

The 96th Annual Meeting of the American Society of Parasitologists

July 26th and 27th, *Accelevents* virtual event platform



Program and Abstracts

Welcome

We would like to welcome you to the 96th annual meeting of the American Society of Parasitologists.

Founded in 1924, the American Society of Parasitologists comprises a diverse group of about 700 scientists from academia, industry, and government involved in the study and teaching of the scientific discipline of parasitology. Society members contribute to the development of parasitology as a discipline, as well as to primary research in behavior, biochemistry, ecology, immunology, medicine, molecular biology, physiology, systematics, and other related fields of science.

Thanks to everyone who helped make this virtual meeting possible.

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All times are EDT	
JULY 26	
10:30 am-12:30 pm	Welcome/ President's Symposium
12:45-1:45 pm	2020 H. B. Ward Lecture
1:45-2:45 pm	Lunch Lounges
3:00-4:00 pm	Session 1A Taxonomy, Systematics & Phylogeny
3:00-4:00 pm	Session 1B Host & Parasite Interactions
3:00-4:00 pm	Session 1C Genomics & Molecular Biology
4:15-5:15 pm	Session 2A Taxonomy, Systematics & Phylogeny
4:15-5:15 pm	Session 2B Biochemistry & Physiology/ Chemotherapy & Drug Resistance
4:15-5:15 pm	Session 2C Life Cycles & Epidemiology
5:30-7:00 pm	Poster session
7:00-8:30 pm	Networking Lounges
JULY 27	
10:30-11:30am	President's Address
11:35 am-12:35 pm	2021 H. B. Ward Lecture
12:45-1:45 pm	Session 3A Taxonomy, Systematics & Phylogeny
12:45-1:45 pm	Session 3B Host & Parasite Interactions
12:45-1:45 pm	Session 3C Evolutionary Ecology
12:45-1:45 pm	Education Workshop
1:45-2:45 pm	Lunch Lounges
2:45-4:45 pm	Student Symposium
5:00-6:00 pm	Session 4A Taxonomy, Systematics & Phylogeny/ Life Cycles & Epidemiology
5:00-6:00 pm	Session 4B Host & Parasite Interactions
5:00-6:00 pm	Session 4C Evolutionary Ecology
6:15-7:15 pm	Session 5A Life Cycles & Epidemiology
6:15-7:15 pm	Session 5B Host & Parasite Interactions/ Immunology
6:15-7:15 pm	Session 5C Vector Biology/ Genomics & Molecular Biology
7:30-8:30 pm	Auction results and closing comments

Monday 26th July

10:30 am-12:30 pm **WELCOME TO ASP 96TH MEETING AND ASP PRESIDENT'S SYMPOSIUM**

Presiding: **Tami Cook**, Sam Houston State University.

Theme: "Retooling parasite ecology and for genomics and metagenomics era".

10:40 (1) **Stephen Greiman.** Hidden communities: seasonal cestode and bacterial community dynamics within the guts of two North American *Sorex* shrew species.

11:10 (2) **Holly Lutz.** Associations between Afrotropical bats, eukaryotic parasites, and microbial symbionts.

11:40 (3) **Spencer Galen.** Parasite genomic resources: challenges and opportunities.

12:10 Questions. Closing remarks.

12:30-12:45 pm **BREAK**

12.45-1.45 pm **2020 H. B. WARD LECTURE**

Thomas Platt. Introduction of the 2020 H. B. Ward Medal recipient.

Stephen Ash Bullard. "Acceptance of the 2020 Henry Baldwin Ward Medal"

1:45-2:45pm **LUNCH BREAK**

Please visit one or more of the themed lounges so you can socialize and network with other parasitologists.

2:45-3:00 pm **BREAK**

3:00-4:00 pm **Session 1A: Taxonomy, Systematics & Phylogeny**

3:00 (4) Redescription of *Cathariotrema selachii* (MacCallum, 1916) Johnston and Tiegs, 1922 (Monogenoidea: Monocotylidae), emendation of monotypic *Cathariotrema* Johnston and Tiegs, 1922, and proposal of a new subfamily based on morphological and nucleotide evidence.

Stephen A Bullard, Micah B Warren, Haley R Dutton.

3:15 (5) Fresh insights into the New World members of the Family Nippostrongylinae.
Guinevere O Drabik, Agustín Jiménez.

- 3:30 (6) A new species of Harmotrema (Digenea: Liolopidae) infecting the intestine of side-necked turtles (Pleurodira: Pelomedusidae) in Mozambique and South Africa.
Haley R. Dutton, Louis H. DuPreez, Stephen A. Bullard.
- 3:45 (7) How many origins of parasitism in copepods? A new count with a review of the evidence from phylogenetics, morphology, and natural history.
James P Bernot, Geoffrey A Boxshall.

3:00-4:00 pm Session 1B : Host & Parasite Interactions

‡ denotes student presentation in the Best Student Presentation Competition

- 3:00 (8)‡ Reduction of *Ascaridia galli* pathology by *Salmonella typhimurium* in broiler chicken.
Eric Igor Sop Foka, Cedric Yamssi, Ben Enyetoranye, Christelle Nadia Noumedem Anangmo, Mpoame Mbida, Theodore B Mayaka.
- 3:15 (9) Forecasting endemic spillover hosts for zoonotic pathogens in South Africa using network analyses.
Heike Lutermann, Dina Fagir.
- 3:30 (10)‡ Invasive parasites: A survey of endoparasites from *Salvator merinae* populations in Florida.
Marisa Fonseca, Gabriel Langford.
- 3:45 (11) Comparison of endohelminths of the black drum (*Pogonias cromis*) and the red drum (*Sciaenops ocellatus*) from an estuarine system.
Hannah C McNeese, Autumn J Smith-Herron, Tamara J Cook.

3:00-4:00 pm Session 1C: Genomics & Molecular Biology

‡ denotes student presentation in the Best Student Presentation Competition

- 3:00 (12) Factors regulating *Strongyloides stercoralis* male development differ from *Caenorhabditis* species.
Damia Gonzalez Akimori, Emily J Dalessandro, Thomas J Nolan, Christopher R Stieha, James B Lok, Jonathan DC Stoltzfus.
- 3:15 (13)‡ Elucidation of the role of dense granule 1 in *T. gondii* and its application in a diagnostic assay.
Hannah E Steinberg, Amanda Haymond, Andrea Diestra, Weidong Zhou, Lance A Liotta, Nancy E Freitag, Maritza Caleron, Vernon B Carruthers, Alessandra Luchini, Robert H Gilman.
- 3:30 (14) Characterization of the highly diverse genomic regions of an important African vector of schistosomiasis.
Ryan Burd, Jared Cayton, Tom Pennance, Jacob A Tennesen, Fredrick Rawago, Maurice Odieri, George Owino, Michelle L Steinauer.

3:45 (15) Population genomic structure in marine tapeworms: The importance of host species versus geographic locality.
Kaylee S Herzog, Kirsten Jensen.

4:00-4:15 pm BREAK

4:15-5:15 pm Session 2A: Taxonomy, Systematics & Phylogeny

‡ denotes student presentation in the Best Student Presentation Competition

4:15 (16) The parasites of Oneida Lake fishes: Then and now.
Florian B Reyda, Emma Nielsen, Isaiah Crosbourne, Stephen Curran, Thomas Brooking.

4:30 (17) Integrative taxonomy of *Posthodiplostomum*.
Kari D Waddle, Isa Blasco-Costa, Autumn Smith-Herron, Nicci Carpenter, Kristin Herrmann.

4:45 (18) Redescription and molecular barcoding of a transatlantic monogenean *Allogastrocotyle bivaginalis* Nasir & Fuentes Zambrano, 1983, parasites of *Trachurus picturatus* off the southern Mediterranean Sea.
Chahinez Bouguerche, Fadila Tazerouti, Delphine Gey, Jean-Lou Justine.

5:00 (19)‡ A new species and emendation of *Pseudoparamacroderoides* Gupta and Agarwal, 1968 (Digenea: Macroderoididae), with comments on the systematics of macroderoidid genera.
Triet N Truong, Stephen S Curran, Haley R Dutton, Stephen A Bullard.

**4:15-5:15 pm Session 2B: Biochemistry & Physiology
Chemotherapy & Drug Resistance**

‡ denotes student presentation in the Best Student Presentation Competition

4:15 (20)‡ Glycogen branching and debranching enzymes from the parasitic protist *Trichomonas vaginalis*.
Karoline Dittmer, Prajakta Pradhan, Quentin C Tompkins, Andrew Brittingham, Wayne A Wilson.

4:30 (21)‡ Efficacy of a combinational drug therapy against chronic *Toxoplasma gondii*.
LeeAnna M Lui, Austin G Sanford, Alexander Wallick, Braydon Dreher, Paul H Davis.

4:45 (22)‡ Comprehensive study of parasites of the Texas state bison herd: Part 2.
Sara B Boggan, Heather A Mathewson, Kristin Herrmann, Donald Beard, Gui Verocai.

5:00 (23)‡ Field application of salt, magnesium sulfate, Dylox, formalin, and hydrogen peroxide for killing parasitic copepods (Siphonostomatoida: Lernaepodidae: *Achtheres*) infecting white bass (*Morone chrysops*) and striped bass (*Morone saxatilis*).
Justin D Krol, John Damer, Haley Dutton, Steve Curran, Stephen A Bullard.

4:15-5:15 pm **Session 2C: Life Cycles & Epidemiology**

‡ denotes student presentation in the Best Student Presentation Competition

- 4:15 (24) Development of selected tapeworms of the round stingray, *Urobatis halleri* (Myliobatiformes: Urotrygonidae), in Southern California.
Ralph G Appy.
- 4:30 (25)‡ Current status of intestinal parasites among elementary school children in Sohag, Egypt.
Eman Fathi Fadel.
- 4:45 (26) Flat-headed mayflies (Heptageniidae) as a likely paratenic host of *Chordodes morgani* (Nematomorpha).
John F Shea, James Marchant, Anna Sniezek.
- 5:00 (27)‡ Five thousand trout and 400 oligochaetes later: Geographic distribution of *Myxobolus cerebralis*, the first diagnosed case of salmonid whirling disease, and detection in two non-*Tubifex tubifex* oligochaetes in the Southeastern United States.
Steven P Ksepka, Jacob M Rash, Brandon Simcox, Doug Besler, Micah B Warren, Haley R Dutton, Stephen A Bullard.

5:15-5:30 pm **BREAK**

5:30-7:00 pm **POSTER SESSION**

‡ denotes student presentation in the Best Student Presentation Competition

Host & Parasite Interactions

- (28) Assessing the healthcare burden of parasites: An analysis of hospital discharge records for characterizing patients and analyzing trends in human cestode cases in Nevada for 2013-2019.
Chad L Cross, Brianna Rivera, Francisco Sy.
- (29) Nanoparticle-enhanced mass spectrometry: Discovery of novel *Trypanosoma cruzi*-specific urinary peptides in Chagas disease congenitally infected infants.
Raghad Almofeez, Paul Russo, Weidong Zhou, Ruben Magni, Hannah Steinberg, Kathryn Cassels, Yagahira Castro, Freddy Tinajeros, Manuela Versategui, Edith Malaga, Beth J Condori, Caryn Bern, Robert Gilman, Lance Liotta, Alessandra Luchini.
- (30)‡ Dead end host? Altered behavior in aquatic snails infected with cysts of *Paragordius varius*
Benjamin J Engle, John F Shea.
- (31) Fish health and biodiversity at Lily Lake, Pennsylvania.
Genevieve Ivec.

Evolutionary Ecology

- (32) Can competition among parasite species be detected in field-collected samples of fishes?
Michael Barger.
- (33) Atypical trematode life cycle decreases within-host clonal diversity
Sarah Cobb, Sarah A Orlofske, Robert C Jadin, Devon Keeney.

Education

- (34) Increasing education initiatives in ASP.
Jeffrey Bell, Nicole Chodkowski, Makedonka Mitreva, Sarah Orlofske, J Trevor Vannatta.

Taxonomy, Systematics & Phylogeny

- (35) Morphological and molecular characteristics of *Telorchis* (Digenea: Plagiorchoidea: Telorchidae) obtained from indigenous and introduced freshwater turtles in Japan.
Misako Urabe, Tomoyoshi Tsubouchi, Kei Okayama, Yusuke Miyamura, Hiroaki Wakita.
- (36) Investigation of genetic and trait variability of *Gyrinicola batrachiensis* (Nematoda: Oxyurina) across North America.
Matthew A Walker, Matthew G Bolek, Elliott A Zieman, Gabriel J Langford, Jason L Brown, F Agustín Jiménez.
- (37) Expanded geographic distribution and redescription of *Octospinifer macilentus*. Van Cleave 1919 (Acanthocephala) from *Catostomus commersonii*.
Claire E Curtin, Florian B Reyda.
- (38) Morphological and molecular characterization of *Trichuris* (Nematoda: Trichuridae) parasite of *Heteromys irroratus* (Rodentia: Heteromyidae) in central Mexico.
René Josué Monzalvo-López, Jorge Falcón-Ordaz, Norma Leticia Manríquez-Morán.
- (39) The University of Wisconsin - Stevens Point Parasitology Collection: Integration of teaching and research
Sarah A Orlofske.

7:00-8:30 pm SOCIAL HOUR

Please visit one or more of the themed lounges so you can socialize and network with other parasitologists.

Tuesday 27th July

10:30-11:30 am PRESIDENT'S ADDRESS

Scott D. Snyder. Introduction of Vasyl Tkach's presidential address.

Vasyl Tkach. "Parasitology and technology: A perfect symbiosis".

11:35 am-12:35 pm 2021 H. B. WARD LECTURE

Vasyl Tkach. Introduction of the 2021 H. B. Ward Medal recipient

Sarah Bush. "Acceptance of the 2021 Henry Baldwin Ward Medal: Parasite forms most beautiful".

