive host, coyotes (*Canis latrans*), to develop a map of parasite distribution and prevalence across different regions of New York

State. During the winter of 2021-2022, we collected fecal samples and gastrointestinal tracts (GIT) from coyotes and analyzed fecal samples a multiplex PCR test specific to *E. multilocularis* DNA and examined GIT samples using a sedimentation filtration counting technique. Preliminary sampling in the southern region of New York yielded 7.5% (3/40) coyote fecal samples testing positive for *E. multilocularis*. DNA sequences of the *nad1* gene amplified from our samples appear most similar to European variants of the parasite. These data support the idea that coyotes are acting as sylvatic definitive hosts in New York and are likely driving the spread of *E. multilocularis* into new areas of the state. The commonplace and vagile nature of coyotes across the state could allow *Echinococcus* parasites to exploit a diversity of environments, including human-dominated and peri-urban spaces, which could increase the likelihood for zoonotic transmission.

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Endohelminth parasites of alligator gar (*Atractosteus spatula*) and spotted gar (*Lepisosteus oculatus*) from Sabine Lake.

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Alligator gar (*Atractosteus spatula*) and spotted gar (*Lepisosteus oculatus*) are predatory, primitive fishes native to North America. These species have an overlapping distribution throughout the gulf coast in fresh and brackish water and are frequently found in highly vegetated habitats with slow moving, occasionally hypoxic water. The parasites of these fishes are understudied throughout their range, particularly in coastal Texas. This study examined the gastrointestinal helminth communities of these 2 species collected from Sabine Lake, an estuary on the Texas-Louisiana border that is formed by the confluence of the Sabine and Neches Rivers and the Gulf of Mexico. Helminths were collected from 40 alligator gar and 40 spotted gar captured in the spring and summer of 2018. From these samples, 3,501 individual parasites representing 13 species were identified (5 trematodes, 4 nematodes, 2 cestodes, and 2 acanthocephalans), 10 of which were shared by both host species. Of the 13 parasite species found, 9 represent new host records. The lack of parasitological studies conducted on these two species as well as the findings from this study highlight the need for additional studies of parasite communities in these fishes throughout their range.

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Utilizing Insect Diversity and Horsehair Worm Presence to Measure an Ecosystem's Health.

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Horsehair worms [Nematomorpha] live in terrestrial freshwater environments. Their complex parasitic life cycle begins with adults laying eggs in water. After the larvae hatch, they encyst in a paratenic host which can include larvae of various aquatic insects such as mosquitos, caddisflies and mayflies. When these hosts metamorphose into terrestrial adults they are consumed by a definitive terrestrial host, usually a larger arthropod such as a cricket, roach, or grasshopper. Here, the horsehair worms develop into juveniles. Once mature, they manipulate their host into entering water where they exit the host and mate. Previous studies have linked healthy, functioning ecosystems with abundant insect diversity. Such insect diversity provides horsehair worms with many hosts, paratenic or definitive, throughout its lifecycle. Therefore, we predict that horsehair worm presence at a site will correlate with high insect diversity. To test this, we collected adult caddisflies using a caddisfly attracting ultraviolet light trap at four sites. We collected aquatic insects by hand and from four clay tiles placed at each site over 7 days. We hand collected twenty *Physa* snails and examined them for the presence of horsehair worm cysts. Finally, we measured nitrate, DO, pH, salinity, and atrazine levels. One of the four sites tested positive for atrazine. Initial analysis showed that site 1 has a cyst prevalence of 50% with an intensity of 21.6. Site

42 was measured to have a horsehair worm cyst prevalence of 65%, with an intensity of 2.7. We calculated insect biodiversity using the Shannon-Weiner diversity index and found indices of 1.126, 1.378, 1.331, and 0.3747 at the sites. Correlation of these data will help us assess the relative health of each site. This information could be used to predict the impact of climate change, agriculture, or other disturbances on these aquatic ecosystems.

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Phylogeographic analysis of *Plasmodium vivax* and *P. falciparum p47*, *p48/45*, and *pimms43* as markers for parasite-vector compatibility in invasive mosquito vector settings.

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Malaria remains a major source of infant mortality in Africa. The impact of the recent detection of the Asian vector *Anopheles stephensi* in Ethiopia, Djibouti, Sudan, and Somaliland on malaria transmission in East Africa is a growing concern. Questions remain about the compatibility between the invasive vector and local *Plasmodium* species. *Plasmodium* genes involved in key vector-related interactions have all been identified as potential markers for parasite-vector compatibility at a continental level. Here, we analyzed the diversity of *p47*, *p48/45*, and *pimms43* genes to assess their potential as markers for malaria parasite-vector compatibility in invasive vector settings in East Africa. We sequenced the three genes in samples of *P. falciparum* and *P. vivax* DNA from Ethiopia and extracted available corresponding global sequence data from nucleotide and genome databases. We performed phylogenetic analysis using a maximum-likelihood approach to detect geographic differentiation as an indicator of vector-parasite specificity. Analysis of the Ethiopian *Plasmodium* protein sequences revealed evidence of both shared and Ethiopia-exclusive haplotypes in multiple genes for both *P. falciparum* and *P. vivax*. Level of differentiation between African and Asia sequences varied across species and genes. Phylogenetic analysis of *P. falciparum pfs47* revealed geographic differentiation between African, Southeast Asian, and South American samples, with Ethiopian sequences clustering with other African sequences. Differentiation was not observed between African and South Asian *P. falciparum pfs48/45* and *P. vivax pvs47* and *pvs48/45* sequences. Phylogenetic analyses of *P. falciparum* and *P. vivax pimms43*, were more inconclusive, due to limited available sequence data and the detection of multiple insertion/deletions in the alignment. Overall, our findings confirm significant continental differentiation at the *pfs47* gene in *P. falciparum* between Africa, Southeast Asia, and South America, and evidence of subcontinental specific haplotypes in the vector-interacting genes. The stronger signal of differentiation between Ethiopian and Asian sequences in *pfs47* may suggest higher vector-parasite specificity for *P. falciparum* compared to *P. vivax* with implications for different levels of compatibility with non-East African malaria vectors between the two *Plasmodium* species.

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Helminth parasites and body condition in brown-headed cowbirds (*Molothrus ater ater*).

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The understanding of how common avian parasites affect the health and condition of their hosts is crucial to understanding how populations are affected. We documented parasite load of helminths in brown-headed cowbirds (*Molothrus ater*) and related it to body condition in 24 male and female brown-headed cowbirds. The brown-headed cowbird is a commonly occurring species of brood parasite that reproduces by laying an egg within the nests of other species of birds, leading to the decline of many endangered bird species, as the cowbird young absorb all the attention of the parents. Cowbirds feed largely on seeds but also include insect prey in their diet. There are few studies that have examined cowbird body condition in an attempt to link it to parasite load. We found very few internal parasites in

the cowbirds we examined. We will discuss the parasites found and relationships with cowbird condition.

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Alteration of behavior in aquatic snails due to larval infections of *Paragordius varius.*

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The hairworm, *Paragordius varius* [Nematomorpha], parasitizes multiple hosts. When fully grown in the terrestrial, definitive host, the hairworm can manipulate the behavior of its host, causing them to enter aquatic environments where the fully developed worms emerge, mate, and lay eggs. After hatching, the larvae encyst in a paratenic host that transfers the hairworm's cyst stage from the aquatic to the terrestrial environment. Typically, this paratenic host is an aquatic insect, but cysts are commonly found in aquatic snails (*Physa* sp.). Aquatic snails do not regularly enter the terrestrial environment but could do so if manipulated. This study asks if aquatic snails can serve as a paratenic host for *P. varius* by comparing the behavior of infected and uninfected snails in a 20-hour period. If hairworms manipulate the behavior of their paratenic host to facilitate their transmission to the terrestrial environment, then infected snails will be more active, and/or spend more time above the water line than uninfected snails. Preliminary trials did not find significant differences in snail behavior between cyst infected and uninfected snails, but this may have been the result of insufficient sample size, using field-collected snails, using a habitat with vertical walls, and failing to account for circadian rhythms in snails. If aquatic snails can serve as a paratenic host for *P. varius*, then this will represent another example of parasite manipulation of the host to facilitate the parasite's life cycle. The life cycle of *P. varius* should be more stable because the parasite can better persist in the environment while encysted in aquatic snails which can overwinter.

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Temporal dynamic of the *Octopus maya* parasite-fauna from Campeche and Yucatan, Mexico.

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Monthly and bimonthly samplings of the pick octopus (*Octopus maya*) were carried out throughout a year at four locations of the states of Yucatán (Celestun and Progreso) and Campeche (Isla Arena and Campeche). For each location and sampling date between 24 and 30 fresh specimens were examined. For each sample the total number of parasites and total number species parasites were recorded together with infection parameters (mean intensity, mean abundance, and prevalence). Furthermore, the relationship between the infection parameters and the sex and size of the hosts were investigated. After parasitological analysis of between 203 and 260 octopuses from the Yucatan localities and between 68 and 51 octopuses from the Campeche localities, a total of 21 metazoan parasites were identified (8 species of cestodes, 8 digenean trematodes, 4 nematodes and a copepod). Both the total number of species and the total number of parasites collected per locality differed significantly between localities. The most frequent and abundant species were the cestode *Prochristianella* sp. 1, and the copepod *Octopicola* sp. These two species were present though the year with a prevalence between 70 and 80%. They also presented the highest mean abundances and represented more than 96% of the total parasites collected. The differences in total parasites between localities are highly influenced by the presence of *Prochristianella* sp. 1 and *Octopicola* sp. A positive relationship was found between the parasite load and the size of the collected octopuses in all locations, no significant differences were found with respect to sex, except in the case of *Prochristianella* sp. 1 in Celestun, where males were significantly more parasitized than females. Undoubtedly, the greatest influence on parasite community parameters in all cases is highly influenced by the cestode *Prochristianella* sp. 1. However, other

cestodes such as *Eutetrarhyncus* sp., and the trematode Cryptogonimidae gen. sp. were present consistently through the year but with low values of prevalence and abundance.