12:35-12:45 pm BREAK

12:45-1:45 pm Session 3A: Taxonomy, Systematics & Phylogeny

‡ denotes student presentation in the Best Student Presentation Competition

- 12:45 (40)‡ Fish blood flukes (Digenea: Aporocotylidae) from Indonesia: Two new genera and species infecting the banded eagle ray, *Aetomylaeus nichofii* (Bloch and Schneider, 1801) Capapé and Desoutter, 1979 (Myliobatiformes: Myliobatidae) from Borneo. Micah B Warren, Stephen A Bullard.
- 1:00 (41)‡ New Species of *Mathevolepis* Spassky 1948 from the dusky shrew *Sorex monticolus*. Joshua E Anderson, Vasyl V Tkach, Stephen Greiman.
- 1:15 (42) First record of *Psorospermium* cf. *haeckeli* (Class: Mesomycetozoa) in Northern Clearwater crayfish, *Faxonius propinquus* Girard 1852 (Decapoda: Cambaridae) from Michigan, USA. Christina Anaya.
- 1:30 (43) Walking with dinosaurs: Phylogeography and systematics of proterodiplostomid digeneans parasitic in crocodilians. Tyler J Achatz, Eric E Pulis, Kerstin Junker, Jeffrey A Bell, Francisco Tiago de Vasconcelos Melo, Vasyl V Tkach.

12:45-1:30 pm Session 3B : Host & Parasite Interactions

‡ denotes student presentation in the Best Student Presentation Competition

- 12:45 (44) Zoonotic and non-zoonotic tick borne pathogens in wild cervids of Tapada (Portugal). Nélida Fernández, Irene Aguilar, Luis Miguel González, Estrella Montero, Jorge Soares.
- 1:00 (45) *Giardia lamblia* in commercial oysters (*Crassostrea virginica*) and mussels (*Mytilus edulis*) from the Bronx, New York City.

Ghislaine Mayer, Sireen Mastrooq, Viola Marcia.

- 1:15 (46)‡ *Tarantobelus jeffdanielsi* n. sp. (Panagrolaimomorpha, Panagrolaimidae), a nematode parasite of tarantulas.
Jacob Schurkman, Kyle Anesko, Joaquin Abolafia, Irma Tandingan De Ley, Adler Dillman.

12:45-1:45 pm Session 3C: Evolutionary Ecology

‡ denotes student presentation in the Best Student Presentation Competition

- 12:45 (47) Shake it off: Behavior of a freshwater snail during and after parasite attack
J Trevor Vannatta, Jason T Hoverman, Dennis J Minchella.
- 1:00 (48)‡ Quantifying bilateral infections in the trematode *Alloglossidium renale*.
Jenna M Hulke, William H Ellenburg, Derek A Zelmer, Charles D Criscione.
- 1:15 (49) Downstream effects: Impact of antibiotic pollution on an aquatic host-parasite interaction.
Hannah G Melchiorre, Stephanie O Gutierrez, Dennis J Minchella, Jonathan T Vannatta.
- 1:30 (50) Unidirectional stream drift, dendritic ecological networks and host dispersal: Parasite gene flow in riverine habitats.
Mary J Janecka, Jan E Janecka, Charles D Criscione.

12:45-1:45 pm EDUCATION WORKSHOP

- 12:45 (51) Lessons learned from teaching parasitology in the non-traditional classroom
Jeffrey Bell, Nicole Chodkowski, Makedonka Mitreva, Sarah Orlofske, J Trevor Vannatta.

1:45-2:45 pm LUNCH BREAK

Please visit one or more of the themed lounges so you can socialize and network with other parasitologists.

2:45-4:45 pm STUDENTS' SYMPOSIUM

Presiding: Margaret L Doolin, University of Utah.

Theme: "Perspectives on the trajectory of parasitology"

- 2:45 **Margaret L Doolin.** Introduction.
- 2:50 (52) **John Janovy Jr.** A parasitological life in the shadow of H. B. Ward and Harold W. Manter.
- 3:10 (53) **Timothy G Geary.** Looking back and looking ahead.

3:30-3:35 pm BREAK

- 3:35 (54) **Jimmy Bernot.** Parasitology methods looking forward: genomics, phylogenomics, Iso-Seq, single-cell RNA-Seq, and spacial transcriptomics.
- 3:55 (55) **Jasmine Childress.** Trajectory of parasitology: Looking to the future using environmental DNA detection methods.
- 4:15 (56) **John Barthell.** The postdoctoral research fellowships in biology: An overview for conference participants.
- 4:35 Questions. Closing remarks.

4:50-5:00 pm BREAK

**5:00-6:00 pm Session 4A: Life Cycles & Epidemiology
Taxonomy, Systematics & Phylogeny**

‡ denotes student presentation in the Best Student Presentation Competition

- 5:00 (57) An outbreak of canine schistosomiasis in Utah: acquisition of a new snail host (*Galba humilis*) by *Heterobilharzia americana*, a pathogenic parasite on the move. Martina R Laidemitt, Scott Z Dolginow², Suzanne Pape, Colin D Topper, Pilar Alda, Jean P Pointier, Erika T Ebbs, Melissa C Sanchez, Guilherme G Verocai, Randall J DeJong, Sara V Brant, Eric S Loker.
- 5:15 (58)‡ Revealing identities of digenean metacercariae in fishes in the upper Midwest: Some progress and more questions. Jakson R Martens, Tyler J Achatz, Vasyl V Tkach.
- 5:30 (59)‡ Filling the flap gap: New "tetracystid" diversity in stingray and guitarfish hosts. Kara M Heilemann, Janine N Caira.
- 5:45 (60)‡ Jumping the continents and major host lineages: A curious case of the Cryptotrochidae. Taylor P Chermak, Tran Thi Binh, Vasyl V Tkach.

5:00-6:00 pm Session 4B: Host & Parasite Interactions

‡ denotes student presentation in the Best Student Presentation Competition

- 5:00 (61)‡ Physiological and behavioral interactions of *Drosophila* and two symbionts: *Spiroplasma* and an ectoparasitic mite. Collin J Horn, Taekwan Yoon, Monika K Mierzejewski, Lien T Luong.
- 5:15 (62)‡ Mapping parasitism onto host geographic ranges: Do host populations differ in their levels or types of parasitism between range edges and range centers? Anaí Novoa, Ryan F Hechinger.

- 5:30 (63) Parasite transmission in a milkweed patch: How are parasites transmitted in insects specializing on milkweed hosts?
Matthew G Bolek, Ryan P Shannon, Jillian T Detwiler, David D Berman, Kristen A Baum.
- 5:45 (64)‡ The role of gut microbial diversity in *Heligmosomoides bakeri* infections in mice
Margaret L Doolin, Sara B Weinstein, LeAnn Lindsey, W Zac Stephens, June L Round, M Denise Dearing.

5:00-6:00 pm Session 4C: Evolutionary Ecology

‡ denotes student presentation in the Best Student Presentation Competition

- 5:00 (65) Phylogenetic patterns of *Posthodiplostomum* metacercariae in Texas.
Josue H Zuniga, Isabel Blasco-Costa, Kristin K Herrmann.
- 5:15 (66)‡ The increasing prevalence and intensity of the invasive copepod, *Salmincola californiensis* in salmonids in Lake Ontario.
Brian R Mullin, Florian B Reyda.
- 5:30 (67) Drought and infection complexity: Insights from over twenty-years of research on a sand fly-transmitted malaria parasite.
Allison T Neal, Joshua Sassi, Joseph J Schall, Anne M Vardo-Zalik.
- 5:45 (68) Alpha and beta diversity trends of parasite communities in English sole (*Parophrys vetulus*) in Salish Sea, Washington, USA over the past nine decades.
Whitney C Preisser, Rachel L Welicky, Katie L Leslie, Natalie Mastick, Evan Fiorenza, Katherine Maslenikov, Luke Tornabene, John M Kinsella, Chelsea Wood.

6:00-6:15 pm BREAK

6:15-7:00 pm Session 5A: Life Cycles & Epidemiology

‡ denotes student presentation in the Best Student Presentation Competition

- 6:15 (69) Parasites of the Gulf wedge clam, *Rangia cuneata*, from the tidal reaches of the Pascagoula River, Mississippi.
Stephen S Curran, Micah B Warren, Stephen A Bullard.
- 6:30 (70)‡ Freeze tolerance of the dinoflagellate *Amyloodinium ocellatum*.
Robert D Gonzales, Haley Dutton, Reginald B Blaylock, Stephen A Bullard.
- 6:45 (71)‡ Unraveling the role of ostracod and snail hosts in turtle acanthocephalan life cycles.
Ryan W Koch, Matthew G Bolek.

6:15-7:00 pm Session 5B: Host & Parasite Interactions/ Immunology

‡ denotes student presentation in the Best Student Presentation Competition

- 6:15 (72) The occurrence of mesomycetozoon (Dermocystida) infecting American toads (*Anaxyrus americanus*) from central Illinois.
Elliott A Ziemann, Mathew G Bolek.
- 6:30 (73)‡ Mediterranean and African parasites in North America: Coccidia from introduced populations of the Mediterranean house gecko, *Hemidactylus turcicus* and the tropical house gecko, *H. mabouia*.
Allison Bryant, Matthew Bolek, Gabriel Langford.
- 6:45 (74)‡ Immune-related thioester-containing proteins (TEPs) in the *Biomphalaria glabrata* embryonic (Bge) cell line.
Deblina Misra, Maria G Castillo.

6:15-7:15 pm Session 5C: Vector Biology/ Genomics & Molecular Biology

‡ denotes student presentation in the Best Student Presentation Competition

- 6:15 (75)‡ The heart-associated immune response is conserved across insect evolution.
Yan Yan, Julián F Hillyer.
- 6:30 (76) Conserved immune signaling pathways drive heart-associated immune responses in mosquitoes.
Julian F Hillyer, Yan Yan, Tania Y Estévez-Lao, David C Rinker, John A Capra.
- 6:45 (77) The hirudin superfamily.
Christian H Mueller, Phil Lukas, Jan-Peter Hildebrandt.
- 7:00 (78) DNA metabarcoding methods for parasite surveillance and diet analyses of San Miguel Island foxes.
Ana E Garcia Vedrenne, Jasmine N Childress, Kevin D Lafferty.

7:30-8:30 pm AUCTION ANNOUNCEMENTS AND CLOSING COMMENTS

97TH ANNUAL MEETING OF THE
AMERICAN SOCIETY OF
PARASITOLOGISTS



BACK TO SCHOOL: A&M HOSTS ASP

JULY 9-12, 2022
COLLEGE STATION, TX

VENUE &
ACCOMMODATIONS:
CAVALRY COURT HOTEL &
THE GEORGE HOTEL



COLLEGE STATION

Learn more about the meeting, venue,
travel, and ART CONTEST online at
TAMU Biology's ASP Website

Abstract Listings

1. Hidden Communities: seasonal cestode and bacterial community dynamics within the guts of two North American *Sorex* shrew species.

Stephen Greiman

Georgia Southern University, Statesboro, GA, USA.

The mammalian gut microbiome is extremely complex and has been shown to be essential to host fitness and health, assisting in both nutrient acquisition from diet, as well as protection from pathogens. This community of microorganisms: bacteria, viruses, fungi, and even multicellular parasites, can all interact with each other and their host. In this talk, I will discuss the seasonal community composition of both cestodes and bacteria within the intestines of two North American shrew species, *Sorex monticola* and *Sorex cinereus*. Specimens were collected approximately every three weeks from May to October during 2016 and 2017 as well as during April and May of 2018 and September of 2009 from the Sangre de Cristo Mountains in Cowles, New Mexico. A total of 186 shrews were collected and surveyed for cestode and bacterial taxa. Bacterial and cestode communities were estimated based on next generation amplicon sequencing of 16S rDNA (for bacteria) and 28S rDNA (for cestodes).

2. Associations between Afrotropical bats, eukaryotic parasites, and microbial symbionts.

Holly Lutz.

Field Museum of Natural History, Chicago, IL, USA.

Skin is the largest mammalian organ and the first defensive barrier against the external environment. The skin and fur of mammals can host a wide variety of ectoparasites, many of which are phylogenetically diverse, specialized, and specifically adapted to their hosts. Among hematophagous dipteran parasites, volatile organic compounds (VOCs) are known to serve as important attractants, leading parasites to compatible sources of blood meals. VOCs have been hypothesized to be mediated by host-associated bacteria, which may thereby indirectly influence parasitism. Host-associated bacteria may also influence parasitism directly, as has been observed in interactions between animal gut microbiota and malarial parasites. Our work uses Afrotropical bats, hematophagous ectoparasitic bat flies, and malarial parasites transmitted by bat flies as a model to test the hypothesis that the vertebrate host microbiome is linked to parasitism in a wild system. We identified significant correlations between bacterial community composition of the skin and dipteran ectoparasite prevalence across four major bat lineages, as well as striking differences in skin microbial network characteristics between ectoparasitized and nonectoparasitized bats. We also identified links between the oral microbiome and presence of malarial parasites among miniopterid bats. Our results support the hypothesis that microbial symbionts may serve as indirect mediators of parasitism among eukaryotic hosts and parasites.

3. Parasite genomic resources: challenges and opportunities.

Spencer Galen.

The University of Scranton, Scranton, PA, USA.

The widespread use of genomic data for ecological and evolutionary analyses has not taken off within the field of parasitology, even as genomic data has become standard for the study of free-living organisms. The challenges that parasitologists face to build genomic resources for their focal taxa are

multi-faceted, ranging from the difficulty of obtaining samples from poorly-studied species to isolating high-quality parasite genomic DNA that is free from host contamination. However, a largely untapped body of parasite genomic data exists from genomic and transcriptomic studies of host organisms that has the potential to accelerate our understanding of parasite ecology and evolution for some taxa. Here, I illustrate how parasitologists can use these data to build genomic resources that can be applied to a wide variety of research directions. First, I describe two case studies from research on haemosporidians and trypanosomes to show how these resources can be used for phylogenomics. I also discuss how these data can inform our understanding of parasite ecology, particularly at the level of within-host communities. Collectively, this body of research provides a path forward for expanding our understanding of the evolutionary ecology of many poorly-understood parasite clades.

4. Redescription of *Cathariotrema selachii* (MacCallum, 1916) Johnston and Tiegs, 1922 (Monogenoidea: Monocotylidae), emendation of monotypic *Cathariotrema* Johnston and Tiegs, 1922, and proposal of a new subfamily based on morphological and nucleotide evidence.

Stephen A Bullard^{1,2}, Micah B Warren¹, Haley R Dutton¹.

¹Auburn University, Auburn, AL, USA. ²Southeastern Cooperative Fish Parasite and Disease Laboratory, Auburn, AL, USA.

We herein redescribe the enigmatic *Cathariotrema selachii* based on the holotype, paratypes, and newly-collected specimens infecting the nose of 5 shark species from the Gulf of Mexico (all new host records): scalloped hammerhead shark, *Sphyrna lewini*; great hammerhead shark, *Sphyrna mokarran*; blacktip shark, *Carcharhinus limbatus*; spinner shark, *Carcharhinus brevipinna*; and Atlantic sharpnose shark, *Rhizoprionodon terraenovae*. These specimens were morphologically indistinguishable from each other and from MacCallum's holotype and paratypes. Those sequenced had identical first internal transcribed spacer and large subunit ribosomal DNA nucleotide sequences. This report is the first of new specimens of *C. selachii* in the Atlantic Ocean Basin in 95 yr. We herein emend monotypic *Cathariotrema* and propose a new subfamily for it plus 4 genera all formerly assigned to Merizocotylineae. Species of these genera infect the nose of sharks and a chimaera. The new subfamily differs from Merizocotylineae by having a 3-part attachment organ. It was sister to Merizocotylineae, which were together were sister to monophyletic Calicotylineae. These subfamilies comprise a monophyletic group of monocotylids that have a double vagina and infect extra-branchial, enclosed niches (urogenital system, body cavity, olfactory chamber/nose) on their shark, ray, and chimaera hosts (all other monocotylids have a single vagina and infect the gill or body surfaces of rays only).

5. Fresh insights into the New World members of the Family Nippostrongyliinae

Guinevere O Drabik, Agustín Jiménez.

Southern Illinois University Carbondale, Carbondale, Illinois, USA.

Nippostrongyliinae is a globally distributed subfamily of trichostrongylid nematodes that occur commonly in rodents of the families Muridae, Cricetidae, and Sciuridae. The more than 80 species of nippostrongylids currently known have been allocated to around 12 genera classically diagnosed based on the reduction of the buccal cavity, the presence of 13 or more continuous cuticular ridges that compose the synlophe, a 2-2-1, 1-3-1, or mixed 2-2-1 and 2-3 arrangement of the rays of the copulatory bursa, the shape of the copulatory bursa, and the structure of the female tail and reproductive system.

Due to the taxonomic practice of using the same structures to define different hierarchical levels in this group, there is some uncertainty in diagnoses of nippostrongyline genera. To assess ancestor-descendant relationships and increase the number of characters used to enable more accurate estimation of these relationships, we conducted a phylogenetic analysis using morphological characters and DNA sequences derived from Internal Transcribed Spacer (ITS) and mitochondrial gene Cytochrome C Oxidase subunit 1 (COX1) trees for several species of New World Nippostrongylineae. A phylogeny was estimated for selected specimens among representatives of seven New World genera, including: *Carolinensis*, *Guerrerostrongylus*, *Hassalstrongylus*, *Longistriata*, *Malvinema*, *Mazzanema*, as well as species of *Vexillata* and *Heligmosomoides* as outgroups were also included. The phylogenies suggests that both *Carolinensis* and *Hassalstrongylus* represent paraphyletic assemblages of species. Further, *Vexillata* should be included in the Nippostrongylineae. The phylogenetic pattern suggests that the symmetry of the bursa, the non-hypertrophied nature of the genital cone, and the size of the ridges in the synlophes are homoplastic traits.

6. A new species of *Harmotrema* (Digenea: Liolopidae) infecting the intestine of side-necked turtles (Pleurodira: Pelomedusidae) in Mozambique and South Africa.

Haley R Dutton¹, Louis H DuPreez², Stephen A Bullard¹.

¹Auburn University, Auburn, AL, USA. ²North-West University, Potchefstroom, South Africa.

Liolopidae comprises 12 species assigned to 4 genera (*Liolope*, *Helicotrema*, *Harmotrema*, *Dracovermis*) that collectively infect the intestine of a salamander, iguana, snakes, crocodylians, and turtles. To date, only 3 liolopids are known to infect 4 turtles: *Helicotrema spirale* infects the big-headed Amazon River turtle, *Peltocephalus dumerilianus* (Pleurodira: Podocnemididae) and the yellow footed tortoise, *Testudo tabulate* (Cryptodira: Testudinidae) in Brazil; *Helicotrema asymmetricum* infects the Columbian wood turtle, *Rhinoclemmys melanosterna* (Cryptodira: Geomydidae) in Panama; and *Liolope dollfusi* infects the east African black mud turtle, *Pelusios subniger* (Pleurodira: Pelomedusidae) in Democratic Republic of Congo. Herein, we collected specimens of a liolopid from the intestine of serrated hinged terrapins, *Pelusios sinuatus* (Nwanedzi River, Mozambique) and South African helmeted terrapins, *Pelomedusa galeata* (ephemeral ponds in Tembe Elephant Park; northern KwaZulu-Natal Province, South Africa). Based on morphology, these specimens represent a new species. This is the first report of a liolopid infection in a turtle from Africa since 1950, and only 1 African turtle previously was known as a liolopid host. The 28S phylogenetic analysis recovered a monophyletic Liolopidae (only 1 other liolopid, *Liolope copulans*, has been sequenced; the new species differed from it by 103 [92%] nucleotides in the 28S), which was sister to all other taxa included in the analysis. Given that only 6 of 356 (2%) extant turtle species are known as liolopid hosts, and given that liolopids are known from all continents except Australia, Eurasia, and Antarctica, we expect that many innominate liolopids exist.

7. How many origins of parasitism in copepods? A new count with a review of the evidence from phylogenetics, morphology, and natural history.

James P Bernot¹, Geoffrey A Boxshall².

¹Smithsonian National Museum of Natural History, Washington, DC, USA. ²Natural History Museum, London, UK.

The Copepoda is a clade of pancrustaceans containing over 14,400 species that are extremely varied in their lifestyle. More than 5,000 species are parasites associated with every major phylum of marine

metazoans. It is clear that copepods have evolved to be parasitic multiple times, but just how many transitions to parasitism have occurred has yet to be evaluated in detail, especially in light of recent copepod phylogenetic efforts. We apply an operable definition of parasitism to copepods and identify at least 13 independent clades of parasites, which is likely an underestimate given how poorly resolved the copepod phylogeny remains. Nonetheless, molecular phylogenetic data support 10 transitions to parasitism. The remaining 3 transitions to parasitism are supported by morphological data, though it has not always been evaluated in an explicit phylogenetic context. The molecular, morphological, and albeit limited, fossil data supporting these parasitic clades are examined, as is the life history data that supports their qualification as parasites. The species diversity of each clade is reviewed, which ranges from a single species to 2,427 species. What remains a major challenge to improving our understanding of parasitic copepod evolution is elucidating the nature of the association symbiotic copepods have with invertebrate hosts. More than 2,000 species of copepods are associated with marine invertebrate hosts and, in most cases, little is known regarding the nature of their association. In some instances, modified morphology is a practical indicator of parasitism, such as sucking or scraping mouthparts, or robust clawed appendages for attachment, but this is far from a perfect approximation, especially for those copepods associated with invertebrates that are relatively unmodified from their free-living relatives.

8. Reduction of *Ascaridia galli* pathology by *Salmonella typhimurium* in broiler chicken.

Eric Igor Sop Foka¹, Cedric Yamssi², Ben Enyetornye³, Christelle Nadia Noumedem Anangmo⁴, Mpoame Mbida¹, Theodore B. Mayaka¹.

¹Department of Animal Biology, Faculty of Sciences, University of Dschang, Dschang, Cameroon.

²Department of Biomedical Sciences, Faculty of Health Sciences, University of Bamenda, Bamenda, Cameroon. ³School of Veterinary Medicine, University of Ghana, Accra, Ghana.

⁴Department of Microbiology, Hematology and Immunology Faculty of Medicine and Pharmaceutical Sciences, University of Dschang, Dschang, Cameroon.

Previous studies have reported interactions between *Salmonella spp* and some helminths coinfections. In this study, *S. typhimurium* and *Ascaridia galli* co-infections were analyzed and the consequences on therapy proposed. In a first experiment where the effect of the bacteria on the nematode was evaluated, thirty 42 days-old broiler chickens were divided into 3 groups and co-infected with both parasites. The rate of *A. galli* eggs inoculum was kept constant at 500/ml while that of *S. typhimurium* varied as follow: T₀ (500 *A. galli* eggs/ml), T₁₀₄ (500 *A. galli* eggs/ml + 10⁴ *S. typhimurium* CFUs) and T₁₀₆ (500 *A. galli* eggs/ml + 10⁶ *S. typhimurium* CFUs). EPG and parasitic load were measured using the McMaster technique and number of worms and their length also measured. It was found that T₁₀₆ containing 10⁶ CFUs of *Salmonella* significantly reduced the EPG values and this group recorded the lowest worm load ranging from 18-21 worms. Likewise, the length of the worms obtained with T₁₀₄ and T₁₀₆ appeared to be shorter than those of the control (T₀). In a second experiment to assess the effects of the nematode on the bacteria, thirty 42 days-old broiler chickens were divided into 3 groups and co-infected with both parasites. The rate of *S. typhimurium* inoculum was kept constant at 10⁶ CFUs while that of *A. galli* varied as follow: T₀ (10⁶CFUs), T₅₀₀ (500 *A. galli* eggs/ml + 10⁶ *S. typhimurium* CFUs) and T₇₅₀ (750 *A. galli* eggs/ml + 10⁶ *S. typhimurium* CFUs). Bacterial load was measured using the Voogt technique. We observed that: T₅₀₀ increased the colonization time and prolonged the duration of *S. typhimurium* secretion. *Salmonella* appears to be a hyperparasite considering the deleterious effect on *A. galli*. Due to this, it may be prudent to combine anti-*Salmonella* treatment with anthelmintic so as to effectively treat pathologies caused by these two pathogens.

9. Forecasting endemic spillover hosts for zoonotic pathogens in South Africa using network analyses.

Heike Lutermann, Dina Fagir.

University of Pretoria, Pretoria, South Africa.

The loss of biodiversity has been suggested to increase the risk of zoonotic spillovers of pathogens and parasites from wildlife posing a challenge to human and animal health. At the same time, predicting and identifying potential wildlife sources of zoonotic pathogens and/or parasites is difficult, particularly for poorly studied wildlife communities such as those of endemic rodents in many regions of Africa. Using field collections of ecological and parasitological data from eleven sympatric small mammal species (nine rodents, two insectivores) and their ectoparasitic arthropods (ten tick species, 14 mite species, 5 flea species and 4 louse species) we analyzed network metrics including modularity and node centrality to evaluate the relative epidemiological importance of the rodent species captured in Telperion /Ezemvelo Nature Reserve, Gauteng Province, South Africa. Networks showed an intermediate level of nestedness. However, in both bipartite and unipartite networks two closely related murid rodents, *Micaelamys namaquensis* and *Aethomys ineptus*, emerged as sharing a large number of arthropod vectors with other rodents that also affect livestock and humans. These include ticks and fleas that may act as vectors for pathogens of medical (*Rickettsia conorii*, *Yersinia pestis*) and veterinary importance in the region (*Theileria parva*, *Anaplasma marginale*, *Babesia bigema* and *Ehrlichia bovi*). The two murids appear to be habitat generalists compared to other sympatric rodents and have been recorded as human commensals in parts of South Africa. As the geographic range of *M. namaquensis* includes most of sub-Saharan Africa and they are host to several *Bartonella* spp., including those of zoonotic concern, our findings suggest that this species may act as a source of zoonotic spillovers in the future. Thus, more detailed studies of its biology and pathogen/parasite community are needed to prevent the emergence of zoonotic diseases from this host.

10. Invasive Parasites: A survey of endoparasites from *Salvator merinae* populations in Florida.

Marisa Fonseca, Gabriel Langford.

Florida Southern College, Lakeland, FL, USA.

The Argentine Black and White Tegu (*Salvator merinae*) 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. Thirty-one Argentine Black and White Tegus from central and southern Florida were necropsied to perform an extensive parasite examination of these invasive populations. The necropsies revealed that the tegus brought three species of exotic nematode to Florida from South America (*Physaloptera tupinambae*, *Diaphanocephalus galeatus*, *Cruzia lauroi*) 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.

11. Comparison of endohelminths of the black drum (*Pogonias cromis*) and the red drum (*Sciaenops ocellatus*) from an estuarine system.

Hannah C McNeese¹, Autumn J Smith-Herron², Tamara J Cook¹.

¹Sam Houston State University, Huntsville, Texas, USA. ²Texas Invasive Species Institute at Sam Houston State University, Huntsville, Texas, USA.

The black drum (*Pogonias cromis*) and the red drum (*Sciaenops ocellatus*) are two closely related fish species that occur throughout the Gulf of Mexico. These species utilize estuarine systems as brooding grounds for their young, which offers protection, and food sources to juveniles. This study sought to understand how endo-parasitic communities of the juvenile and sub-adult individuals of the two drum species compared, and to determine what the effects of host size and habitat salinity were on the parasitic communities in and between fish species. We conducted a helminth survey on black drum (n=59) and red drum (n=61) taken from Sabine Lake in spring and summer 2018. We identified 38 parasite species (23 nematodes, 6 trematodes, 5 acanthocephalans, and 4 cestodes). Significance for the interaction of host size and parasitic intensity was realized, though the model did not adequately explain the relationship. The Jaccard index value was 0.2895, or 28.95% similarity between the communities, and Hutcheson-t did show significant difference in diversity between the two communities. The results did show the predicted relationship for host size and parasite intensity, but a relationship was not found for habitat salinity and diversity. This study is significant as a primary helminth survey from Sabine Lake, and as new host and locality documentations for several parasite species.

12. Factors regulating *Strongyloides stercoralis* male development differ from *Caenorhabditis* species.

Damia Gonzalez Akimori¹, Emily J Dalessandro¹, Thomas J Nolan², Christopher R Stieha¹, James B Lok², Jonathan DC Stoltzfus¹.

¹Millersville University, Millersville, PA, USA. ²University of Pennsylvania, Philadelphia, PA, USA.