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***Chordodes morgani* Effect on Host Growth and its Development Time in Differing Diet and Temperature Conditions.**

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Chordodes morgani (also known as a hairworm) belong to the Phylum Nematomorpha, employ a parasitic lifestyle, and are found in Nebraska. Recent work identified the wood roach (*Parcoblatta* spp.) as its terrestrial definitive host and flatheaded mayflies as their aquatic paratenic host. Yet two important questions remain unanswered. First, many parasites have detrimental effects on their hosts, resulting in slower growth rates. However, experimentally infected wood roaches showed faster growth rates than uninfected wood roaches. One possible answer to this is the fact that the wood roaches grow through the process of molting and the internal stress and pressure from the growth of the hairworms could result in an increase of speed at which they are forced to molt. Also, the initial trials on growth rates lacked sufficient sample sizes. Second, wild wood roaches are infected with *C. morgani* via infected mayflies in late summer. Yet, adult *C. morgani* worms are not found until July, suggesting around a 9-month development. In the lab this finding contrasts with lab-infected wood roaches in which adult worms emerged 2-3 months post infection. One possible answer to this is the difference in diet and temperature between field and lab conditions. To address both questions, this study measures growth rate in infected and uninfected roaches as well as *C. morgani* development time using a four-block design with limited and unlimited food as well as at cold and room temperatures. Initial analysis at 11 weeks post-exposure showed no significant differences among the treatments, but this pilot study suffered from high mortality and a low sample size. This study will help understand how these parasites survive in different seasons and temperatures as well as the variation in emergence time of *C. morgani*.

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Parasites of spotted skunks (*Spilogale* sp.) in the eastern and central United States.

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To date, few studies exist on the extent of the parasitic fauna found on and within spotted skunks (*Spilogale* sp.). Most research has focused either on skunks from a portion of their range, or on a specific parasite group, creating a bias towards heterogeneous sampling efforts and incomplete sampling. As such, the goal of this project is to report on the parasite community of spotted skunks collected across their ranges. Skunks collected represent eight states and were obtained from vehicle-killed animals, mortalities from previous research projects, donations from natural history collections, and legally harvested animals by fur trappers. We have performed fifty total necropsies on spotted skunks: eight of which were western spotted skunks (*S. gracilis*) and forty-two were eastern spotted skunks (*S. putorius*). When possible, both an internal and external evaluation was performed. Endoparasites (acanthocephalans, cestodes, and nematodes) have been found in thirty-five hosts and ectoparasites (fleas, lice, mites, and ticks) were found on fifteen hosts. Additional ectoparasites were obtained from a radio collar project in Harris County, Texas. Identification based on morphological keys of the collected parasites is ongoing.

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Biodiversity of parasites in freshwater snails: How common are non-trematode parasites in freshwater snails?

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Most studies on parasites of freshwater gastropods have concentrated on trematodes which are intimately linked in physical space and over evolutionary time with their gastropod intermediate hosts. However, other symbionts including annelids, nematodes, nematomorphs, acanthocephalans, cestodes, and coccidia are also found in snails but are not commonly reported. Thus, the commonality of non-trematode symbionts in freshwater snails remains unclear. To assess this data gap, we examined a total of 1,500 *Physa acuta* snails from 60 sites (17–53 per site) and 600 *Planorbella* cf. *P. trivolvis* snails from 25 sites (9–150 per site) throughout Oklahoma, but also from Nebraska and/or Wisconsin for trematode, annelid, nematode, nematomorph, acanthocephalan, and coccidian infections. Although trematode and annelid infections were ubiquitous in both snail species, we commonly detected nematomorph, nematode, acanthocephalan, and/or coccidian infections in one or both snail species. For example, at least 3 nematomorph species (cyst types of *Paragordius varius*, *Gordius terrestris*, and/or *Chordodes*/*Neochordoes*) infected *P. acuta* snails at 70% of localities. In contrast, *P. trivolvis* snails were infected with 2 species of nematodes, including *Daubaylia potomaca* at 53% of sites and *Spiroxys contortus* at 7% of sites. Both snail species were infected with cystacanths of the acanthocephalan, *Neoechinorhynchus emydis*, and *P. trivolvis* was infected at 30% of sites and generally had a much higher prevalence of cystacanths (5–70% per site) than *P. acuta* (8–23% per site). Finally, we report an undescribed species of coccidian in the genus *Pfeifferinella* infecting *P. trivolvis* snails. More broadly, our work indicates that freshwater snails serve as either intermediate, paratenic, or definitive hosts for a broad range of symbionts from at least 6 phyla and can be used to evaluate the biodiversity and distribution of parasites over large geographical areas.

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The effect of trematode parthenitae infection on the reproduction and mortality of freshwater mussels of Texas.

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Freshwater mussels act as first intermediate hosts for trematodes, which infect gonadal tissue and can negatively affect fitness. Fifteen of ~52 mussel species in Texas are state-threatened, of which *Cyclonaias petrina* and *Lampsilis bracteata* reportedly contain castrating trematodes. This research aims to monitor the long-term effects of trematode parthenitae in freshwater mussels. Six mussel species were marked at two sites on the San Saba River in July and November 2021. Recapture was attempted in August and November 2021 at Site 1 and November 2021 at Site 2. A syringe technique was used to withdraw gonadal fluid to screen for trematode presence. In July, trematode prevalence at Site 1 was low to absent across marked mussels: *Lampsilis bracteata* (0/28), *Tritogonia verrucosa* (0/3), and *Utterbackia imbecillis* (1/3). Trematode prevalence at Site 2 was low in July for *Amblema plicata* (0/14) and *T. verrucosa* (2/20), but high for *C. petrina* (10/11) and *C. pustulosa* (9/17). In November, 14 mussels were recaptured, including three previously infected *C. petrina*, of which two were deceased, and the other remained infected. Ten previously uninfected mussels (six *A. plicata*, one *C. pustulosa*, and three *T. verrucosa*) were recaptured. The *C. pustulosa* was found deceased, and all others had no change in

infection. All infected hosts carried bucephalid sporocysts and did not appear to contain gametes. Thus far, no individual mussel has recovered from infection. No new infections were observed, but new infections in the spring may occur when trematode miracidia are hatching. Of the two imperiled species, *L. bracteata* and *C. petrina*, only *C. petrina* has been found to contain gonad-infesting trematodes. The high prevalence (91%) and recorded mortality in *C. petrina* are concerning, as successful reproduction leads to population persistence. The high infection rate in the mussel genus *Cyclonaias* also suggests host-specificity, though further research is needed.

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Characterization of TbCatL Recombinant protein in a CHO-S mammalian model.

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The eukaryotic parasite, *Trypanosoma brucei*, is responsible for African Trypanosomiasis, a disease that has killed many animals. Humans are resistant to the affliction due to apolipoprotein-1 (APOL1), a trypanolytic lipoprotein that forms ion channels in the parasite membranes, resulting in lysis. *Trypanosoma brucei* Cathepsin-L (TbCatL), a protease, is hypothesized to degrade APOL1 and thus allows for the evasion of trypanolysis. To test this hypothesis, pure recombinant TbCatL will be incubated with rAPOL1 embedded in an artificial lipid bilayer, which mimics the membranes of the parasite. The rAPOL1 will be activated, which results in open channel conformation and ion flux. If rTbCatL can degrade APOL1 in the bilayer, we hypothesize that the ion flux will stop.
First, we must purify rTbCatL. We utilized Chinese Hamster Ovary suspension cells (CHO-S), exceptional for protein expression and secretion, to produce rTbCatL. The efficiency of this CHO-S line to produce rTbCatL for protein purification was determined via transfection with a pcDNA/TbCatL vector. The enzymatic activity for both the transfected and non-transfected cells was evaluated with the concentrated culture supernatant, which was measured with the Z-Phe-Arg-AMC fluorogenic substrate for rTbCatL by spectrofluorometry. Results show that enzymatic activity of the supernatant from transfected CHO-S was equivalent to a cathepsin-like positive control (papain), while the non-transfected supernatant had none. For purification of the rTbCatL, affinity and size exclusion chromatography techniques were used, resulting in ~90% purity.
Analyses of the literature revealed that 16 hours of proteolytic activation of rTbCatL results in the degradation of almost all contaminating proteins in the supernatant, therefore purifying the enzyme. We found that 21 hours of proteolytic activation resulted in a single prominent band with rTbCatL activity, which was confirmed by Western blot using an antibody to TbCatL. Work to optimize this process to obtain purer rTbCatL is underway.
We have shown that this novel expression system generates good quality, functional, 90% pure rTbCatL. We will evaluate if rTbCatL can degrade and inactivate rAPOL1 channels in membranes. Thereby, allowing the parasites to evade trypanolysis by the human APOL1, a new player in the molecular arms race.

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***In vitro* models of macrophage activation in *Trypanosoma brucei* infection.**

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Pathogenesis in African trypanosome infection is associated with a dysregulation of inflammatory regulation and an over-activation of type 1 macrophage responses. This is driven in part by components of the variant surface antigen, though other factors have been implicated. The mechanisms of this process are poorly understood. The requirement for MyD88 signalling provides circumstantial evidence of TLR signalling, but no direct evidence has been presented for this. We are developing experimental

platforms to define the interaction of trypanosomes with innate immune receptors, with the aim of identifying key immunomodulatory parasite components. In an in vitro system using murine macrophage-like RAW264 cells, we demonstrate that culture adapted *T. brucei*, conditioned medium and lysate caused upregulation of inflammatory cytokine production (specifically TNF-α and IL-6). We confirmed these findings in RAW264 reporter cells that express alkaline phosphatase after PRR signalling leading to NF-KB activation. We also have used TLR overexpressing HEK reporter cells to demonstrate that the parasites trigger signalling via TLR4 and TLR2 *in vitro*. We will use this system to identify the ligands involved in these responses.

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Understanding the Mechanism of Lysing *Trypanosoma Brucei* by TLF as Followed by the Release of the Variant Surface Glycoprotein Coat.