The parasitic nematode *Strongyloides stercoralis*, which typically infects humans and canines, can alternate between a parasitic generation of parthenogenetic females and a free-living generation of sexually reproducing males and females. The genetic and environmental factors controlling male development are not well understood. We identified rhabditiform L4/adult males in the large intestine of a permissive host treated with corticosteroids and undergoing autoinfection, suggesting that steroid hormones can regulate male development. We also examined changes in gene expression between free-living adult males and females by RNA-Seq. We identified two gene clusters, each encoding a novel family of putative transmembrane proteins, which are highly up-regulated in free-living males, in addition to other male-specific transcripts. We also sought to determine whether genes that control sex determination in *Caenorhabditis* species are conserved in *S. stercoralis* and whether any of the transcripts from these homologs are regulated in a sex-specific manner. We found that homologs of the transcription factors encoded by *tra-1* and *mab-3* appear to have similar functions between the two species. By contrast, we found three paralogs of the mRNA-binding protein encoded by *gld-1* with sex-specific transcripts as well as an expansion of genes encoding pumilio domain proteins with sex-specific transcripts in *S. stercoralis*. We additionally sought to test the “bottom up hypothesis” and determine whether down-stream genes in the sex determination pathway are more conserved across Nematoda than up-stream genes. We found a broad conservation of the down-stream transcription factors encoded by *tra-1* and *mab-3* across nematode species; however, we found that the male-specific ligand encoded by *her-1* in *Caenorhabditis* species appears to have been lost in several lineages, and we were unable to identify its receptor, encoded by *tra-2*, outside of *Caenorhabditis* species. Together, our

results suggest that different factors may control sex determination in *S. stercoralis* and potentially other parasitic nematodes than in *Caenorhabditis* species.

13. Elucidation of the role of dense granule 1 in *T. gondii* and its application in a diagnostic assay.

Hannah E Steinberg¹, Amanda Haymond², Andrea Diestra³, Weidong Zhou², Lance A Liotta², Nancy E Freitag¹, Maritza Caleron³, Vernon B Carruthers⁴, Alessandra Luchini², Robert H Gilman⁵.

¹University of Illinois, Chicago, Chicago, IL, USA. ²George Mason University, Fairfax, VA, USA. ³Universidad Peruana Cayetano Heredia, Lima, Peru. ⁴University of Michigan, Ann Arbor, MI, USA. ⁵Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA.

Opportunistic neurological infections in persons living with HIV (PLHIV) are challenging to diagnose. CT and MRIs with a clinical suspicion can guide treatment, but definitive diagnosis remains elusive for many patients. *Toxoplasma gondii* (*T. gondii*) is known to cause Toxoplasmic Encephalitis in PLHIV. Though difficult to diagnose, it has up to 90% clinical response rate to treatment. Innovations in *T. gondii* diagnostics, such as our team's urine-based diagnostic western blot utilizing hydrogel nanoparticle antigen concentration, require laboratory equipment and skilled personnel, limiting its range. To expand access to the diagnostic assay, we initiated structural and functional studies of the antigen of interest, dense granule 1 (GRA1), to allow for transition to a lateral flow assay. We have tested 8 antibody clones for their ability to form a sandwich around GRA1, resulting in an antibody pair with detection to 62.5pg/ml of recombinant antigen. Despite this high sensitivity in recombinant antigen, formation of the sandwich is not observed in urine from *T. gondii*-infected patients who are positive for GRA1 via western blot. Immunoprecipitations into mass spectrometry of *T. gondii* identified SAG2, a surface antigen, as a binding partner to GRA1. This interaction has been confirmed by western blotting. Circular dichroism studies suggest that GRA1 has a 96% alpha helical structure that refolds in the presence of calcium or increasing pH. Enzymatic digestion studies suggest that GRA1 undergoes N-linked glycosylation on the 30th amino acid. This glycan is estimated to be one third the size of the total GRA1 structure and may be obstructing antibody binding. Despite being a known secretory protein, GRA-1's function and structure is currently unknown; our data sheds light on GRA1's signaling role and structural modifications, which impact design of lateral flow immunodiagnostics. Moving forward, we will use a mass spectrometry based protein-protein interaction identification technique to map the binding sites of the 8 antibody clones as well as SAG2 to GRA1. This data will assess if the antibodies are impeded in their binding by the glycan or binding partners.

14. Characterization of the highly diverse genomic regions of an important African vector of schistosomiasis.

Ryan Burd¹, Jared Cayton¹, Tom Pennance², Jacob A Tennesen³, Fredrick Rawago⁴, Maurice Odiere⁴, George Owino⁴, Michelle L Steinauer².

¹College of Osteopathic Medicine of the Pacific, Western University of Health Sciences, Pomona, California, USA. ²College of Osteopathic Medicine of the Pacific-NW, Western University of Health Sciences, Lebanon, Oregon, USA. ³Harvard T.H. Chan School of Public Health, Boston, Massachusetts, USA. ⁴Neglected Tropical Diseases Research Unit, Center for Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya.

Schistosomiasis is a neglected tropical disease that impacts the health of hundreds of millions of people worldwide, primarily in regions of poverty. Schistosomes are parasitic blood flukes that cause a chronic

inflammatory disease and infection can lead to severe morbidities including cirrhosis, abdominal pain, reproductive infertility, and cancer. Additionally, infections in children can lead to reductions in physical growth and cognitive abilities. Humans become infected via contact with freshwater containing schistosome cercariae, the infectious larval stage, which emerge from freshwater snails and penetrate the skin of their vertebrate hosts. Because development within snails is necessary for the schistosome to infect humans, preventing development of schistosomes within the snail host would disrupt transmission to humans and thus improve human health. We have taken a bioinformatic approach to finding and characterizing pathogen recognition genes in an important snail vector in North-Eastern Africa, *Biomphalaria sudanica*. We have scrutinized genomic sequences of five inbred lines of *B. sudanica* (Lake Victoria, Kenya) to identify and annotate highly polymorphic regions that may be under balancing selection, a type of selection which favors the maintenance of multiple alleles within a population and has been associated with immune related gene regions in other host-pathogen systems. Like vertebrates, these snail species employ pathogen recognition proteins to trigger granular, phagocytotic and encapsulated immune responses against pathogens. We have identified and characterized polymorphic proteins through predictive peptide models and comparisons to the annotated genome of a related snail species (*B. glabrata*) and to reference sequences in GenBank. Promising candidates include pathogen recognition receptors known to impact schistosome resistance in related snail species and those that have not been recognized previously. This project represents a significant contribution to the annotation of the *B. sudanica* genome, providing an important resource for the research community.

15. Population genomic structure in marine tapeworms: The importance of host species versus geographic locality.

Kaylee S Herzog, Kirsten Jensen.

University of Kansas, Lawrence, KS, USA.

Tapeworms as a group demonstrate a wide range of geographic distributions and specificities for their definitive vertebrate hosts; however, the relative importance of these factors (among others) in structuring tapeworm populations at the genomic level remains unclear. To explore this question, we designed a study that leverages the wide range of specificities of trypanorhynch tapeworms for their definitive shark and ray hosts and the power of next generation multi-locus sequence data in combination with a comprehensive global sampling strategy. This study will allow us to (1) measure population-level genomic diversity in two species of marine tapeworms, (2) estimate relatedness among tapeworms collected from a single host specimen, and (3) assess the relative roles of host specificity and geographic distribution in marine tapeworm population-level genomic structure. Two species representing both trypanorhynch suborders were targeted for a restriction site associated multiplex shotgun genotyping (MSG) approach. For *Rhinoptericola megacantha* (suborder Trypanobatoidea), 39 tapeworms were sequenced from 19 ray hosts representing three species of *Rhinoptera* from four geographic localities in the northern Atlantic Ocean. For *Callitetrarhynchus gracilis* (suborder Trypanoselachoidea), 47 tapeworms were sequenced from 17 shark hosts representing five species in two genera from five geographic localities in the Atlantic and Pacific oceans. We hypothesize that geographic locality will be an important driver in structuring trypanorhynch genomic diversity at the population level, and that tapeworms recovered from the same host individual will be more closely related than will tapeworms recovered from different host individuals of the same species, or different species of hosts. Data processing is underway, and the results of this study are expected to lay an initial foundation upon which future population-level studies on marine tapeworms can build to address, for example, questions regarding infection dynamics.

16. The parasites of Oneida Lake fishes: Then and now.

Florian B Reyda¹, Emma Nielsen¹, Isaiah Crosbourne¹, Stephen Curran², Thomas Brooking³.

¹SUNY Oneonta, Oneonta, NY, USA. ²Auburn University, Auburn, AL, USA. ³Cornell University Biological Field Station, Bridgeport, NY, USA.

Pioneering North American parasitologists H. J. Van Cleave and J. F. Mueller published several papers in which they reported on the fish parasites they encountered following an extensive (1929-1931) survey of Oneida Lake, New York. Their foundational work included descriptions of a remarkable total of 31 new species of parasitic worms (digeneans, monogeneans, nematodes, and cestodes) in 34 species of fish examined! Since then, Oneida Lake has experienced a variety of well-documented changes, including loss of various species of mollusks, including both gastropods and bivalves, and the addition—via exotic introductions—of others. Our study aims to compare the species composition of the fish parasites of Oneida Lake today with what was originally reported almost a century ago. One of our objectives is simply to determine whether all 31 species of helminths originally described from Oneida Lake remain present at their type locality today. To date, we collected and examined ~400 specimens representing 28 species and 12 families of fishes via gill-netting, trap nets, or electrofishing via boat or backpack. Our primary emphasis was the digestive system, though we examined other organs in a subset of the fish. Our survey activities will continue for at least another year. At this stage we can report some overlap between our survey results and the original study, but with notable differences. For example, we have encountered each of the four species of acanthocephalans found by Van Cleave & Mueller, as well as four additional species of *Neoechinorhynchus*, including two new species. Even though our sample size of *Perca flavescens* (yellow perch) is relatively large (n=84), we have so far collected only one of the five digeneans described from that host in Oneida Lake and its tributaries. Conversely, we have encountered helminths not previously reported, including the invasive tapeworm *Schyzocotyle acheilognathi* (in cyprinid fishes), and multiple species of the nematode genus *Rhabdochona* in five different families of fishes. Although a diversity of species of fish parasites have withstood the environmental changes that have taken place at Oneida Lake, some species may be lost from the system while others have been added.

17. Integrative taxonomy of *Posthodiplostomum*.

Kari D Waddle¹, Isa Blasco-Costa², Autumn Smith-Herron³, Nicci Carpenter⁴, Kristin Herrmann¹.

¹Tarleton State University, Stephenville, Texas, USA. ²Natural History Museum of Geneva, Geneva, Switzerland. ³Sam Houston State University, Huntsville, Texas, USA. ⁴Texas Parks and Wildlife, San Marcos, Texas, USA.

Parasitologists have been operating under the assumption that there is a single representative species of *Posthodiplostomum* found in North America, and currently, specimens found within the North American continent are deemed to be *Posthodiplostomum minimum*. Metacercariae in fish are more easily accessible than adult specimens found in herons, but lack of morphological differentiation at this life stage makes determining species unlikely. More recently, phylogenetic studies conducted on *Posthodiplostomum* metacercariae in fish hosts have found genetic differences and have shown host and tissue specificity within *Posthodiplostomum*. Our study incorporates integrative taxonomic methodology to delineate species of *Posthodiplostomum* based on adult specimens. Specimens belonging to *Posthodiplostomum* were obtained from nuisance herons at a Texas fish hatchery by their biologist. A subset of specimens was relaxed and fixed in steaming saline, then tissue samples were removed and preserved in 100% ethanol for DNA extraction. The remainder of each specimen was

stored in 70% ethanol for staining and morphological measurements. After DNA extraction, gene-specific primers were used for PCR amplification of two genes (CO1 and ITS). For morphological examination, specimens were dehydrated in a graded ethanol series, stained, and cleared with xylene then mounted on microscope slides in Canada Balsam. Various organ measurements are being recorded for morphological comparison of hologenophores. Maximum likelihood and Bayesian phylogenetic analysis is being conducted for COI and ITS sequences from our study and those obtained from GenBank. Currently, our results suggest four distinct morphologies that line up with species descriptions for *P. centrarchi*, *P. nanum*, *P. minimum*, and *P. macrocotyle*. Additionally, we have obtained one specimen that has not matched any morphological species descriptions, which may represent a new undescribed species. Further, preliminary phylogenetic analysis of COI indicates that this specimen of a putative new species matches metacercariae obtained from Western mosquitofish, *Gambusia affinis*. Thus far, preliminary data reveals unrecognized and undocumented diversity within *Posthodiplostomum* in North America.

18. Redescription and molecular barcoding of a transatlantic monogenean *Allogastrocotyle bivaginalis* Nasir & Fuentes Zambrano, 1983 parasites of *Trachurus picturatus* off the southern Mediterranean Sea.

Chahinez Bouguerche^{1,2}, Fadila Tazerouti¹, Delphine Gey^{3,4}, Jean-Lou Justine².

¹Laboratoire de Biodiversité et Environnement: Interactions – Génomes, Université des Sciences et de la Technologie Houari Boumediene (USTHB), Alger, Algeria. ²Institut Systématique Évolution Biodiversité (ISYEB), Muséum National d’Histoire Naturelle (MNHN), Paris, France. ³Service de Systématique Moléculaire, Muséum National d’Histoire Naturelle (MNHN), Paris, France. ⁴MCAM, Muséum National d’Histoire Naturelle (MNHN), Paris, France.

Allogastrocotyle bivaginalis Nasir & Fuentes Zambrano, 1983, the sole species of *Allogastrocotyle* Nasir & Fuentes Zambrano, 1983, was described from the rough scad *Trachurus lathami* (Carangidae) off Venezuela and never recorded since. We found monogeneans on the blue jack mackerel *Trachurus picturatus* off the Algerian coast, Mediterranean Sea, which had the characteristics of the genus, including, especially, paired vaginae. We compared them to the single available specimen of *A. bivaginalis*, the holotype. Unfortunately, this holotype does not show clamp structure nor soft internal anatomy. Our specimens were similar to *A. bivaginalis* in most characteristics such as body shape, vaginal openings, and number of testes, clamps and hooks in genital atrium. We detected minor differences in clamp structure but could not ascertain if these were the result of incomplete observations in the original description of real morphological differences. The host fish of our specimens were barcoded (cox1) confirming their specific identity. A phylogenetic analysis of cox1 sequences showed that our sequences of *A. bivaginalis* were distinct from those of *Pseudaxine trachuri* Parona & Perugia, 1889 (distance > 15%) and of several other gastrocotylids. Finally, we could not distinguish our Mediterranean specimens from *A. bivaginalis*, neither on the base of morphology (because the original description is incomplete) nor on molecules (because molecular information is lacking on *A. bivaginalis* from Venezuela) and ascribe them to *A. bivaginalis*. However, hosts are different, and localities are widely separated, so it is likely that future studies will show that the species from the Mediterranean is a distinct, new, species.

19. A new species and emendation of *Pseudoparamacroderoides* Gupta and Agarwal, 1968 (Digenea: Macroderoididae), with comments on the systematics of macroderoidid genera.

Triet N Truong, Stephen S Curran, Haley R Dutton, Stephen A Bullard.

Auburn University, Auburn, Alabama, USA.

We herein resurrect and emend *Pseudoparamacroderoides* Gupta and Agarwal, 1968 (Digenea: Macroderoididae), a cryptic genus previously restricted to species ranging on the Indian sub-continent. We also describe a new species of the genus based on specimens infecting the intestine of the riverine catfish, *Mystus mysticetus* (Siluriformes: Bagridae) in the Mekong River, Vietnam. Species of *Pseudoparamacroderoides* (*P. seenghali* Gupta and Agrawal, 1968; *P. vittatusi* Kakaji, 1969; *P. raychaudhurii* Agarwal and Kumar, 1984; and *P. keni* Agarwal and Agarwal, 1985) each has an elongate body with broadly rounded ends, a subterminal and spinous oral sucker, oral and ventral suckers of approximately equal diameter, testes in a diagonal configuration, a cirrus sac that is lateral to the ventral sucker, a genital pore that is immediately anterior to the ventral sucker, an ovary that is posterolateral to and abutting the ventral sucker, and symmetrical vitelline fields extending posteriad to mid-level of the post-testicular space. *Pseudoparamacroderoides* is distinct from other macroderoidid genera by having a forebody that is not strongly dorsoventrally-flattened, an oral sucker that is sub-spherical and nearly equal to the diameter of the ventral sucker, a ventral sucker with a typical lumen (non-vestigial), caeca extending posteriad beyond the testes and terminating near the posterior body extremity, small testes (diameter nearly equal to or $<1/3$ maximum body width), a cirrus sac that is lateral to the ventral sucker, a seminal receptacle, a vitellarium comprising two symmetrical lateral fields that remain separated (not confluent) anteriorly and posteriorly (not restricted to inter-gonadal space), and a wholly post-ovarian excretory bladder that is I-shaped and courses between the testes. The new species differs from its congeners by having an elongate hindbody ($>2 \times$ forebody length) and an excretory bladder extending anteriorly beyond anterior testis. This is the first record of a species of *Pseudoparamacroderoides* from beyond the Indian sub-continent, from *M. mysticetus*, and from the Mekong River or from Vietnam. Diagnostic keys to macroderoidid genera and *Pseudoparamacroderoides* spp. are presented.

20. Glycogen branching and debranching enzymes from the parasitic protist *Trichomonas vaginalis*.

Karoline E Dittmer, Prajakta Pradhan, Quentin C Tompkins, Andrew Brittingham, Wayne A Wilson

Des Moines University, Des Moines, Iowa, USA.

The protist *Trichomonas vaginalis* is an obligate parasite of humans and the causative agent of trichomoniasis, the most common non-viral sexually transmitted infection worldwide. Like all parasitic organisms, *T. vaginalis* is dependent upon the host for many nutrients. While the microenvironment of the vaginal epithelium is rich in carbohydrates, the availability of nutrients in males is less understood. Previous studies have demonstrated that *T. vaginalis* accumulates large amounts of glycogen, a branched polymer of glucose. It is thought that this glycogen may support parasite survival during periods of nutrient limitation. However, the enzymes required for the synthesis and degradation of glycogen by *T. vaginalis* have been little studied. Previously, we characterized *T. vaginalis* glycogen synthase and glycogen phosphorylase, the key enzymes of glycogen synthesis and degradation, respectively. We determined that their regulatory properties differed from those of well-characterized animal and fungal enzymes. Here, we address how glycogen attains its branched structure. We first determined that the glycogen from *T. vaginalis* resembled that from a related organism, *Trichomonas*

gallinae. To determine how the branched structure of *T. vaginalis* glycogen arose, we identified open reading frames encoding putative *T. vaginalis* branching and debranching enzymes. When the open reading frames TVAG_276310 and TVAG_330630 were expressed recombinantly in bacteria, the resulting proteins exhibited branching and debranching activity, respectively. Specifically, recombinant TVAG_276310 had affinity for polysaccharides with long outer branches and could add branches to both amylose and amylopectin. TVAG_330630 displayed both 4- α -glucanotransferase and α 1,6-glucosidase activity and could efficiently debranch phosphorylase limit dextrin. Furthermore, expression of TVAG_276310 and TVAG_330630 in yeast cells lacking endogenous glycogen branching or debranching enzyme activity, restored normal glycogen accumulation and branched structure. We now have access to the suite of enzymes required for glycogen metabolism in *T. vaginalis*. Given that glycogen can comprise up to 20% of the dry weight of a trichomonad cell, we reason that it must play an important role in the physiology of the organism. Better understanding glycogen metabolism will give us insight into core biochemical processes of an important human pathogen, which may reveal novel therapeutic targets.

21. Efficacy of a combinational drug therapy against chronic *Toxoplasma gondii*.

LeeAnna M Lui¹, Austin G Sanford^{1,2}, Alexander Wallick^{1,2}, Braydon Dreher¹, Paul H Davis¹.

¹University of Nebraska at Omaha, Omaha, NE, USA. ²University of Nebraska Medical Center, Omaha, NE, USA.

Toxoplasma gondii is an intracellular parasite that infects 30% of the world's population. Toxoplasmosis, the disease caused by *T. gondii* infection, causes mild cold symptoms in its host initially. Existing in its tachyzoite stage, *T. gondii* replicates and infects quickly. However, weeks after infection, the parasite transforms into a slow replicating, bradyzoite stage that forms within cells as cysts. As bradyzoites, *T. gondii* forms in the host's brain, eyes, and muscle tissue. Currently, there is no treatment for this cyst stage, which can reemerge and cause lethal toxoplasmic encephalitis. Our work suggests that a novel combination of already approved drugs significantly reduces and potentially eradicates cyst burden. Through *in vitro* tissue culture and *in vivo* murine drug studies, we examine the efficacy of this cocktail and its ability to clear cyst burden in chronic infection models. If successful, we will be closer to creating a combinational approach with FDA approved drugs that eradicate the chronic infection of *T. gondii*.

22. Comprehensive study of parasites of the Texas state bison herd: Part 2.

Sara B Boggan¹, Heather A Mathewson¹, Kristin Herrmann¹, Donald Beard², Gui Verocai³.

¹Tarleton State University, Stephenville, Texas, USA. ²Texas Parks and Wildlife Department, Austin, Texas, USA. ³Texas A&M University, College Station, Texas, USA.

Parasites can have a significant effect on the typical growth, weight gain, and milk production of hoofstock. Therefore, infections are often managed with common antihelminthics. Texas Parks and Wildlife Department (TPWD) biologists manage the Texas State Bison herd at Caprock Canyons State Park (CCSP), Briscoe County, Texas, and base management plans on restoring native prairies to preserve the historic herd of Southern Plains Bison (*Bison bison*). The purpose of this study is to 1) identify the species of intestinal parasites present and 2) compare parasite load in treated and untreated bison. In January 2020 and February 2021, TPWD treated half of the sampled bison ($n = 50$) with Cydectine (moxidectine) leaving the remaining half ($n = 50$) untreated. Fecal samples were collected prior to treatment during examination of individuals. Samples were processed for intestinal parasites using a

modified McMaster's fecal float protocol. We observed 4 different parasite types: *Coccidia*, *Moniezia*, *Strongyloides*, and Strongylid-type. The Baermann technique was added for samples collected in February 2021 to test for the lungworm, *Dictyocaulus*. Difference in parasite load between the sampling dates was calculated. We assessed the effect of treatment and age on difference in parasite load using a generalized linear model for strongylid nematodes. We found no effect of treatment; however, juveniles had a greater decrease in parasite load after one year compared to adults. Further, there was a greater decrease in parasite load in juveniles for *Moniezia* than adults. The study will continue for the next year and samples will be assessed again at the end of the 2-year study. To improve management, we will provide TPWD with an assessment of effectiveness of antihelminthic treatment by age group.

23. Field application of salt, magnesium sulfate, Dylox, formalin, and hydrogen peroxide for killing parasitic copepods (Siphonostomatoida: Lernaepodidae: *Achtheres*) infecting white bass (*Morone chrysops*) and striped bass (*Morone saxatilis*).

Justin D Krol¹, John Damer², Haley Dutton¹, Steve Curran¹, Stephen A Bullard¹.

¹Auburn University, Auburn, AL, USA. ²Georgia DNR, Armuchee, GA, USA.

We tested field efficacy of salt (5-50 ppt), magnesium sulfate (30,000 mg/L with salt 7,000 mg/L), organophosphate (Dylox 420 SL; 0.25-2 ppm), formalin (Parasite-S; 250 mg/L), and hydrogen peroxide (35% Perox-Aid; 150 mg/L-1,500 mg/L) treatments in killing parasitic copepods (*Achtheres* sp.) infecting striped bass (*Morone saxatilis*) and white bass (*Morone chrysops*). Basses were electroshocked from Georgia waters (Etowah River, Flat Creek, Oostanaula River) in February and March. The agency required a method of treating the fish in transit from the capture locality to the hatchery. A trout hauling truck with 5, 454 L compartments was used to expose the wild-caught, infected basses to the respective treatment. Females of *Achtheres* sp. periodically were removed from the buccal cavity and viewed with high magnification using a stereo-dissecting microscope and compound microscope, respectively. Copepods were considered dead if no body movement nor tidal haemocoel movement was observed, and term eggs (having visible nauplii) were assessed similarly. The hydrogen peroxide (750 mg/L) treatment was recommended because female copepods were killed after 1 hour of exposure. A noteworthy outcome is that the purported effective treatment concentrations for salt, Dylox, formalin, and magnesium sulfate had no apparent effect on female copepods nor nauplii.

24. Development of selected tapeworms of the round stingray, *Urobatis halleri* (Myliobatiformes: Urotrygonidae), in Southern California.

Ralph G. Appy.

Cabrillo Marine Aquarium, San Pedro, California, USA.

The large abundance and relative accessibility of the round stingray, *Urobatis halleri*, in shallow nearshore habitats in Southern California provided an opportunity to examine the biology/transmission of its diverse tapeworm fauna. Eggs expelled from gravid tapeworm proglottids taken from round stingrays were fed to the tidepool copepod, *Tigriopus californicus*, which were examined at various intervals post-exposure. Larval development occurred in *Rhinebothrium urobatidium*, *R. gravidum* and *Ruptobothrium ditesticulum* (Rhinebothriidea), *Acanthobothrium parviuncinatum* (Oncoproteocephalidea), and *Dollfusiella schmidti* and *Mecistobothrium myliobati* (Trypanorhyncha). In addition, successful transmission to a second intermediate/transport host was documented for *R. urobatidium* and *A. parviuncinatum* (plerocercoid in small benthic fish) and *D. schmidti* (plerocercus in

ghost shrimp). Some observations based on this limited number of tapeworm species suggest the following: 1) the proceroid apical organ is specialized for adhering (*R. urobatidium*, *A. parviuncinatum*) or penetrating (*Ru. ditesticulum*) depending on the parasite's location in the second intermediate host; 2) a cercomer is present/visible only in the non-trypanorhynch species examined; 3) among the non-trypanorhynch species *Ru. Ditesticulum* is exceptional in having an appendage attached to a plerocercus-like larva in the second intermediate host; and 4) the scolex of the trypanorhynchs *D. schmidtii* and *M. myliobati* develop bothria and tentacles in the first intermediate host (copepod), which then withdraw into a cyst/blastocyst. Infection studies of round stingrays born and raised in captivity are underway.

25. Current status of intestinal parasites among elementary school children in Sohag, Egypt.

Eman Fathi Fadel.

Sohag University, Sohag, Egypt.

Intestinal parasitic infections (IPIs) are of the maximum generic of human infections international, causing extensive morbidity and mortality particularly in children. Our aim was to estimate the situation of IPIs in stool and fingernail samples among elementary schoolchildren in Sohag, Egypt. In this cross-sectional research, stool specimens from 200 schoolchildren were inspected macroscopically and microscopically by formol-ether sedimentation and after that stained with Kinyoun's modified acid-fast stain. Fingernail cuts of the children were gathered, put in tubes including 10% KOH before examination by light microscope for detection of parasites. A detailed questionnaire about clinical symptoms was done. Univariate and multivariable logistic relapse models were calculated for interpretation of the danger figures for parasitic infection. 63.5% of children harbored at least one type of intestinal parasite. There were significant differences regarding infections in contrast to residence and family size. Monoparasitized children constituted 40%, while 23.5% were polyparasitized. Protozoa were more frequent than helminths parasitizing (53.5% vs 4%) of the studied children. *Cryptosporidium* sp., *G. duodenalis* and *E. histolytica/ dispar* were the majority regular parasites found, with prevalence rates of 34%, 14.5% and 13% respectively. The predominant helminthic infection was *H. nana* (5%). Polyparasitized children were more frequently symptomatic than monoparasitized children. A significant difference was detected between diarrhea and polyparasitized children. *E. vermicularis* and *H. nana* eggs were found in 2% of the fingernail clippings. Age, gender, residence, and also family size were not danger figures to polyparasitism after calculation of univariate, and what's more, multivariable logistic relapse models. IPIs were very common among Sohag schoolchildren. Hence, there is an insistent requirement to execute an integrated project to decrease the predominance and intensity of these infections.

26. Flat-headed mayflies (Heptageniidae) as a likely paratenic host of *Chordodes morgani* (Nematomorpha).

John F Shea, James Marchant, Anna Sniezek.

Creighton University, Omaha, NE, USA.