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African Trypanosomes are unicellular, eukaryotic, bloodborne parasites that cause a major agricultural burden in Sub-Saharan Africa. Humans and some non-human primates are protected against infection by some species of *Trypanosoma* due to the innate immune complex Trypanosome Lytic Factor (TLF). The parasites evade the host's adaptive immune system through antigenic variation of the densely packed Variant Surface Glycoprotein (VSG) coat. VSGs are present at the parasite surface as homodimers, anchored into the extracellular face of the membrane by a glycosylphosphatidylinositol (GPI) anchor. The VSG coat can be released by cleavage of the GPI anchor by an endogenous GPI-phospholipase C (GPI-PLC) during hypotonic lysis of the parasites. We hypothesize that TLF lyses trypanosomes by causing osmotic imbalance, leading to hypotonic lysis. To determine if the VSG coat is shed as a component of the TLF-mediated lysis mechanism, trypanosomes were treated with TLF for defined times, the surface was labeled with Alexa fluorophore-conjugated wheat germ agglutinin (a lectin that binds GPI anchored VSGs), and cellular fluorescence was monitored using Flow Cytometry. A parallel set of trypanosomes were monitored for lysis, using propidium iodide. The results show a gradual decrease in wheat germ agglutinin fluorescence over 60 minutes of TLF treatment, and no change in propidium iodide. This suggests that the VSG coat is shed as a result of TLF treatment, which occurs before the parasites die, supporting the hypothesis that TLF causes hypotonic lysis. The next step will be to use a trypanosome line deficient in GPI-PLC, rendering it unable to release the VSG coat, testing if the shedding of the VSG coat is required for or a consequence of lysis by TLF.

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The site specificity of *Blabericola haasi* and *Protomagalhaensia wolfi* (Apicomplexa: Eugregarinida: Blabericolidae) parasitizing the speckled cockroach *Nauphoeta cinerea* (Dictyoptera: Blattaria: Blaberidae).

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We investigated the site specificity of *Blabericola haasi* and *Protomagalhaensia wolfi*, two species of eugregarines parasitizing laboratory colonies of the speckled cockroach *Nauphoeta cinerea*. Overall infection prevalence was 94% (44 of 48 cockroaches were infected with both gregarine species, while a single cockroach was infected with *B. haasi* only). Overall infection intensity of *B. haasi* was higher than infection intensity of *P. wolfi* (941.5 vs. 281.3). *Blabericola hassi* was found throughout the length of the midgut, but intensity was 50% higher in the anterior portion of the midgut. *Protomagalhaensia wolfi* was also found throughout the length of the midgut, but intensity was 37% higher in the posterior

portion of the midgut. In the single host that was infected only with *B. hassi*, all gregarines were found in the anterior portion of the midgut.

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Monitoring of *Toxoplasma gondii* in Marine Species from the Indian River Lagoon, Florida.

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Toxoplasma gondii is a protozoan parasite increasingly associated with morbidity and mortality of marine mammal species. Certain fish species have been shown to harbor the *T. gondii* oocysts in their tissues, while the commonly consumed Eastern Oyster (*Crassostrea virginica*) has also been known to filter sporulated *T. gondii* oocysts from seawater. The highly urbanized Indian River Lagoon on the Atlantic coast of Florida is a biodiverse estuary that attracts important marine mammal species such as dolphins and manatees to its waters for breeding and feeding periods. This ecosystem is also an important sport and commercial fishery. Currently, the prevalence of *T. gondii* in this ecosystem is unknown, but exposure to *T. gondii* through the consumption of the resident marine species presents a valid concern. As a trial project, tissues from a total of 118 fish and 30 oysters were collected from the Indian River Lagoon and tested for the presence of *T. gondii* DNA using PCR analysis. Neither oysters nor fish tested positive by *T. gondii* specific PCR, suggesting that either *T. gondii* was not present in this system under these limited sampling parameters. Inherent limits of the assay system may also have contributed to the results. Although incomplete, PCR testing of fish tissues, including gill and muscle, has yet to reveal the presence of *T. gondii* specific sequences in any of the animals or tissues tested. Once complete, these analyses may provide a baseline for future monitoring efforts of *Toxoplasma gondii* prevalence in this important aquatic ecosystem.

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Prevalence of *Toxoplasma gondii* among cat populations in Southeast Nebraska.

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Domestic cats (*Felis catus*) are beloved companions and important animals that many humans live close to or encounter every day. However, cats are also profoundly important carriers for many zoonotic diseases. One of the unicellular eukaryotic parasites which cause a deadly disease in humans and are transmitted via cats is toxoplasmosis. The causative agent of this debilitating disease is the protozoan parasite *Toxoplasma gondii*. 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. Keeping in mind the high prevalence of this zoonotic disease among our population it was decided to investigate the prevalence of this parasite among the cat population. This survey was tailored to determine the percentage of cats which are harboring *Toxoplasma gondii*. Fresh fecal samples were collected from individual houses and outdoor cats in Southeastern Nebraska. The samples were transported in vials of 10% formalin to the laboratory. After filtration and centrifugation, the fecal material was re-suspended in diluted ethyl acetate. Following a vigorous shaking process and a second round of centrifugation, the fecal material was resuspended in water. The identification of the parasite was performed under light microscopy. Overall, 95% of the fecal samples were infected with one or more parasites. The most prevalent protozoan parasite (91%) found was *T. gondii* followed by *Entamoeba histolytica* (50%), *Chilomastix mesnili* (41%) and *Endolimax nana* (29%). Some of the animals were also infected with *Giardia intestinalis*. The details of this study will be presented at the meeting.

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Infection patterns of two species of eugregarines (Apicomplexa: Eugregarinida: Blabericolidae) parasitizing the speckled cockroach Nauphoeta cinerea (Dictyoptera: Blattaria: Blaberidae).

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Two species of eugregarines in the family Blabericolidae (*Blabericola haasi* and *Protomagalhaensia wolfi*) were found to cooccur in laboratory colonies of the speckled cockroach *Nauphoeta cinerea* (Dictyoptera: Blattaria: Blaberidae). We investigated infection patterns in three host size classes: juveniles <12 mm (size class 1; n = 15), juveniles 20-30 mm (size class 2; n = 9), and adults (size class 3; n = 39). In size class 1, 14/15 individuals were infected with at least one species of eugregarine; 11/15 were infected with *B. haasi* (mean intensity = 45.6; range 14-100) and 7/15 were infected with *P. wolfi* (mean intensity = 26.0; range 2-50). In size class 2, 7/9 individuals were infected with at least one eugregarine; 7/9 were infected with *B. haasi* (mean intensity = 92.6; range 12-194) and 6/9 were infected with *P. wolfi* (mean intensity = 28.7; range 1-52). In size class 3, 38/39 individuals were infected with both species of eugregarine; mean intensity of *B. haasi* was 1097.9 (range 29-5640) while mean intensity of *P. wolfi* was 321.0 (range 10-1867). In the two juvenile size classes, prevalence of *B. haasi* was higher than the prevalence of *P. wolfi* and in all three size classes, mean intensity of *B. haasi* was higher than the mean intensity of *P. wolfi*.

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Morphological and molecular characterization of *Crepidostomum* sp. (Trematoda: Allocreadiidae) from the Mountain Whitefish (*Prosopium williamsoni*) in Oregon.

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The diversity of *Crepidostomum* species in salmonid fishes of the Pacific Northwest has not been fully explored using morphological and molecular data. Two typical salmonid specialists, *Crepidostomum farionis* (=*Stephanophiala farionis*) and *C. metoecus*, have been reported from this region. During a survey of fish parasites from the Deschutes River system in Oregon, gravid individuals of a *Crepidostomum* species were collected from the gallbladder of Mountain whitefish (*Prosopium williamsoni*). Anatomical measurements were taken from stained and whole mounted specimens. This form resembles *C. farionis* in size, organization of internal organs and oral papillae, but also resembles *C. metoecus* in having an excretory bladder that extends to the anterior testis and a large opening of the ventral sucker. Molecular data were obtained from the 28S rRNA gene, internal transcribed spacer region (ITS), and cytochrome c oxidase subunit 1 (COI) gene. A BLAST search indicated that the amplified COI region (407 bp) of *Crepidostomum* sp. differed from *C. farionis* by 5 bp (1.2%). Phylogenetic analyses of the 28S and ITS regions, using Maximum Likelihood and Neighbor Joining methods, indicate the form is most closely related to *C. farionis*. The site of infection of the form in this study is identical to that of *C. wikgreni*, a parasite of *Coregonus acronius* in Finland (Gibson D.I. & Valtonen, E.T. 1988; *Syst. Parasitol.* 12: 30-41), but molecular data for this species are not currently available. Based on host specificity, morphology, and molecular evidence, the form in Mountain Whitefish appears to be distinct from other *Crepidostomum* species.

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Parasites of heptapterid catfishes in streams of Soberania National Park, Chagres River drainage, Panama.

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Between 2010 and 2019, a survey of fish parasites was conducted in tributaries of the Chagres River system in Panama. In total, 19 species of fishes belonging to 7 families were examined, including two species of heptapterid catfishes (Siluriformes: Heptapteridae), namely *Pimelodella chagresi* and *Rhamdia quelen*. Eight species of helminths and one species of Protista were found as follows: 5 Trematoda (*Acanthostomum gnerii*, *Creptotrema* sp., *Genarchella* sp., *Phyllodistomum* sp. and metacercariae of Diplostomoidea gen. sp.), 1 Nematoda (*Cucullanus pimelodellae*), immature cestodes of Onchoproteocephalidea gen. sp., 1 Monogenea (*Kritskyia* sp.), and 1 opalinid species. Four helminths, *Acanthostomum gnerii*, *Genarchella* sp., *Phyllodisotomum* sp. and *Cucullanus pimelodellae,* occurred in both host species. The parasites are characterized using morphological and molecular data. Overall, the parasite fauna is an extension of the neotropical parasite fauna found in catfishes in South America. The species of *Genarchella* and *Phyllodistomum* in this study are similar to *G. isabellae* and *P. scotti* in heptatpterid catfishes farther north in neotropical Middle America. In contrast, helminths such as the *Creptotrema* sp. and *Kritskyia* sp., or their congeners, have not been found in studies of heptapterid catfishes farther north, and Panama may mark the current limits of their northern distribution.

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A new species of *Neoechinorhynchus* (Acanthocephala) from two species of redhorse (Catostomidae: *Moxostoma erythrurum* and *Moxostoma macrolepidotum*) in North America.

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We encountered a new species of *Neoechinorhynchus* (Acanthocephala) during extensive fish parasite survey work in North America that focused on catostomid fishes (suckers). Among our samples of *Moxostoma* specimens from the Red River in Manitoba, Canada, the Kanawha River in West Virginia, and the Allegheny River in Pennsylvania we encountered specimens of genus *Neoechinorhynchus* inconsistent with previously known species. All fish utilized in this study were captured via boat electroshocking, and subsequently examined with a dissecting microscope for parasitic worms. All acanthocephalans encountered were stored in tap water and after ~24 hours switched to 70% ethanol. They were then stained and mounted onto slides with Canada Balsam and subsequently examined with a Leica DM 2500 microscope. Measurements of 9 male and 12 female specimens of this new species were then compared to available published data for other North America fish-parasitizing species of *Neoechinorhynchus*, and in some cases, to type specimens. This new species differs from all but six of the 30+ species of *Neoechinorhynchus* from the USA and Canada in its possession of body walls that are thicker dorsally than ventrally, and in having lemnisci that are markedly unequal in length. Although the new species is similar to *N. buckneri*, *N. bullocki*, *N. carinatus*, *N. cristatus*, *N. prolixoides*, and *N. prolixus* in terms of body wall thickness and lemnisci, it can be distinguished from each of those species based on hook lengths of anterior, middle, and posterior hooks on the proboscis. Our morphologically-based conclusion that that this species is distinct from each of those 6 species is corroborated by sequence data for the large ribosomal subunit obtained in another ongoing study. Our study calls attention to the potential for more discovery of novel species in North America.

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Re-evaluation of the diversity of *Psilochasmus* Lühe, 1909 (Digenea: Psilostomidae) and descriptions of two new species from Europe and North America.

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Digeneans of the genus *Psilochasmus* Lühe, 1909 (Echinostomatoidea: Psilostomidae) are known to parasitize the intestines of their avian definitive hosts, primarily waterfowl, on all continents except Antarctica. Members of this genus are characterized by typical psilostomid morphology as well as the presence of a protrusible, retractile muscular tail-like process at posterior end of its body. Taxonomic history of *Psilochasmus* is complex and its taxonomic content remains unclear. In the opinions of some authors the genus is monotypic, while other authors consider the genus to contain up to eight species. Prior molecular phylogenetic studies on the Psilostomidae have only included DNA sequences from two species of *Psilochasmus*. One of them was tentatively identified as *Psilochasmus oxyurus*, the type-species, collected in Europe. Unfortunately, the original description of *P. oxyurus* was poor and subsequent descriptions based on European material were incomplete. In the present study, we generated nuclear ribosomal and mitochondrial DNA sequences from *P. oxyurus* and two new *Psilochasmus* spp. collected from birds in Europe and North America. Newly generated and previously published DNA sequences were used to study the interrelationships of the genus. Our data provides insight into the evolutionary history of *Psilochasmus*. The high quality of our specimens allowed for a detailed description of *P. oxyurus* and the two new species. Future studies must focus on collecting well-fixed adult specimens of *Psilochasmus* and test the validity of the other nominal *Psilochasmus* spp. using molecular tools.

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Parasites lost (and found): Filling in gaps of parasite distributions with newly digitized collections.

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Parasite-host relationships and their geographic distributions are a critical component to understanding ecosystems and biogeography. However, these important data are often limited to specimens referenced in the published literature while information from museums and teaching collections is often unavailable to the broader scientific community. Recently, the Terrestrial Parasite Tracker project has begun addressing this knowledge gap by digitizing ectoparasites from over 22 collections and institutions in the United States. In this study, we examine a small subset of this newly available data by focusing on ectoparasite specimens from raptors in the Stephen J. Taft Parasitology collection at the University of Wisconsin – Stevens Point (UWSP-PARA). Our research objective was to investigate how these newly digitized collections could contribute to our knowledge of parasite diversity and distributions in Wisconsin and the upper Midwest. Currently, the UWSP-PARA collection has digitized records of over 2100 slide-mounted ectoparasite specimens from fifteen raptor taxa. We focused on more than 1700 records from eight of the most common host species for our analysis. Parasite records that are accurately identified include two species of Hippoboscid flies, four genera of lice, one species of flea, and one species of mite, while other parasites were only identified to family or order. Using a systematic literature search, we collected data on published parasite-host relationships and geographic distributions. Although our identified parasite-host relationships in the UWSP-PARA are not novel, our study uncovered a gap in distribution records from Wisconsin. Furthermore, many of these specimens were deposited from 1970-2000 and therefore represent a historical record that can be used as a baseline for future comparisons. This research highlights the utility and importance of including small, orphan collections to larger, publicly accessible databases to increase our broader understanding of parasite relationships and their distributions. Future improvements to the collection and digitized records include georeferencing specimen localities for more precise distribution data as well as addressing the limited taxonomic resolution of many specimens.

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A new species of *Neoechinorhynchus* (Acanthocephala) from white sucker (Catostomidae: *Catostomus comersonii*) from Oneida Lake, New York.

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We encountered a new species of *Neoechinorhynchus* (Acanthocephala) in New York state after several years of extensive fish parasite survey work in North America. The emphasis of the surveys was on catostomid fish (suckers), but other fish species were also collected via electrofishing boat, backpack shocking, or gill net. In New York state we examined a total of 391 *Catostomus commersonii* (white sucker) between 2008 and 2021 from multiple drainage basins including Lake Ontario (n = 139 fish examined), Mohawk River (n = 13), Susquehanna River (n = 215), Delaware River (n = 6), and Hudson River (n = 18). The neoechinorhynchids *Octospinifer macilentus* and *Neoechinorhynchus bullocki* were found in white sucker in most of the drainage basins, but the new species of *Neoechinorhynchus* was only found in the Lake Ontario Basin; in Oneida Lake and in an eastern tributary stream of Lake Ontario. The new species appears to be quite rare–only 4 of 139 white sucker examined from Lake Ontario Basin were infected—at least for our sample, which was biased towards summer months. Acanthocephalans encountered were stored in tap water, later switched to 70% ethanol, stained with Semichon's acetocarmine, mounted onto slides with Canada balsam and subsequently examined with a Leica DM 2500 microscope. Measurements of 2 male and 3 female specimens of this new species were compared to available published data for other species of *Neoechinorhynchus* from the USA and Canada, and with museum specimens of some species. The new species can be distinguished from its congeners based on a combination of features including hook sizes and the possession of a relatively large cement gland in males. Further evidence that these specimens represent a unique species was obtained in a separate study in which DNA sequence data of the large ribosomal subunit was compared to other species of *Neoechinorhynchus* in the USA and Canada. The discovery of a new species of acanthocephalan in Oneida Lake, New York—site of a classic 1932 survey study by H. J. Van Cleave and J. Mueller—speaks to the importance of continued survey work using a diversity of tools.

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Towards the understanding of gregarine diversity: development of single-cell whole-genome sequencing and 18S barcoding approaches to inform the phylogeny and systematics of gregarines (Apicomplexa) in insects.

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Recent phylogeny-aware high-throughput metabarcoding 18S eDNA data have prompted the idea that a protist group known as gregarines is one of the most diverse eukaryotic lineages in terrestrial environments. Gregarines belong to the Apicomplexa, a phylum that is better known for including vertebrate parasites of medical importance responsible for diseases such as malaria. They, however, do not infect vertebrates but instead, inhabit a broad arrange of invertebrate lineages including insects. The fact that they utilize insects as hosts have been used to explain its putative great diversity in terrestrial environments as it is thought that gregarines and insects have coevolved. However, this hypothesis has not been formally tested because we virtually ignore gregarine molecular biology, which has prevented the understanding of their phylogenetic diversity.
Here, we present a methodology that facilitates the generation of whole-genome sequence information coming from gregarine single-cell isolates. This approach involves the use of multiple displacement amplification to increase the number of copies of genomic DNA and Illumina sequencing. Although this pipeline retrieves genomes with a variable degree of completeness, the merging of libraries from different cell isolates can improve this value. Additionally, we developed a pipeline that allows the

generation of a nearly complete 18S fragment from gregarine single-cell isolates using a nested PCR approach first using universal eukaryotic primers, and then a pair of newly designed primers that in silico simulations seem to perform well for a broad arrange of gregarine species. This method eliminates the need for molecular cloning and can be readily used to molecularly delineate gregarine morphospecies. Using this approach, we have been able to sequence the gregarine 18S loci from distantly related orthopteran hosts. The integration of both approaches along with the available eDNA sequence data and morphology will largely benefit the understanding of the phylogenetic diversity and systematics of gregarines in insects.

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Identification of Ixodid ticks of the Cumberland Gap Region of Appalachia (2016-2020).

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Tick-transmitted diseases are increasing in incidence, and tick spatial distributions and phenology may be shifting as well due to habitat change and/or climate change. Data on the questing seasonality of ticks are sparse, especially in rural Appalachia. The purpose of this project was to investigate the phenology, diversity, abundance, and hosts of Ixodid ticks in the Cumberland Gap Region of Tennessee, Virginia, and Kentucky. From May 2016 to December 2020, ticks were collected via dragging or opportunistically collected via submission from the public and from other projects at Lincoln Memorial University College of Veterinary Medicine. Over 2900 ticks have been collected from the following genera: *Dermacentor* (32.2%), *Amblyomma* (21.9%), *Ixodes* (19.6%), *Rhipicephalus* (25.4%), and *Haemaphysalis* (0.76%). *Dermacentor variabilis* were the most frequently identified tick to date. Current data suggests year-round tick activity. Ticks will be screened for common tick-transmitted pathogens. Once complete, these findings will provide insight for future studies of Ixodid ticks in rural Appalachian areas. These data will also help us to understand the natural history of ticks in the Cumberland Gap Region as well as allow us to determine changes in seasonality or shifts in species composition.

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Distribution of *Dirofilaria immitis* vectors among neighborhoods of different socio-ecological status.