Horsehair worms (Nematomorpha) have complicated life cycles requiring at least two hosts. Juveniles develop in a terrestrial arthropod such as a cricket or roach. When mature, they manipulate the host into entering water where the worms emerge, mate and lay eggs. The eggs develop into larvae that encyst in a paratenic host, which transfer the parasite from the aquatic to the terrestrial environment. These paratenic hosts are often the larval stages of aquatic insects such as midges and mayflies. When

they metamorphosize into adults and move over land, they are consumed by the definitive host. Wood roaches serve as a definitive host for the hairworm, *Chordodes morgani*, in eastern Nebraska. However, identifying its paratenic host is difficult because the larvae encyst in a wide variety of aquatic invertebrates, including dead-end hosts such as aquatic snails. To identify a likely paratenic host, we sampled three sites where *C. morgani* occurs. Because this hairworm lays its eggs on sticks, we collected submerged sticks, noting the presence or absence of eggs, placed them individually in Ziplock bags and froze the bags in a conventional freezer. We later removed all the invertebrates from each stick, identified them to the lowest taxonomic level, classified them according to how they obtain food (scraper or non-scraper) and dissected them to count the number of cysts. We predicted that scrapers found on sticks with eggs would have the highest prevalence of infected invertebrates and those invertebrates would harbor the largest number of cysts and so indicate the likely paratenic hosts for *C. morgani*. 82% of invertebrate scrapers that occurred on sticks with eggs were infected. The average intensity of cyst infection was 17.2 (n=50) for scrapers on sticks with eggs and 31.2 (n=47) for scrapers found on sticks without eggs. Scrapers consisted of aquatic snails (*Physa* sp.) and flat-headed mayflies (*Heptagenia elegantula*). The lifecycle of mayflies makes them a likely paratenic host for *C. morgani* in eastern Nebraska.

27. Five thousand trout and 400 oligochaetes later: geographic distribution of *Myxobolus cerebralis*, the first diagnosed case of salmonid whirling disease, and detection in two non-*Tubifex tubifex* oligochaetes in the Southeastern United States.

Steven P Ksepka¹, Jacob M Rash², Brandon Simcox³, Doug Besler², Micah B Warren¹, Haley R Dutton¹, Stephen A Bullard¹.

¹Auburn University, Auburn, AL, USA. ²North Carolina Wildlife Resources Commission, Marion, NC, USA. ³Tennessee Wildlife Resources Agency, Nashville, TN, USA.

Myxobolus cerebralis, the etiological agent of whirling disease, was detected in 2 river basins in North Carolina during 2015, which initiated the largest spatial–temporal monitoring project for the disease ever conducted within the southeastern US. A total of 3,157 rainbow trout (*Oncorhynchus mykiss*), 1,700 brown trout (*Salmo trutta*), and 787 brook trout (*Salvelinus fontinalis*) were screened from 198 localities within 8 river basins during July 2015 through October 2019. Infections were detected by pepsin–trypsin digest, microscopy, and the species-specific nested PCR from 25 localities across 7 river basins. Myxospore morphology was indistinguishable from the published literature. Five rainbow trout symptomatic for whirling disease were processed for histopathology. Myxospores were detected in the calvarial cartilage of two deformed trout with associated erosion of the cartilage consistent with whirling disease. Additionally, 452 oligochaetes from 31 localities within 7 river basins were screened for infection by *M. cerebralis*. The species-specific nested PCR was positive for 8 oligochaetes from 3 sites across 2 river basins. We barcoded *M. cerebralis*-positive oligochaetes using cytochrome oxidase 1 primers and conducted a Bayesian inference phylogenetic analysis. We identified 2 oligochaete genotypes: one sister to a clade comprising *Limnodrilus udekemianus* and another sister to *Limnodrilus hoffmeisteri*. This is the first report of *M. cerebralis* in Tennessee, the first histologically confirmed cases of whirling disease in the southeast US, the first detection of *M. cerebralis* from an oligochaete in the southeast US, and the first detection of *M. cerebralis* from an oligochaete other than *Tubifex tubifex*.

28. Assessing the healthcare burden of parasites: An analysis of hospital discharge records for characterizing patients and analyzing trends in human cestode cases in Nevada for 2013-2019

Chad L Cross, Brianna Rivera, Francisco Sy.

University of Nevada, Las Vegas, Las Vegas, NV, USA.

Cestodes are ubiquitous vertebrate parasites. Human infections are common globally, but less is understood about cases in the United States. Since there is no routine surveillance for these parasites, little is known about their public health impacts. To understand the potential impact of primary cestode infection (*Echinococcus granulosus*, *Taenia* spp., *Hymenolepis nana*, and *Diphyllobothrium latum*) and symptomatic infection (*Taenia solium* cysticercosis) on human health, we adopted a big data analytics approach utilizing secondary inpatient (IP), outpatient (OP), and emergency department (ED) records from Nevada as a case study because Southern Nevada is a busy tourist destination with a growing immigrant population. Data were obtained from the UNLV Center for Health Information Analysis from 2013-2019. We developed a brute-force algorithm to scrape ICD9/10 diagnostic codes for helminthiases from over 20 million patient discharge records. Nearly 15,000 records of vector-borne and parasitic diseases were found, and 372 records were from cestode parasitism. Most came from IP (50.3%) or OP (24.5%) visits. Diagnostically, *Taenia solium* taeniasis (30.9%) and nervous system cysticercosis (38.4%) were most common, with comorbid organ involvement occurring in 7.8% of patients. IP stays had a median stay of 3 days (range: 1-344), resulting in high cost (med=\$54,851). Patient races differed significantly ($p < 0.001$) and were predominantly Hispanic (49.5%) or white (32.0%). The majority were female (56.2%), and over the age of 40 (72.8%). There were no noticeable temporal trends ($p = 0.128$), with an average of 53 (SD=9.9) cases per year. This analysis serves as a case study for using patient record databases, in the context of One Health, as a means of indirect parasitic disease surveillance that may prove to be useful for understanding the sociodemographic characteristics of patients most at risk for these infections and may assist in obtaining population-based estimates of parasite disease burden for underfunded public health surveillance programs.

29. Nanoparticle-enhanced mass spectrometry: Discovery of novel *Trypanosoma cruzi*-specific urinary peptides in Chagas disease congenitally infected infants.

Raghad Almofeez¹, Paul Russo¹, Weidong Zhou¹, Ruben Magni¹, Hannah Steinberg², Kathryn Cassels¹, Yagahira Castro³, Freddy Tinajeros³, Manuela Versategui⁴, Edith Malaga⁴, Beth J Condori⁴, Caryn Bern⁵, Robert Gilman³, Lance Liotta¹, Alessandra Luchini¹.

¹Center for the Applied Proteomics and Molecular Medicine, George Mason University, Manassas, VA, USA. ²Department of Microbiology and Immunology, University of Illinois Chicago, Chicago, Illinois, USA. ³Department of International Health, Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland, USA. ⁴Universidad Peruana Cayetano Heredia, Lima, Peru. ⁵University of California San Francisco School of Medicine, San Francisco, CA, USA.

Chagas disease (CD), caused by the protozoan *Trypanosoma cruzi*, is mainly transmitted through vectors, blood transfusions or from mothers to their infants. It is estimated that around 25% of new CD infections occur through congenital transmission. In most CD cases, the infection remains asymptomatic for years; and being undetected and untreated, it can cause cardiac or gastrointestinal complications or even unexpected death. Detecting and treating CD in the asymptomatic phase is critical as it allows for more efficient treatment before tissue damage progresses to an irreversible stage. CD is endemic in parts of Latin America and due to immigration, it's been growing to be a global public health concern. For that reason, there is a need for a low cost, specific and sensitive test to screen for CD in areas of high

prevalence and for immigrants. Current tests use blood specimens for diagnostics and most lack sensitivity and are unreliable without a combination of another test. Our study presents a novel non-invasive nanoparticle-enhanced mass spectrometry test to detect *T. cruzi* peptides in the urine of infants with Chagas disease. Nanoparticles harvest and concentrate low abundance protein markers, preventing their degradation while excluding high molecular weight, abundant proteins. Novel *T. cruzi* specific urinary markers are identified with high sensitivity and specificity in patients congenitally infected with Chagas disease. Over a 100 unique *T. cruzi* derived peptides were identified in 15 Chagas patients living in endemic areas. Of the identified peptides, mucin-associated surface protein, trans-sialidase and dispersed gene family protein 1 were highly represented in the urinary peptidome of Chagas patients. Members of those family groups are involved in host invasion and pathogenesis. In this study, we demonstrate for the first time that the nanoparticle-enhanced mass spectrometry test is able to detect urinary *T. cruzi* peptides in patients with Chagas disease. Introducing a low cost and non-invasive test can be valuable for universal screening of Chagas disease for immigrants and for increasing endemic areas diagnostic testing. Next step for this project is to verify identified markers with orthogonal technologies.

30. Dead end host? Altered behavior in aquatic snails infected with cysts of *Paragordius varius*.

Benjamin J Engle, John F Shea.

Creighton University, Omaha, NE, USA.

Paragordius varius (Family Gordiidae) is one of the most prevalent horsehair worms throughout the western hemisphere. Definitive hosts, typically crickets and grasshoppers, become infected when they consume the cyst stage. When mature, *P. varius* manipulates their terrestrial host into entering water where the worms emerge, mate and lay eggs. Upon hatching, larvae encyst in an aquatic paratenic host such as midge or mayfly larvae. When these aquatic insects become adults, they transfer *P. varius* to the terrestrial environment. Cysts of *P. varius* are found in a variety of aquatic organisms, showing low host specificity. Aquatic snails (*Physa* spp.) contain *P. varius* cysts but are considered dead end hosts in the life cycle. However, if infected snails exit the water, they would be susceptible to predation by the definitive host and so could play a role in maintaining *P. varius*'s life cycle. We examined altered behavior, comparing the activity level and location at the waterline between infected and uninfected snails. We predicted that infected snails would stay closer to the waterline than uninfected ones and would be more active. Two experiments were run from before sunrise to after sunset. One tested the behavior of individual snails while the other tested groups of snails. Waterline preference was tested using an aquarium tank with 30 snails and marking their locations each hour. Physical activity was tested by recording the distances traveled by 6 snails each hour. Initial analysis did not find any significant difference in infected and uninfected snails. While statistically not significant, the drop in p value observing the mid-day hours of snail physical activity from 2-7pm could suggest a possible future significance. Sample size for that part of the experiment could have been a limiting factor (t-test, n= 6, p= 0.208). If infected snails are more active during the day, it could increase the chances of them being dead, dried out and available for predation by definitive hosts, signifying that aquatic snails may play an important role in the life cycle of *P. varius*. Further studies will examine if there is behavioral difference by manipulation of the parasite.

31. Fish health and biodiversity at Lily Lake, Pennsylvania.

Genevieve Ivec.

SUNY-ESF, Syracuse, NY, USA.

Parasites are components of a healthy ecosystem which can also impact fish health and fitness. Understanding fish parasite communities to interpret fish health is essential for the conservation of natural ecosystems and for optimizing managed fisheries. In this study, a comprehensive survey was conducted on parasite communities in 3 fish species at a private lake near Dalton, PA. We sampled *Lepomis macrochirus* (Bluegill) and *Pomoxis nigromaculatus* (Black Crappie) using a fyke net, and *Micropterus salmoides* (Largemouth Bass) using hook-and-line gear. There were 13 species of parasites present in all hosts combined. Bluegill and Largemouth Bass each had 10 of those species, while Black Crappie only had 6 species. Parasites represented the following taxonomic groups: nematodes (3 species), trematodes (3 species), monogeneans (3 species), copepods (2 species), and cestodes (2 species). Bluegill and Bass each had 2 species of nematodes, while none were in Crappie. The metacercarial stage of the digenean *Posthodiplostomum minimum* was the most abundant parasite in Bluegill and Bass with 100% prevalence. Mean abundance of this parasite was also high with 2289 parasites per fish in Bluegill and 2662 parasites per fish in Bass. This parasite was notably found to be completely absent in Crappie. *Ergasilus* sp., a copepod parasite, was also absent in Crappie and occurred rarely in Bass, but had a 66% prevalence in Bluegill with mean abundance of 22 parasites per fish. One of the monogenean species was found to specialize only on Bass. Otolith microchemistry analysis was conducted to compare parasite burden with concentrations of trace elements over time of the lightest and heaviest parasitized fish for Bluegill and Crappie were chosen. Analysis revealed that Bluegill expressed a positive correlation with parasite abundance and concentrations of manganese in ratio to calcium. The Mn:Ca ratio is indicative of hypoxia and the trend persisted when Mn was rationed against magnesium to correct for effects from growth. Both the high and low parasitized Black Crappie analyzed had markedly lower abundances than the Bluegill and did not reveal high levels of hypoxic conditions. Future directions of this work should be to conduct the analysis with more individuals.

32. Can competition among parasite species be detected in field-collected samples of fishes?

Michael Barger.

Stephens College, Columbia, Missouri, USA.

Parasite communities of fishes are thought to be absent of competitive interactions regulating species composition and abundance. However, most studies in these systems are conducted using field surveys, and it is unclear if observed communities carry the stamp of past competitive interactions. It is also unclear whether the methods used to test for competition are able to do so in field collected datasets. Data from a two-decade long study of the intestinal helminth communities of creek chub (*Semotilus atromaculatus*) were used to explore the potential of commonly available methods to detect negative interactions among parasite species in species-poor, low-intensity communities typical of many freshwater fishes. True to most past studies, analyses of parasite abundance (interspecific correlations) and co-occurrence (logistical regression and null model analyses) revealed no patterns consistent with negative interactions. Modelling approaches were then utilized to build parasite communities structured by competition to determine the conditions under which these methods can discern the presence of strong competitive interactions. Model communities behaved similarly to observed communities from creek chub. Four models of competition increased the number of negative correlations among species by 42%, but only 9% of these were significantly negative, despite very strong underlying competitive

effects. Logits were twice as likely to be negative in competitively structured model communities than when competition was absent, but none of the logits explained much variation in infracommunity species composition. Null model analyses of infracommunity species composition produced mixed results, with some randomization models and metrics of co-occurrence performing poorly in all circumstances, e.g., always or never rejecting the null hypothesis, and the rest performing in an unbiased, but highly imprecise, manner. Two additional experiments were performed, one increasing the prevalence of parasite species, and the other increasing the number of parasite species in the component community. Results from these will help to winnow away those methods incapable of detecting competition, and unreliable in doing so, from those that merit further study and use.

33. Atypical trematode life cycle decreases within-host clonal diversity.

Sarah Cobb¹, [Sarah A Orlofske](#)², Robert C Jadin², Devon Keeney³.

¹Department of Pharmacology, University of Texas Southwestern Medical Center, Dallas, TX, USA. ²University of Wisconsin - Stevens Point, Stevens Point, WI, USA. ³Department of Biological and Environmental Sciences, Le Moyne College, Syracuse, NY, USA.

Digenean trematodes use multiple hosts to complete their life cycles and commonly infect different species at each developmental stage. Vagile second intermediate hosts (e.g. fish, crustaceans) have been shown to accumulate diverse trematode clones after clonal reproduction of trematodes in previous snail hosts. *Cotylurus* sp. has an atypical life cycle and can utilize the same snail species as first and second intermediate hosts. We developed novel microsatellite loci and used them to identify the clonal diversity of *C. sp. tetracotyles* within 22 *Stagnicola exilis* second intermediate hosts. Specimens were collected from three sites (two in Illinois within 1 km of each other and one in Wisconsin, USA ca. 75 km away) in 2015. Our goal was to examine how the use of the same, relatively immobile, host species influences trematode genetic diversity within hosts. Snails from all sites possessed large numbers of identical clones, including numerous sets of identical clones within single snails. Identical trematode clones were also recovered from different snails within sites. These findings suggest that the alternative life cycle of *C. sp.* increases the frequency of identical clones within second intermediate hosts and the likelihood of different host individuals encountering the same parasite clone.

34. Increasing education initiatives in ASP.

Jeffrey Bell¹, [Nicole Chodkowski](#)², Makedonka Mitreva³, Sarah Orlofske⁴, J Trevor Vannatta⁵.

¹University of North Dakota, Grand Forks, ND, USA. ²Lawrence University, Appleton, WI, USA. ³Washington University in St. Louis, St. Louis, MO, USA. ⁴University of Wisconsin- Stevens Point, Stevens Point, WI, USA. ⁵University of Minnesota, Minneapolis, MN, USA.

The American Society of Parasitologists by-laws contain three primary goals: to improve teaching, promote investigation, and advance knowledge of parasitology. The goal of the ASP Education Committee is to assist in fulfilling these goals. As one step towards the realization of these goals, the committee distributed a survey during the 2019-2020 academic year soliciting feedback on current and desired educational needs of our society membership. With these results, the committee redefined their goals to better serve members of the community, generated ideas for how we can better engage with other societies and educational resources and began working to create an accessible teaching repository for our members. The committee's main goals were to curate freely-available open educational resources (OERs) and work with society members to contribute their own resources to the broader

community. By doing this, our society can gain recognition as a source of educational material, our members can publicize resources used for tenure and promotion, and we can centralize and distribute the resources that have already been created. The committee is currently working on ways to generate a searchable repository of published OERs to serve our current membership, retain and expand on membership, and increase the frequency of communication within the society by highlighting resources that can be used in a variety of classroom settings. 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.

35. Morphological and molecular characteristics of *Telorchis* (Digenea: Plagiorchoidea: Telorchidae) obtained from indigenous and introduced freshwater turtles in Japan.

Misako Urabe, Tomoyoshi Tsubouchi, Kei Okayama, Yusuke Miyamura, Hiroaki Wakita.

The University of Shiga Prefecture, Hikone, Shiga, Japan.

Genus *Telorchis* Lühe, 1899 is a digenean parasite observed widely in reptiles and amphibians. In Japan, four species [*T. clemmydis* (Yamaguti, 1933), *T. geoclemmydis* (Yamaguti, 1933), *T. konoii* (Ogata, 1934) and *T. megacotyle* (Fukui et Ogata, 1934)] have been reported from both the indigenous pond turtle (*Mauremys japonica*) and from the introduced Reeve's turtle (*M. reevesii*), and red-eared slider (*Trachemys scripta elegans*). Because of their morphological variation and the lack of molecular studies, it has been uncertain whether these scientific names are valid or not. Therefore, we obtained new specimens of *Telorchis* species in Japan from freshwater turtles, and conducted their morphological and molecular characterization. Morphological study was carried out based on 74 *Telorchis* specimens obtained from 16 pond turtles, 34 Reeve's turtles and 156 red-eared sliders. The mitochondrial COI were sequenced for 57 samples, and 28S rDNA were for 20 samples. A phylogenetic tree based on 28S rDNA sequences showed that at least three *Telorchis* species are included in our samples. All samples from red-eared sliders were identified as *Telorchis corti* Stunkard, 1915, based on their morphological and molecular characteristics, suggesting that they were introduced into Japan with their host sliders. *Telorchis* sp. 1, which resembles *T. geoclemmydis* morphologically, was obtained from *M. japonica* and *M. reevesii*. However, their measurements sometimes overlapped with those of *T. corti* and it was difficult to distinguish these two species by morphology. *Telorchis* sp. 2 was infected to *M. japonica*, and its morphology did not match any species reported in Japan in past studies. Our study showed that the taxonomic status of *Telorchis* in Japan is still confused and that there are some undescribed species. Moreover, it suggests that the species composition of this genus has been disturbed by non-native species introduced with their host turtles.

36. Investigation of genetic and trait variability of *Gyrinicola batrachiensis* (Nematoda: Oxyurina) across North America.

Matthew A Walker¹, Matthew G Bolek², Elliott A Zieman³, Gabriel J Langford⁴, Jason L Brown¹, F Agustín Jiménez¹.

¹Southern Illinois University, Carbondale, IL, USA. ²Oklahoma State, Stillwater, Oklahoma, USA.

³Eastern Illinois University, Charleston, IL, USA. ⁴Florida Southern College, Lakeland, FL, USA.

Gyrinicola includes six species of oxyurid mutualists found within the intestinal tract of numerous larval anuran host species. The species include the sympatric *Gyrinicola tba* (Dinnik, 1930) and *Gyrinicola chabadamsoni* (Brigitte, 2008) in Europe, *Gyrinicola chabaudi* (Araujo & Artigas, 1982) in Argentina,

Gyrinicola japonica (Yamaguti, 1938) in Japan, *Gyrinicola dehradunensis* (Maity, Rizvi, Burse & Chandra, 2019) in India and *G. batrachiensis* (Walton, 1929) in North America. The latter is the only recognized species across North America. The relative morphological variation of the species has been analyzed in diecious metapopulations of *G. batrachiensis* from Oklahoma and diecious and parthenogenetic metapopulations of *G. batrachiensis* from Nebraska. The analysis of character variability did yield statistically significant differences among worms collected from different host species, but none of these differences were proposed as diagnostic or an indicator of species identity. These results suggest that a single species of nematode occurs in various species of sympatric anurans. To further examine their putative diversity we sampled populations of these nematodes from across the Midwest and the Gulf of Mexico and evaluated them for genetic diversity for the first time using the nuclear markers 28S, ITS1, 5.8S and ITS2. The resolution of the phylogenies suggests that at least two clades exist among the nematodes collected across the Midwest. Examination of female anatomy suggests that some caudal traits may help in defining each of the two clades. Further taxonomic and gene sampling are necessary to determine the extant diversity of *G. batrachiensis* across North America.

37. Expanded geographic distribution and redescription of *Octospinifer macilentus*. Van Cleave 1919 (Acanthocephala) from *Catostomus commersonii*.

Claire E Curtin, Florian B Reyda.

SUNY Oneonta, Oneonta, NY, USA.

The acanthocephalan *Octospinifer macilentus* Van Cleave 1919 was described from *Catostomus commersonii* (white sucker) from Douglas Lake, Michigan. Since its original description, *O. macilentus* has been reported from a diversity of states in the eastern and northern USA. In spite of its frequent reports in surveys, the morphology of *O. macilentus* has received little attention since it was first described, and hence the information about this taxon is limited. The current study was possible because we conducted extensive survey work in North America in order to obtain a diversity of intestinal helminths of catostomids. The fish were obtained via backpack or boat electrofishing and from gill and trap nets during our survey. We acquired specimens of *O. macilentus* from *C. commersonii* from several localities in New York State, and from New Hampshire and Virginia. Our study also incorporated specimens from Wisconsin and Manitoba, Canada from a collaborator. Twenty-two male and 14 female specimens of *O. macilentus* were studied and measured using light microscopy, and proboscides of several individuals were examined with scanning electron microscopy. We also prepared scientific illustrations of a female and male worm, and of female genitalia, using a camera lucida. This presentation includes a comparison of the morphological data we obtained with that provided by Van Cleave in 1919, as well as scientific illustrations that are more highly detailed than those provided in the original description. Our study also includes the first scanning electron micrographs of *O. macilentus* and an expanded geographic distribution for this taxon. This project is part of a bigger collaboration to improve reference information and taxonomy for species of Neoechinorhynchidae in North American freshwater fishes.

38. Morphological and molecular characterization of *Trichuris* (Nematoda: Trichuridae) parasite of *Heteromys irroratus* (Rodentia: Heteromyidae) in central Mexico.

René Josué Monzalvo-López, Jorge Falcón-Ordaz, Norma Leticia Manríquez-Morán.

Centro de Investigaciones Biológicas, Universidad Autónoma del Estado de Hidalgo., Pachuca, Hidalgo, Mexico.

Studies of *Trichuris* parasites of heteromyid rodents in Mexico have been scarcely addressed, represented only by morphological studies that include five described species and one identified at genus level (*T. elatoris*, *T. dipodomis*, *T. fossor*, *T. muris*, *T. silviae*, and *Trichuris* sp.) reported in 10 host species of the genus: *Chaetodipus*, *Dipodomys* and *Heteromys*. In the particular case of *H. irroratus*, there are three records, belonging to *Trichuris* sp., *T. fossor*, and *T. muris*, the last two being considered as doubtful species, in addition to the absence of their deposited material in scientific collections, which makes it difficult to corroborate the identifications. To contribute to the morphological and molecular knowledge of the genus *Trichuris* parasite of *H. irroratus*, morphological and morphometric studies were carried out in localities of central Mexico (Hidalgo, Querétaro, State of Mexico and Tlaxcala) while molecular analyses were performed for the localities corresponding to Hidalgo state. The organisms were measured and observed by optical and scanning electron microscopy, comparing them with the 30 described species that parasitize rodents in America. The morphometric study was performed with a generalized discriminant analysis (GDA) using 12 morphological characteristics in males and eight in females. The morphological study of the specimens of the present work shows differences with 29 of the 30 described species, the specimens in the study are characterized by the presence of a spicular tube, cylindrical sheath with acute projections in males, and semiprotusive vulva in females, characteristics that the studied organisms share along with the attributes with *T. guanacastei*, parasite of *H. salvini* from Costa Rica, which makes the species separation difficult. Regarding morphometric analysis, GDA showed significant differences between three of the four populations compared, forming three distinct groups, positively and negatively correlated with some morphologic attributes such as fusiform length, total length, and proximal cloacal tube length, suggesting variations among the localities considered, mainly, related to non-distinctive attributes (except for the proximal cloacal tube). *Trichuris* sp. is described for *H. irroratus* and its phylogenetic position within the genus is also indicated.

39. The University of Wisconsin - Stevens Point Parasitology Collection: Integration of teaching and research.

Sarah A Orlofske.

University of Wisconsin - Stevens Point, Stevens Point, WI, USA.

The Stephen J. Taft Parasitology Collection in the UWSP Museum of Natural History was established in 2004 when Dr. Stephen (Steve) J. Taft retired after 33 years of teaching and research at UWSP. The mission of the Parasitology Collection is to serve as a foundation for research and training, primarily of undergraduates, in parasitology and related scientific and applied disciplines. The collection was largely acquired and amassed through the work of Steve Taft and the numerous students he mentored over the decades of his tenure at UWSP. The collection is impressive in its magnitude and faunistic scope, with over 20,000 slide mounted specimens and hundreds of additional wet preserved specimens in vials and jars. Strengths of the collection include avian ectoparasites (lice and mites) as well as endoparasites (helminths and blood protozoa). The collection contains many invaluable specimens, such as those from hosts that have declined in Wisconsin, or others from hosts for which lethal sampling is no longer permissible. Faculty-mentored student curation of the arthropod components of the collection is possible with the support of the National Science Foundation through the collaborative Terrestrial Parasite Tracker Project. In addition to physical improvements in the management of the collection, this project has supported the development of an efficient digitization workflow which allows students to contribute high resolution slide images and label data to the Symbiota Collections of Arthropods Network (SCAN) portal for use by other data aggregators like iDigBio and ultimately the larger community of scientists and educators. The digital resources supported by the Terrestrial Parasite Tracker Project also inspired the development of several innovative teaching resources for parasitology

and introductory biology courses in response to the transition to online instruction due to the COVID-19 pandemic. Future plans for the collection include the development of parasitology related exhibits in conjunction with the modernization of the UWSP Museum of Natural History public galleries.

40. Fish blood flukes (Digenea: Aporocotylidae) from Indonesia: Two new genera and species infecting the banded eagle ray, *Aetomylaeus nichofii* (Bloch and Schneider, 1801) Capapé and Desoutter, 1979 (Myliobatiformes: Myliobatidae) from Borneo.

Micah B Warren, Stephen A Bullard.

Auburn University, Auburn, AL, USA.

Specimens representing two species of blood flukes (Digenea: Aporocotylidae), were collected from the banded eagle ray, *Aetomylaeus nichofii* (Bloch and Schneider, 1801) Capapé and Desoutter, 1979, in Borneo, Indonesia. *Aetohemecus kirstenjensenae* infected the heart of a banded eagle ray from Manggar, East Kalimantan, Borneo, Indonesia, and differs from its congeners by having an oviducal ampullae, an oötype posterior to all genitalia, and a uterus that extends anterior to the ovary. *Aetohemecus kirstenjensenae* resembles *Selachohemecus* spp., which infect requiem sharks (Carcharhinidae) in the Northwestern Atlantic Ocean and Gulf of Mexico, by having a single ventrolateral row of large C-shaped tegumental spines, X- or H-shaped intestine, and a post-caecal ovary. Specimens of *Homestios janinecairae* infected the heart of a banded eagle ray from Takisung, South Kalimantan, Borneo, Indonesia. *Homestios janinecairae* resembles other blood flukes that infect rays (Batoidea) by having a single, curving testis and an inverse U-shaped intestine as well as by lacking tegumental spines. It differs from all aporocotylids infecting batoids that lack spines by having a uterus that extends anterior beyond the level of the seminal vesicle. The present study comprises the first record of an aporocotylid from Indonesia or from an eagle ray (Myliobatidae). To our knowledge, these are the first trematodes reported from a species of *Aetomylaeus*. The proposals of new genera and the description of two new species herein brings the total number of nominal chondrichthyan blood flukes to 13 species of 11 genera.