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The socioeconomic status (SES) and degree of urbanization of neighborhoods is known to affect the diversity, distribution, and abundance of medically important mosquito species. There are at least 25 mosquito species that are naturally infected with *Dirofilaria immitis* and previous studies have shown that the degree of urbanization plays a role in which mosquito species are considered to be the primary vectors. The geographic region also influences which mosquito species vector *D. immitis*. San Antonio, TX is one of the most economically segregated cities in the U.S. and is considered to be a high-risk area for heartworm. The unrestrained dog population is considerable, with 34,636 unrestrained dogs within the city at any given time, and most are found in lower-income areas. Therefore, the aim of our study is to identify the primary vectors of heartworm in residential areas of San Antonio and to investigate the socio-ecological neighborhood characteristics that may affect heartworm prevalence in mosquitoes. We collected mosquitoes in more than 70 neighborhoods over 10 epiweeks during the summer of 2021. Each neighborhood was classified by the SES, housing density, degree of urbanization, shade and impervious surface coverage, and dog population density. We have not yet conducted PCR to analyze mosquitoes for presence of *D. immitis* due to institutional biosafety delays, but preliminary analysis of mosquito data shows that collection week and SES did not significantly affect mosquito population density. Housing density did not differ amongst neighborhoods and therefore was not used. We found that dog population density was significantly higher in low SES compared to moderate or high. During

the summer and fall of 2022 we will conduct additional mosquito collections, use PCR to determine *D. immitis* infection in mosquitoes, and analyze these data in predictive models using the socio-ecological neighborhood characteristics.

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Implementing course-based undergraduate research experiences of waterfowl parasitology across the curriculum.

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Inquiry-based science education is considered an essential component for students to obtain authentic skills in scientific investigation. One of the most effective methods for implementing inquiry is through Coursed-based Undergraduate Research Experiences (CUREs) where students are directly involved in original faculty led research in their basic biology courses. We developed CUREs involving novel parasite surveys of hunter donated waterfowl carcasses for upper-level parasitology elective courses and introductory biology. Implementation of the CUREs involved guiding student scientists in developing their own novel research questions tied to the larger project goals of parasite community assessment and isolating potential mechanisms shaping species interactions. Hands-on lab activities included practicing dissection methods, adhering to approved biosafety procedures, following published protocols for museum specimen preservation as well as DNA extraction, PCR amplification, and sequencing. Students gained familiarity with data analysis through implementing statistical tests to address their research questions in small groups and then expanded their public speaking and scientific communication experience by presenting their results to the class as the final assessment. Each course was adapted in a unique way based on the instructor, student population, and specific research questions explored. In addition to meeting course learning outcomes, this opportunity supported a group of undergraduate research students as peer-mentors that assisted with all aspects of the projects and then used class-collected data in their own research presentations at campus symposia and regional scientific meetings. Furthermore, these CUREs resulted in publication quality data, supported faculty research at small, teaching-focused institutions, and provided morphological and molecular parasite museum specimens for future research. These course innovations helped students understand not only the concepts of parasitology, but the work involved in becoming a parasitologist. CUREs have the potential to improve access and outcomes for scientific reasoning abilities of all students, reduce barriers to entry into scientific fields, and increase inclusivity critical for recruitment and retention of diversity in science in general and parasitology in particular.

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Integrating Book Club into parasitology courses to promote active student learning.

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Student engagement is a challenge in classrooms today, particularly with the common use of electronics and their association with social media. Additionally, many classrooms have opted to minimize use of textbooks and rely on PowerPoint presentations for class content and as a result, some students have become less engaged in the learning process. The Book Club concept is to help students become actively engaged through discussion and accompanying activities to help demonstrate the role of parasites in the lives of humans in addition to the medical and epidemiological aspects of diseases. The book club concept can be integrated in several ways but I have found a single book in addition to the class's assigned textbook can add enrichment and present parasitology through a different dimension. Alternatively, the use of multiple books over the course of the semester can supplement a lecture series

in lieu of a textbook. This presentation will include an accompanying curriculum for integrating book club into your classroom using Robert S. Desowitz's New Guinea Tapeworms and Jewish Grandmothers: Tales of Parasites and People. The presentation itself will be an active learning activity and I will provide guided resources so that you can implement book club in your classroom with ease.

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Showcasing Educational Resources in Parasitology.

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The goal of the ASP Education Committee is to improve teaching, promote investigation, and advance knowledge of parasitology. In the past year the committee has curated a repository of freely available open education resources (OERs) that is available on the ASP website. These resources have been pulled from other open resource collections and are either directly related to parasitology or to core biology topics. Each resource is identified by tags that allow users to search by topic, course level, class size, and has information about student-access to answer keys and if the resource is available in other languages. The objective of this presentation is to demonstrate how ASP members can use this repository to search for course materials. We will also highlight a selection of resources to demonstrate how they could be implemented in a variety of classrooms. The work of the education committee strives to build an integrated community, promote open communication, and assimilate innovative and inclusive teaching practices to grow the American Society of Parasitologists as a world-renowned organization. Our hope is that this presentation garners interest among members to share educational resources and promote educational initiatives within the society.

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Building an Educational Network for Sharing Resources in ASP.

Elliot Zieman[1], J Trevor Vannatta[2], Sarah Orlofske[3], Makedonka Mitreva[4], Maggie Doolin[5], Nicole Chodkowski[6], Christopher Blanar[7], Jimmy Bernot[8], Jeffrey Bell[9]
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Organismal courses, including parasitology, often have limited offerings at many colleges and universities, which presents several challenges to instructors. One way to address this challenge is to provide a framework to standardize instruction of parasitology by teaching foundational concepts and laboratory skills. The ASP Education Committee is working to develop a system for sharing syllabi/outcomes and physical materials, including laboratory slides. During this interactive presentation, we aim to facilitate a network for creating a collection of syllabi/outcomes, curating slide box repositories, and sharing laboratory materials within ASP for little to no cost to help lower barriers for instructors teaching parasitology courses. Audience members will discuss these topics and ideas and

identify resources that they are willing to share and network to get materials they may need for their courses. We aim to host access to these resources through the ASP website in the near future.

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Description of a new species of *Plagioporus* (Digenea: Opecoelidae) infecting the intestine of two catostomids from the eastern USA, including an emended diagnosis, key to Nearctic congeners, and phylogenetic analysis.

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We herein describe a new species of *Plagioporus* Stafford, 1904 infecting the intestine of two catostomids in the eastern USA. We emend *Plagioporus* to account for Nearctic congeners having ceca terminating at the level of the testes (previously diagnosed as having ceca terminating in the post-testicular space only) and testes in the posterior body extremity (a feature not previously considered as having generic importance). Of the accepted Nearctic species, the new species resembles *Plagioporus serotinus* Stafford, 1904, *Plagioporus hypentelii* Hendrix, 1973, and *Plagioporus hageli* Fayton and Andres, 2016 but differs from them by the distribution of the vitellarium and proportional length and relative extent of the excretory vesicle. The new species has vitelline fields that are discontinuous at the level of the ventral sucker (vs. continuous in *P. serotinus* and *P. hypentelii*) and follicles that surround the ceca (vs. wholly ventral to the ceca in *P. hageli*) and that span the midline dorsal to the testes (vs. slightly overlapping the lateral margins of the testes). The excretory vesicle of the new species is wholly post-testicular and short (6–9% of the body length) (vs. reaching the level of the posterior testis, 14–24% of the body length). Phylogenetic analyses of the 28S, ITS1, 5.8S, and ITS2 rDNA recovered the new species sister to *Plagioporus sinitsini* Mueller, 1934. A key to the Nearctic *Plagioporus* spp. is provided. We regard *Plagioporus shawi* (McIntosh, 1939) Margolis, 1970, *Plagioporus serratus* Miller, 1940, and *Plagioporus loboides* (Curran, Overstreet, and Tkach, 2007) Fayton and Andres, 2016 as *incertae sedis*.

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Even more species diversity in the genus *Stillabothrium.*

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Since its erection in 2016, the rhinebothriidean genus *Stillabothrium* has quickly grown to include 12 species. However, ongoing examination of collections indicates that the genus may be much larger in number than is presently understood. Study material was taken from stingrays and guitarfishes collected from Australia, Borneo, Egypt, India, Mozambique, Senegal and the Solomon Islands. Descriptions of several new species are in progress. Ribosomal sequences have been analyzed for 63 samples (including outgroup taxa), including new and previously published sequences, plus sequences selected from Genbank. Analyses thus far indicate the presence of up to 12 new species of *Stillabothrium*. Host use patterns within the genus reveal both strict and more relaxed host specificity, with species parasitic primarily in dasyatid stingrays, but also found in rhinopristiforms. Species of *Stillabothrium* now have been found in marine waters of Australia, the island of Borneo, Egypt, India, Mozambique, Senegal and Taiwan. No species of *Stillabothrium* have been reported from the Americas, but the type of the sister genus *Escherbothrium* was described from the Pacific coast of Costa Rica.

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Underappreciated diversity and complexity in potentially novel order of cestodes.

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The genus *Caulobothrium* remains one of the more poorly known genera of cestodes that parasitize elasmobranchs. New collections from stingrays in Australia, Ecuador, India, Malaysian Borneo, Mexico, Mozambique, and the Solomon Islands yielded what appears to be additional material of this genus. The aims of this study were to investigate the morphological diversity and phylogenetic relationships of the species discovered in these hosts. Cestode specimens preserved in formalin from each host species were prepared for and examined with light and scanning electron microscopy. Sequence data for the D1–D3 region of the 28S rDNA gene for the subset of these species for which material preserved in ethanol was available were generated and a Maximum Likelihood analysis was conducted to assess their phylogenetic relationships. This material was found to include as many as 15 new species of *Caulobothrium* exhibiting a wide array of morphological and anatomical features. In addition to substantially extending the geographic distribution of the genus, these taxa expanded the hosts of *Caulobothrium* to include species in the genera *Himantura*, *Maculabatis*, *Rhinoptera*, *Urobatis*, and *Urotrygon* as well as additional species of *Myliobatis* and *Pastinachus*. The resulting phylogenetic tree provides multiple instances of species parasitizing the same host species that appear to be only distantly related. This work suggests that the ten described members of the genus represent only a small portion of the morphological diversity, host associations, and geographic distribution of this genus overall. We thank Kirsten Jensen for her assistance with the collection of specimens. This work was supported by NSF grants 1921404 & 1921411.

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Chaos out of orders: It's justified!

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Much progress has been made over the last 15 years with respect to reorganizing the higher classification of cestodes to align it with the more robust understanding of their phylogenetic relationships resulting from analysis of a handful of molecular markers. At present 18 monophyletic orders are recognized. However, a number of issues remain with the morphologically heterogeneous acetabulate groups that parasitize sharks and stingrays (i.e., elasmobranchs) referred to as the "Tetraphyllidean relics". The aims of this work were to critically assess the phylogenetic relationships of these groups based on expanded taxon and molecular sampling and, informed by these results, to identify morphological features to further revise cestode ordinal classification. Approximately 400 novel orthogroups were identified using next generation sequencing protocols. Sequence data for these markers were generated for 840 taxa across acetabulate groups. Our results suggest that establishment of as many as nine additional orders is required if ordinal classification is to reflect the phylogenetic relationships of cestodes. Four of these represent one or two closely related families that merely need to be elevated to ordinal level. The remaining five are novel. Of the resulting 27 cestode orders, 16 are composed entirely of taxa that parasitize elasmobranchs; one includes a mix of elasmobranch-hosted, and freshwater and terrestrial hosted taxa. These orders span the breadth of the cestode phylogenetic tree confirming that elasmobranch-hosted cestodes have played a major role in the evolution of most cestode groups hosted by other major groups of vertebrate taxa. This work was supported by NSF grants 1921404 & 1921411.

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Invasive Parasites: A survey of endoparasites in Salvatormerianae populations in Florida.

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The Argentine Black and White Tegu (*Salvator meriane*) is a large lizard native to South America that has been introduced to central and south Florida. With successful breeding populations in at least two

locations, and the ability to acclimate to many temperate climates of the other southeastern states, it is becoming increasingly more important to monitor all biological aspects of this invasive lizard, including their parasites. No detailed published records exist on the endoparasites from these invasive populations. Eighty-nine Argentine Black and White Tegus from two populations in Florida were necropsied to perform an extensive parasite examination of these invasive populations. The necropsies revealed that the tegus brought four species of exotic nematode to Florida from South America (*Physaloptera tupinambae*, *Diaphanocephalus galeatus*, *Cruzialauroi*, *Cruzia fulleborni*) and were also infected with *Raillietiella orientalis*, a pentastome introduced to Florida via invasive Burmese Pythons (*Python bivittatus*). The invasive pentastome is known to infect native snakes and cause harm to their respiratory tracts. It is unknown how the exotic parasites from the tegus will impact native Florida reptiles, however, the ability for *R. orientalis* to infect the Argentine Black and White Tegu could lead to the rapid spread of this invasive parasite throughout the southeastern United States.

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Cyathostomins and Mucus: Evaluation of the host histopathologic changes in naturally acquired infections.

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Cyathostomins are pervasive parasites of horses that can cause a potentially life threatening disease, “larval cyathostominosis,” which occurs when large numbers of encysted larvae synchronously excyst from the wall of the large intestine and is fatal in 50% of cases. Anthelmintics that are adulticidal only, such as ivermectin, have been implicated in triggering this condition. Alternatively, only moxidectin and fenbendazole are labeled to treat the encysted stages, have also been implied to cause disease. There is limited knowledge of the local inflammatory response to the larvae and to the anthelmintic treatments. The following took place in two parts, Fall 2015 and Fall 2019. In each set, 36 ponies with naturally acquired cyathostomin infections were randomly allocated to 3 groups. In 2015 Group 1 received fenbendazole at 10mg/kg for 5 days, Group 2, Moxidectin at 0.4mg/kg, and Group 3, untreated controls. In 2019, Group 1 received Ivermectin at 0.2mg/kg, Group 2, Moxidectin at 0.4mg/kg, and Group 3 were untreated controls. Tissue samples from the cecum and dorsal and ventral colons were used for histopathological evaluation. Scores were given between 0-3 for all inflammatory cell types, as well as fibrous connective tissue. Larvae observed were counted and classified by stage, and mucosal ulcerations and submucosal granulomas were also enumerated. Between the groups, it was found that the control groups had significantly higher larval scores and inflammation associated with the larvae ($p=$. The treatment groups saw little differences between larval counts and between Inflammatory cell populations ($p>0.05$). Correlations between the larval, weeks post treatment, and goblet cell hyperplasia between groups, with higher numbers of larvae found with increasing goblet cell hyperplasia scores ($p=0.047$). There were also differences noted among timepoints and tissue types, regardless of treatment ($p=0.495$). This also suggests that the organs respond differently to treatment and to the larvae themselves, which may have implications in the disease process and for treatment. These studies illustrate the important host response to parasites within equine tissues.

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Retrospective evaluation of gastrointestinal nematodes in commercial North American bison herds. 2017-2021 at the Texas A&M University Parasitology Diagnostic Laboratory.

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Gastrointestinal nematodes (GIN) are among the main causes of production and economic losses in livestock, including commercial bison. In bison, GIN generally cause subclinical disease; however, reports of clinical disease and mortality are not uncommon, particularly in the southern United States (US). Among the most pathogenic GIN are the abomasal genera *Haemonchus* and *Ostertagia*, for which anthelmintic resistance has been reported in cattle. Using retrospective data from the Texas A&M University (TAMU) Veterinary Parasitology Diagnostic Laboratory, we evaluated the occurrence of GIN reported in commercial North American bison across 15 states from 2017 to 2021. Of the 4,593 fecal samples received, 2,900 (63.1%) were from Texas (TX). Samples were analyzed using a modified Wisconsin double-centrifugal flotation for quantification of trichostrongylid eggs per gram (EPG), and, qualitatively, for the presence of GIN and other endoparasites. Overall, eggs of GIN were found in 3,954 (86.10%) of samples (TX= 2,578, 88.90%). The average EPG for trichostrongylids in TX were evaluated over the five years for calves (2017= 116.9 ± 338.8; 2018= 203.1 ± 307.8; 2019= 172.1 ± 313.1; 2020= 137.3 ± 322.5; 2021= 99.2 ± 242.1), yearlings (2017= 46.7 ± 156.4; 2018= 74.3 ±127.3; 2019= 127.4 ± 264.8; 2020= 198.9 ± 272.6; 2021= 295.9 ± 665.6), and mature bison (2017= 72.5 ± 226.3; 2018= 66.4 ± 135.9; 2019= 75.3 ± 298.7; 2020= 46.2 ± 65.7; 2021= 45.5 ± 141.0). In addition, eleven endoparasite genera were found in flotations, namely: *Eimeria* (US= 52.5%, TX= 45.3%), *Moniezia* (US= 15.1%, TX= 15.0%), *Nematodirus* (US= 6.7%, TX= 1.6%), *Trichuris* (US= 5.9%, TX= 5.5%), *Strongyloides* (US= 1.2%, TX= 1.2%), and *Aonchotheca* (= *Capillaria*) (US= 0.9%, TX= 0.4%). Pooled coprocultures were processed for 75.4% (TX= 71.7%) of the samples for genus-level morphological identification of trichostrongylid third-stage larvae. In summary, the TAMU Parasitology Diagnostic Laboratory confirmed that GIN are ubiquitous endoparasites of commercial bison herds, and their EPG level are highly variable across herds and age classes. This retrospective study highlights the importance of routine fecal examination in bison herds which may inform proper management, including anthelmintic treatments, to mitigate the potential negative impact of GIN on bison production.

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Intestinal parasites of juvenile and adult female bison of the Texas state herd.

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Parasites can have a significant effect on the typical growth, weight gain, and milk production of hoofstock. Therefore, infections are often managed with common anthelminthics. Texas Parks and Wildlife Department (TPWD) biologists manage the Texas herd of Southern Plains Bison (*Bison bison bison*) at Caprock Canyons State Park (CCSP), Briscoe County, in the Texas Panhandle, and base management plans on the health of the heard and on native prairies restoration to preserve the historic herd. The purpose of this study is to determine the need for anthelminthic treatment in the CCSP herd. Our goals are: to 1) characterize the gastrointestinal parasites infecting the herd and 2) compare fecal egg count in treated and untreated bison. In January 2020 and February 2021, TPWD treated half of the bison sampled (n = 50) with a pour-on moxidectin-based product (Cydectin®), leaving the remaining half (n = 50) untreated. Fecal samples were collected prior to treatment during examination of individuals. Fecal samples were opportunistically collected from a subset of the herd nine times in both 2020 and 2021. Samples were processed for intestinal parasites using a modified McMaster's fecal float protocol. The Baermann technique was performed in samples collected December 2020 to April 2021 to test for the lungworm, *Dictyocaulus*. We assessed the effect of treatment and age on differences in fecal egg count in January 2020 using a generalized linear model for strongylid nematodes. We observed four different parasite types: *Eimeria* (adults: 84.5%, juveniles: 60.5%), *Moniezia* (adults: 8.5%, juveniles:

97%), *Strongyloides* (adults: 1%, juveniles: 3%), and strongylid nematodes (adults: 41.5%, juveniles: 69.5%). No *Dictyocaulus* larvae were found in any of the analyzed samples. We found no effect of treatment after 30 days; however, juveniles had a greater decrease in strongylid nematodes infection post treatment compared to adults. Although our sample size was small, TPWD continues anthelminthic treatment of both juvenile and adult bison.

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Periodicity and density-dependent dynamics of migratory bird pathogens.

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The ecological dynamics of host-pathogen systems often change over time, typified in many cases by systemic temporal variation in pathogen prevalence. Long term datasets are crucial to understanding the temporal dynamics of natural populations, allowing for a robust approach in identifying variability of prevalence and diversity over time. In this study, we use a novel data source of data, in the form of a long-term collection of salvaged birds housed at the Field Museum of Natural History in Chicago, Illinois, USA. We document temporal variation in the prevalence of three genera of avian Haemosporidians (*Haemoproteus*, *Plasmodium*, and *Leucocytozoon*) in 4,306 individuals from four species of migratory *Catharus* thrushes collected during spring and fall migration over a 24-year time period (1996-2019). We use heirarchical Bayesian modeling to infer periodicity in pathogen prevalence, identifying cycling patterns unique to each host species-pathogen genus pairing. We complement this with a density-dependent model of migratory bird epizootics and identify parameter ranges inferred from the results of the identified cycles. We determined that avian haemosporidians exhibit distinct seasonality generally exhibiting higher prevalence in the fall than the spring, multi-year periodicity spans 8-19 years depending on the host-pathogen pair, and that factors relating to host population size, such as net fecundity, reasonably replicate the patterns observed in the statistical model, resulting in a plausible mechanism driving periodicity of avian haemosporidians.

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Helminth parasites in migratory bird hosts of the family Turdidae.

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Current federal protections on neotropical migrant songbirds have caused a decline in parasitological research on these hosts. However, fatalities from building collisions provide a unique opportunity to investigate host specificity and parasite diversity among migratory songbirds. The purpose of this research is to survey the community of ocular and intestinal helminth parasites that inhabit migratory birds of the family Turdidae. Songbirds were salvaged and frozen during the migration seasons of 2017-2018 by Audubon's Lights Out Cleveland and processed by the Natural History Museum of Cleveland, where eyes were preserved in formalin and intestines were refrozen. Frozen and fixed tissues were shipped and examined at Sam Houston State University. Parasites are currently being processed and identified. Prevalence and abundance will be determined for each parasite in each host species. Six host species (veery, gray-cheeked thrush, wood thrush, hermit thrush, Swainson's thrush, and American robin) have been processed for eyeworms (n = 3, 9, 10, 33, 16, and 4, respectively) and intestinal helminths (n = 1, 1, 0, 24, 17, and 4, respectively). The veery, gray-cheeked thrush and wood thrush did not harbor any parasites, likely due to the small sample sizes. Five eyeworms, *Oxyspirura* sp., were found in a single hermit thrush, and none were found in any other host species. Thus far, acanthocephalan specimens from the hermit thrush have been identified as *Plagiorhynchus cylindraceus* with a 33.3% prevalence and abundance of 1.83 worms per bird. To date, we have identified several

nematode specimens from the hermit thrush: *Capillaria caudinflata*, *Capillaria contorta*, *Odontoterakis valvata*, *Porrocaecum ensicqudatum*, and *Contracaecum* sp. The two *Capillaria* species have previously been reported only to genus in the hermit thrush. The other three nematodes have never been reported in the hermit thrush, and to our knowledge, the genus, *Odontoterakis*, has not been previously reported in North America.

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The effects of seasonal rainfall on parasitism in bison.

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An essential part of livestock management is the prevention and treatment of parasitic infection to avert disease and developmental issues. The potential for host infection by parasites is heavily dependent on the level of environmental contamination with infective stages, which can be primarily driven by seasonal factors, such as rainfall, humidity, and temperature. One seasonal factor, rainfall, can have an immediate effect on humidity and soil moisture, which are essential for development and survival of environmental stages of various livestock parasites, including gastrointestinal coccidians and helminths. Consequently, this may lead to increased levels of parasitic infection in livestock and other grazing animals with limited mobility. The Texas herd of Southern Plains Bison (*Bison bison bison*) is located at Caprock Canyons State Park and is managed by the local Texas Parks and Wildlife Department biologists to ensure the health of the herd and preservation of the species. Our research seeks to evaluate the relationship, if any, between monthly rainfall and intestinal parasites of adult female and juvenile bison. Starting in January 2020 through October 2021 we collected bison fecal samples 18 times out of the 22-month period. Fecal samples were processed using a modified McMaster's test with 2 grams of fecal matter by Tarleton State University and 5 grams by Texas A&M University Parasitology Diagnostic Laboratory to identify the presence of coccidia and fecal egg count of helminths. We obtained rainfall data from a nearby NOAA gauge in Briscoe County. We calculated monthly rainfall data for 30 and 60 days prior to each collection date. Linear models will be used to assess the effect of prior rainfall on parasite eggs/gram count in the state bison herd.

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Non-invasive sampling revealed not one, but two protostrongylid parasites in white-tailed deer (*Odocoileus virginianus*) in Western Manitoba.

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Wildlife managers are concerned that meningeal worm (*Parelaphostrongylus tenuis*) is negatively affecting moose (*Alces alces*) populations in some areas of Manitoba due to slower than anticipated recovery from decline. Moose are aberrant hosts and experience severe pathology whereas white-tailed deer (WTD, *Odocoileus virginianus*), the common host, experience less pathology and are responsible for spreading larvae into the environment. Meningeal worm prevalence from hunter-harvested WTD heads suggests that moose populations are at higher risk of infection where populations are a concern. However, the shedding rates of larval meningeal worm from WTD in these areas are unknown, particularly because larvae are morphologically indistinguishable from muscleworm (*Parelaphostrongylus andersoni*). We investigated the spatial and temporal variation of protostrongylid larval prevalence in WTD feces (i.e. shedding rate) from four game hunting areas (GHA); two where there is concern for moose populations and two where there is not. We hypothesized that moose would

be at higher risk of infection where and when there are higher shedding rates. Further, we expected to only recover meningeal worm, as muscleworm had only been reported from more northern areas of Manitoba. Over the course of two years, we collected WTD fecal pellets three times throughout the summer along two 700 m transects from six locations in each GHA. We obtained larvae through fecal sedimentation and sequenced the partial cytochrome oxidase I gene to confirm species identity. Zero-inflated models showed that larval parasite prevalence did not differ between collection trip or year but was higher in GHAs where there is concern for moose populations. Genetic analyses of a subset of DSL collected (n = 19) revealed that meningeal worm and muscle worm were both present in Western Manitoba and co-occurred at three of the four GHAs. Our results reveal novel insights for the geographic distribution of muscleworm and emphasize the importance of using genetic analyses to identify protostrongylid larvae in WTD fecal pellets. Our results suggest that risk of parasite infection is higher where there is concern for moose populations, so conservation efforts aimed at preventing moose declines in Western Manitoba should incorporate transmission risk of meningeal worm into management plans.

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Multi-locus phylogenetic relationships among *Onchocerca* isolates from New York and Californian ungulates.

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Recent evidence shows that the biodiversity of *Onchocerca* associated with wild North American ungulates is much greater than previously known. Initial reevaluation of the *Onchocerca cervipedis* species complex has revealed at least four distinct genetic isolates, however, it remains unclear whether two of these isolates (i.e., New York and California) belong to two distinct species or are conspecific. To address this question, we collected ear tissue samples of white-tailed deer (*Odocoileus virginianus*; n= 15) from ten central New York counties and extracted genomic DNA of 5x5cm samples of skin from near the edge of the pinnae. Out of the collected samples, 80% were found to be positive for the same *Onchocerca* isolate previously reported from New York. As currently available molecular data for the New York isolate is scarce, with only a single genetic marker (*nad5*) overlapping with the California isolate, we performed PCR and sequencing targeting three mitochondrial (*cox1*, *nad5*, 12S) and two nuclear (18S, 28S) markers. Genetic distance analyses revealed the two isolates to have an average pairwise distance of 3.95% (3.17-5.62%) for *cox1*, 2.26% (1.82-3.27%) for *nad5*, and 1.77% (1.38-2.22%) for 12S. Distances among these and other North American ungulate *Onchocerca* isolates and other *Onchocerca* species were also calculated. Phylogenetic tree depicted two well-supported clades for markers *cox1* (97%; 99% bootstrap support) and 12S (96%; 89%). In contrast, analysis of *nad5* clustered both isolates in a well-supported clade (95%), divided into three subclades; one comprising all New York isolates (76%) and two comprising the California isolates (94%; 89%). These mitochondrial markers suggest that the New York and California isolates represent two distinct species, however, their phylogenetic relationships remain not fully resolved. The 18S and 28S nuclear markers were very conserved and less informative for species discrimination. These results highlight the need to utilize multiple genetic markers to help discern closely related filarial nematode species and will aid in our efforts to untangle the *Onchocerca* species complex infecting wild North American ungulates.

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Opening a can of (lung)worms: molecular characterization of *Dictyocaulus* (Nematoda; Dictyocaulidae) infecting North American bison (*Bison bison*).

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Dictyocaulus is a globally distributed genus of lungworms of domestic and wild ungulates. *Dictyocaulus* adults inhabit the bronchi, frequently causing subclinical and clinical disease, and that impacts animal health and production. North American bison (*Bison bison*) and cattle (*Bos taurus*) share various parasitic nematode species, particularly in areas where co-grazing occurs. The current assumption is that North American bison share the lungworm *D. viviparus* with cattle, but this has not been confirmed on a molecular basis. The aim of this study was to molecularly characterize *Dictyocaulus* lungworm isolates from North American plains bison (*Bison bison bison*). Fecal samples were collected from 5 wild conservation bison herds located in Iowa, North Dakota, Oklahoma, Colorado, and Montana in 2019 and 2020, and from ranched and feedlot bison from 2 herds in Oklahoma and Texas. First-stage lungworm larvae (L1) were isolated via Baermann technique. Genomic DNA was extracted from L1s of up to 3 samples per herd per year, followed by PCR and sequencing targeting the internal transcribed spacer 2 (ITS2) region of the nuclear ribosomal DNA and the partial cytochrome oxidase c subunit 1 (*cox1*) of mitochondrial DNA. Phylogenetic analyses were performed in MEGA X 10.1 using the Maximum Likelihood method. Generated ITS2 (n=72) and *cox1* (n=68) sequences were deposited in GenBank. Pooled L1 from each herd were deposited in a Museum Collection. Sequences of North American plains bison *Dictyocaulus* belong to a single, uncharacterized species, clustering in well-supported clades (99% and 100% bootstrap support for ITS2 and *cox1*, respectively), differing from *D. viviparus* of cattle in North America and Europe (88.3-90.7% and 87.7-89.1% similarity for ITS2 and *cox1*, respectively), and European bison (*Bison bonasus*) (90.1-90.8% and 87.9-88.8% similarity for ITS2 and *cox1*, respectively). Our results contradict previous assumptions regarding parasite identity, highlighting the need for characterization of this species through morphological and molecular methods, elucidating its biology and host range, and potential impact on host health. Further investigation into the biodiversity of *Dictyocaulus* species infecting bovids and cervids in North America is warranted.

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The emerging view of gregarine phylogeny.

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“Gregarines” constitute a diverse group of protists that are common intestinal parasites of annelids, mollusks, arthropods, urochordates, and echinoderms. Although the group’s diversity is probably largely undescribed, attempts to postulate a plausible phylogeny of the group date to at least 1900. With the advent of accessible small-scale DNA extraction and sequencing, SSU data is now available for a relatively large number of gregarine taxa across a significant breadth of morphologically defined family and superfamily groups. Our phylogenetic analysis of 100 apicomplexan taxa includes 97 species of gregarines and an outgroup of 3 coccidian taxa across an aligned sample of 1,439 bases of the 18s gene. A maximum-likelihood analysis strongly supports 7 in-group clades corresponding to the superfamilies Gregarinoidea, Stylocephaloidea, Actinocephaloidea, Ancoroidea, Lecudinoidea, Cephaloidophoroidea, and Selenidoidea. Although each superfamily clade is strongly supported, the same is not true for the relationships between superfamilies. Superfamily clades and their interior family clades show stronger support with increased taxonomic sampling, but long-branch attraction effects are still obvious in the overall phylogeny. Superfamily and family level clades show strong host associations and support the hypothesis that speciation in gregarines tracks hosts as resources across time. Although prior systematic arrangements have relied heavily on the presence/absence of septa in trophozoites, presence/absence of schizogony in the life cycle, and elaborations of the holdfast structure, these characters are not supported by molecular phylogenetic analysis. Septa in trophozoites have been gained and lost several

times across different superfamilies and existing arrangements based on septa should be abandoned. Similarly, schizogony appears to have been present in early lineages and subsequently lost only to reappeared in a single clade within Actinocephaloidea. Thus, the neogregarines constitute an interior clade of Eugregarina rather than a separate ordinal lineage.

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Hiding in Plain Sight: What can endogenous development tell us about coccidian diversity of *Acroeimeria lineri* and other coccidians from introduced populations of the mediterranean house gecko, *Hemidactylus turcicus* and the tropical house gecko, *H. mabouia*?

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We sampled Mediterranean house geckos, *Hemidactylus turcicus*, from Oklahoma and examined them for coccidia. Thirty-one percent of geckos shed ellipsoid tetrasporocystid oocysts with a smooth bi-layered wall. These oocysts were most similar to *Acroeimeria lineri* previously reported from *H. turcicus* in the United States, Egypt, Israel and Turkey and from the tropical house gecko, *H. mabouia*, from South Africa. However, a recent study on oocyst morphology and endogenous development of *A. lineri* of *H. turcicus* collected from Egypt suggests that *A. lineri* may represent a complex of species. As a result, we expanded our survey and examining the introduced tropical house gecko, *H. mabouia* from Florida for coccidian infections as it has also been reported as a host for *A. lineri* in South Africa. Based on oocysts morphology we identified *A. lineri* infections in *H. mabouia* from Florida. However, using histological techniques our work indicates that the endogenous development of *A. lineri* varied considerably in these two gecko species with eipicytoplasmic development in *H. turcicus* and intracytoplasmic development in *H. mabouia*, suggesting that oocysts identified as *A. lineri* from these two species of geckos may represent multiple species of coccidians. To get a better understanding of these coccidian parasites, we amplified a partial 18s rRNA gene from intestinal endogenous stages from *H. turcicus* and *H. mabouia* shedding oocysts of *A. lineri* and compared them to available partial 18s rRNA sequences of *A. lineri* from *H. turcicus* from Egypt. Our partial 18s rRNA sequences from *H. mabouia* and *H. turcicus* were distinct and differed from available partial 18s rRNA sequences of *A. lineri* from *H. turcicus* from Egypt. More importantly, our phylogenetic analyses of all available 18s rRNA sequences of *Acroeimeria* and *Choleoeimeria* species from New and Old World lizard species indicated two distinct *Acroeimeria* clades with either eipicytoplasmic or intracytoplasmic development. Finally, our work represents the first report of *Acroeimeria lineri* from *H. turcicus* in Oklahoma and the first report of *Acroeimeria* cf. *lineri, Choleoeimeria* sp., *Eimeria dixoni*, and *Isospora hemidactyli* from an introduced population of *H. mabouia* in the United States.

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The dismantling of the "Tetraphyllidea" saga: Proglottids to the rescue!

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The polyphyletic "Tetraphyllidea" has recently undergone major rearrangements. Thus far, the dismantling of the "Tetraphyllidea" has led to the erection of three new orders. However, many taxa remain as relics. To better understand these relics, our study focused on members of the poorly known Clade 1—a group historically allied with the Rhinebothriidea, which parasitize skates, orectolobiform sharks, and electric rays. At present four species are recognized in Clade 1, largely based on their bothridial morphology, which consists of four or five large, facial loculi. Among these, those with five loculi are currently assigned to the genus Pentaloculum, known from orectolobiform sharks and electric rays. The species with four loculi from skates is assigned to the monotypic Zyxibothrium. Examination of

the cestodes of two additional skate species revealed two new cestode species, one with bothridia with five large facial loculi and one with three large facial loculi. Generic assignments based on this morphology suggest that the species with five loculi belongs to Pentaloculum and the one with three loculi may represent a new genus. Sequence data for the partial 28S rDNA gene were generated for both new species. These were combined with comparable data for Pentaloculum, Zyxibothrium, and other elasmobranch-hosted taxa from GenBank in a Maximum Likelihood phylogenetic analysis. The resulting phylogeny confirms that members of Clade 1 likely represent a new order. Surprisingly, only two subclades emerged within Clade 1. One consisted of the existing Pentaloculum species, all with five facial loculi, from electric rays and carpet sharks. The second was a subclade consisting of Zyxibothrium and both new species, collectively with three, four, or five loculi, all of which parasitize skates. Further support for these two subclades comes from proglottid anatomy. Species in the Pentaloculum subclade differ from those in the Zyxibothrium subclade in the location of the genital pore and the number of testes. Conflicting affinities revealed by scolex and proglottid morphologies has been observed in other cestode groups, such as the Lecanicephalidea, and furthers our understanding of the morphological evolution of elasmobranch cestodes in a phylogenetic framework. This work was supported by NSF grants 1921404 & 1921411.

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Measuring variation in drug response in schistosome population using the Single Worm Analysis Movement Pipeline (SWAMP).

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Schistosomes are outbred, sexually reproducing parasites and extensive genomic and phenotypic variation is found within natural and laboratory populations.
We have previously demonstrated that there is standing variation for oxamniquine resistance in *S. mansoni* populations that resulted in treatment failure in Brazil and East Africa. As new anti-schistosomal drugs are developed, it is important to determine levels of pre-existing phenotypic variation in response to these compounds.
We hypothesize that there will be extensive phenotypic and genetic variation for drug response within schistosome populations. Using a newly developed movement assay (SWAMP - Single Worm Analysis Movement Pipeline), we are quantifying phenotypic variation in drug response to nine drugs in our genetically diverse laboratory schistosome populations. The presence of natural genetic variation in drug response within schistosome populations allows use of whole genome association methods to determine the genomic region(s) involved, and ultimately to decipher the mechanism(s) of action of these drugs.
Our ultimate goal will be to examine natural variation of field populations of schistosome from Kenya using SWAMP. This new drug testing platform deployed in Africa would be extremely valuable for testing the efficacy of newly developed, refined or repurposed drugs on genetically diverse field populations of parasites, and identify potentially resistant or highly tolerant parasites to these compounds.

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Novel Therapeutics Against Human Schistosomiasis.

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Human schistosomiasis is a neglected tropical disease caused by parasitic worms. It affects over 250 million people globally. Most human infections are caused by *S. mansoni*, *S. haematobium*, and *S. japonicum*. Currently there is only one method of treatment for human schistosomiasis, the drug praziquantel. Constant selection pressure has caused a serious concern because of the potential development for resistance to praziquantel. This has led to the urgent need for additional pharmaceuticals, with a distinctly different mechanism of action, to be used in combination therapy with praziquantel. Previous treatment of *Schistosoma mansoni* included the use of oxamniquine (OXA), a prodrug that is enzymatically activated by a sulfotransferase, an enzyme produced by *S. mansoni*. Although sulfotransferases are produced by *S. haematobium* and *S. japonicum*, OXA is not effective against these two species. Also, praziquantel is not effective against juvenile stages of the parasite. Structural data have allowed for directed drug development in re-engineering oxamniquine to be effective against *S. haematobium* and *S. japonicum*. Guided by data from Xray crystallographic studies and *Schistosoma* worm killing assays more than 350 OXA derivatives were designed synthesized and tested *in vitro* against the adult parasites. To date, our study has identified reengineered derivatives that are highly effective in killing all three human schistosome species, juvenile stages, and a praziquantel resistance strain *in vitro*. *In vivo* studies revealed that three of these derivatives caused a significant reduction in the number of worms from *S. mansoni*, *S. haematobium*, and *S. japonicum* infected animals. In addition, treating infected mice with these derivatives during juvenile stages of development led to significant reduction in the number of immature worms. The later result is an advance over praziquantel that does not kill immature schistosomes.

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ASP Meeting History

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2014 New Orleans LA
2015 Omaha NE
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* With the American Society of Tropical Medicine; since 1952, American Society of Tropical Medicine and Hygiene
ǂ With the American Institute of Biological Sciences
+ With the Helminthological Society of Washington
§ 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 Association
ϕ With the American Association of Veterinary Parasitologists
ϗ With the Society of Protozoologists
Ↄ With the Society of Nematologists
⊕ With the Parasitology Section of the Canadian Society of Zoologists
Δ With the Sociedad Mexicana de Parasitología
ʊ With the Quebec Molecular Parasitology meeting
¤ With the International Coccidiosis Conference