41. New species of *Mathevolepis* Spassky 1948 from the dusky shrew *Sorex monticolus*.

Joshua E Anderson¹, Vasyl V Tkach², Stephen Greiman¹.

¹Georgia Southern University, Statesboro, GA, USA. ²University of North Dakota, Grand Forks, ND, USA.

Mathevolepis is an understudied genus of hymenolepidid tapeworms infecting shrews exclusively of the genus *Sorex*. There are currently 7 formally described species within this genus; only one of them, *Mathevolepis macyi*, was reported from the Nearctic. Current preliminary molecular data suggests the presence of no fewer than 4 undescribed species within the Nearctic. *Mathevolepis* n. sp. is described based on specimens obtained from the dusky shrew *Sorex monticolus* collected from the Sangre de Cristo Mountains in New Mexico. Cestodes were studied both morphologically using traditional light microscopy techniques, as well as molecularly using the large ribosomal subunit 28S and mitochondrial COI as the target DNA regions. *Mathevolepis* n. sp. is similar to the previously described member from North America as well as the Palearctic representatives of the genus in having serial development of proglottids, a trilobed ovary, and the presence of an oophore within each gravid proglottid. *Mathevolepis* n. sp. is distinguishable from *M. macyi* by having a smaller cirrus sac, longer ovary, shorter suckers, and in the arrangement of the trilobed ovary. *Mathevolepis* n. sp. can be differentiated from all

Palaearctic species excluding *Mathevolepis alpine* and *Mathevolepis skrjabini* by having more proglottids per developmental series, and can be differentiated from *M. alpine* by having a smaller scolex and suckers. *Mathevolepis* n. sp. can be differentiated from *M. skrjabini* by having far fewer proglottids per stage of development. Molecular comparison strongly support the differentiation between *Mathevolepis* n. sp. And *M. macyi*.

42. First record of *Psorospermium* cf. *haeckeli* (Class: Mesomycetozoea) in Northern Clearwater crayfish, *Faxonius propinquus* Girard 1852 (Decapoda:Cambaridae) from Michigan, USA.

Christina Anaya.

University of Nebraska-Lincoln, Lincoln, NE, USA.

Psorospermium cf. *haeckeli* Hilgendorf 1883 is a unicellular, eukaryotic protozoan within the Class Mesomycetozoea. Although only one species has been identified within *Psorospermium*, there have been four morphotypes described in 17 species of crayfish from the Holarctic, Neotropical, and Australasian regions. In the U.S., *Psorospermium* has been documented in Florida, Louisiana, Minnesota, Mississippi, Texas, and Wisconsin but a lack of additional sampling suggests we do not know the full range of *Psorospermium* in the U.S. In September of 2019, eight adult crayfish were submitted to the Parasitology Class at Northern Michigan University by local fishermen. Connective tissue was removed from beneath the carapace and viewed under a light microscope. We found 67% and 60% of crayfish from two locations were infected with three morphotypes of *Psorospermium* cf. *haeckeli* including a less common form known as the 'curved form'. Observations are consistent with previous morphological descriptions but was not surprising since *Psorospermium*, including the curved form, has been found in the neighboring state of Wisconsin. The presence of the curved form represents only the second report of this morphotype in North America but may be more common than previously believed. Whether or not the morphotypes represent distinct species and the ambiguities within Mesomycetozoea will be discussed.

43. Walking with dinosaurs: Phylogeography and systematics of proterodiplostomid digeneans parasitic in crocodilians.

Tyler J Achatz¹, Eric E Pulis², Kerstin Junker³, Jeffrey A Bell¹, Francisco Tiago de Vasconcelos Melo⁴, Vasyly V Tkach¹.

¹University of North Dakota, Grand Forks, ND, USA. ²Northern State University, Aberdeen, SD, USA. ³ARC-Onderstepoort Veterinary Institute, Onderstepoort, South Africa. ⁴Institute of Biological Sciences, Federal University of Pará, Belém, Brazil.

Crocodilians are an ancient group of reptiles that evolved at least 225 million years ago. The ancestors of today's crocodilians already inhabited the supercontinent Pangea prior to its breakup. The geographic range of crocodilians was fragmented and the descendants of early crocodilians were separated from each other by continental drift. Associated speciation and extinction events ultimately shaped today's fauna and distribution of crocodilians. The same likely happened to their parasites. Although parasites of crocodilians have not been studied sufficiently, it has been demonstrated that they possess a relatively rich and highly distinct helminth fauna. One of the most characteristic groups of helminths found in crocodilians is the digenean family Proterodiplostomidae. At least some proterodiplostomids have been found in every region of the planet inhabited by crocodilians. Prior molecular phylogenetic work on proterodiplostomids has been limited to only 2 species, neither of which were collected from

crocodilians. The goal of our study was to infer phylogenetic relationships of proterodiplostomids of crocodilians and properly test the monophyly of most constituent genera using sequences of nuclear ribosomal DNA. The results based on specimens from 3 continents have provided evidence that at least some of today's proterodiplostomid lineages are very ancient and likely evolved before the break-up of supercontinents, thus reflecting long co-evolutionary history between these parasites and crocodilians. In addition, molecular phylogeny has permitted a reassessment of the taxonomic value of some morphological and biological characteristics of proterodiplostomids, resulting in amended systematics.

44. Zoonotic and non-zoonotic tick borne pathogens in wild cervids of Tapada (Portugal).

Nélida Fernández¹, Irene Aguilar¹, Luis Miguel González², Estrella Montero², Jorge Soares³.

¹Alfonso X University, Madrid, Spain. ²National Centre for Microbiology, Madrid, Spain. ³Bewild, Lisbon, Portugal.

Tick borne diseases are present worldwide. Climate change and host availability are factors involved in their geographical spread. Wild and domestic animals allow tick feeding, supporting their survival. In the Iberian Peninsula, wild ungulates, roe deer and fallow deer are common, and are usually parasitized by ticks. These wild animals share habitat with domesticated ruminant species like cattle, sheep or goats and also with humans. This coexistence occurs mostly in peri-urban regions or natural reserves such as "Tapada Nacional, Mafra" (Portugal), where this study has been carried out. The interrelation between wild cervids and tick-transmitted pathogens like some piroplasm species such as *Babesia divergens*, *Babesia microti* and *Borrelia burgdorferi* sensu lato, is frequently threatening the health of both domestic animals and humans. Overall, 560 adult ticks were collected from a total of 12 red deer and 71 fallow deer and were morphologically identified to species. Total DNA was extracted and quantified from ticks. Specific PCR protocols were used to detect piroplasms' DNA of the genera *Babesia*, *Theileria* and *Borrelia burgdorferi* sensu lato. Positive amplicons were sequenced for species identification. *Ixodes* was the most prevalent genus 75.4% (*Ixodes ricinus* 75% and *Ixodes hexagonus* 0.4%). 3.4% of *Haemaphysalis* species, 11.8% *Rhipicephalus sanguineus*, 1.4% *Dermacentor marginatus* and 8% of *Hyalomma* species were found. The results showed a 10% of infected ticks by piroplasms. Coinfections, species analysis and global data of potential zoonotic pathogens isolated have been established. These results verify that wild cervids are parasitized by ticks frequently. The identified tick species can feed not only on wild cervids but also on humans and livestock. Tick borne pathogens observed trigger animal and human diseases. Therefore, establishing control strategies from a one health perspective is essential to avoid animal and human infectious diseases.

45. *Giardia lamblia* in commercial oysters (*Crassostrea virginica*) and mussels (*Mytilus edulis*) from the Bronx, New York City.

Ghislaine Mayer, Sireen Mastrooq, Viola Marcia.

Manhattan College, Riverdale, NY, USA.

Giardia lamblia (*G. lamblia*) is a human intestinal parasite that causes gastroenteritis. It is transmitted through the fecal-oral route by mode of contaminated water. Bivalves are filter feeders that have been previously shown to sequester a number of microbes including protozoan parasites such as *Cryptosporidium parvum* and *G. lamblia*. We have previously shown prevalence of *G. lamblia* in non-commercial bivalves, including oysters and mussels collected from various beach sites in the Bronx, NY. Oysters are very important economically and are commonly consumed raw. Commercial oysters

(*Crassostrea virginica*) were examined for the presence of *G. lamblia* using molecular techniques. A total of 30 oyster and 72 blue mussels (*Mytilus edulis*) specimens were purchased from a popular fish store located in the Bronx in the fall of 2019. Each specimen was dissected to isolate the following tissues: digestive gland, adductor muscle, mantle, gills, and hemolymph. DNA was extracted from each tissue. Nested-PCR was performed using primers that target the β -giardin gene. *G. lamblia* DNA was detected in 20/30 of the oyster specimens with a resulting prevalence of 66.6%. On the other hand, *G. lamblia* DNA was detected in 9/72 blue mussels (12.5%). In the oysters, the mantle and the adductor muscle were the only tissue in which *G. lamblia* DNA was detected with a prevalence of 3.4%, respectively. In blue mussels, *G. lamblia* DNA was observed in the mantle, the gills, the digestive glands, and the foot at a prevalence of 5.5%, 5.5%, and 1.4%, respectively. These data indicate that commercial bivalves are potential sources of *G. lamblia* infection.

46. *Tarantobelus jeffdanielsi* n. sp. (Panagrolaimomorpha, Panagrolaimidae), a nematode parasite of tarantulas.

Jacob Schurkman¹, Kyle Anesko¹, Joaquin Abolafia², Irma Tandingan De Ley¹, Adler Dillman¹.

¹UC Riverside, Riverside, CA, USA. ²Universidad de Jaén, Las Lagunillas, Spain.

Multiple tarantula deaths were reported by a wholesale spider breeder from Virginia Beach, VA, USA in 2018. We received infected *Grammastola pulchra* and *Monocentropous balfouri* from this breeder for diagnostics. Symptoms included white discharge in the oral cavities of the tarantulas, which were composed of nematodes intertwined inside of the tarantula's oral cavity. We examined the nematodes and propose a new species, *Tarantobelus jeffdanielsi* n. sp., in the currently monotypic genus *Tarantobelus* based on a combination of morphological and morphometrical data; and unique nuclear rDNA 28S and 18S sequences. Based on molecular phylogenetic analyses, the previously described *Tarantobelus arachnicida* was relocated, along with *T. jeffdanielsi* into the family Panagrolimidae. We also provide evidence of *T. jeffdanielsi*'s ability to parasitize *Galleria mellonella* larvae and *G. pulchra*. Studies further revealed that the new species has an 11.2-day average lifespan, and a total fertility rate of 158 nematodes/adult.

47. Shake it off: Behavior of a freshwater snail during and after parasite attack.

J Trevor Vannatta^{1,2}, Jason T Hoverman², Dennis J Minchella².

¹University of Minnesota, St. Paul, Minnesota, USA. ²Purdue University, West Lafayette, Indiana, USA.

Parasite avoidance has recently drawn attention from scientists due to its potential role in structuring ecological interactions. Although snails serve as important intermediate hosts for a number of ecologically important trematode species, few studies have considered snail avoidance behavior. Here, we use the common model species, *Physa acuta* host snails and the parasitic trematode, *Echinostoma trivolvis*, to explore how snails respond to attacks by parasites. Snails exposed to parasite cercariae displayed more shell shaking, more surfacing, and less time foraging than unexposed snails. However, these impacts did not persist beyond the initial exposure period. These results suggest that shell shaking, commonly assumed to be an antipredator response, also may be associated with parasite avoidance. The combination of these behaviors is likely to have ecological ramifications including altered interactions with predators, changes in snail foraging, and increased bioturbation.

48. Quantifying bilateral infections in the trematode *Alloglossidium renale*.

Jenna M Hulke¹, William H Ellenburg¹, Derek A Zelmer², Charles D Criscione¹.

¹Texas A&M University, College Station, Texas, USA. ²University of South Carolina Aiken, Aiken, South Carolina, USA.

Within host distributions of parasites can have ecological and evolutionary consequences for both hosts and parasites. Parasites that infect bilateral organs (e.g., eyes, lungs, kidneys) can exhibit 1 of 4 possible distributions: random, uniform, consistent aggregation to one particular organ (e.g., left vs. right), or inconsistent bias (aggregated, but does not favor one side). *Alloglossidium renale* is a trematode that undergoes sexual reproduction within the bilateral antennal glands of grass shrimp. Previous studies have shown that host asymmetry between the bilateral organs can result in a consistent aggregation to one organ. Grass shrimp have no apparent asymmetry between the glands, thus a random pattern is a plausible prediction. However, as *A. renale* is hermaphroditic, a possible need to increase outcrossing opportunities could lead to aggregation. We examined within-host distributional patterns from 4 field-collected samples (3 geographic locations where 1 was sampled at 2 time periods). We used Monte Carlo simulations to determine if the observed patterns differed from that expected by randomly allocating parasites into groups of 2. We explored the use of 3 test statistics, the mean difference in abundance, the mean exact probability, and the mean index of dispersion, as well as kept track of the number of single infections. Single infections can have important genetic consequences as single parasites are forced to self-mate. Results of the simulations showed that the parasite distribution between the antennal glands did not statistically differ from random in 3 of the 4 samples (though one had a tendency towards uniform). In the fourth sample, we observed a statistically significant more uniform distribution than expected by chance. No deficiencies of single infections were observed in any of the samples. As there was no aggregation between glands and that the proportion of worms in single gland infections did not differ from that expected by chance alone, we found no evidence of inbreeding avoidance as might be manifested via a within-host distribution. Overall, *A. renale* displays a random pattern of infection between the glands, but additional samples are warranted to determine the robustness of the possible tendencies to a uniform pattern that we observed.

49. Downstream effects: Impact of antibiotic pollution on an aquatic host-parasite interaction.

Hannah G Melchiorre¹, Stephanie O Gutierrez¹, Dennis J Minchella¹, Jonathan T Vannatta^{1, 2}.

¹Purdue University, West Lafayette, IN, USA. ²University of Minnesota, St. Paul, MN, USA.

The global increase in antibiotic use has led to contamination of freshwater environments occupied by parasites and their hosts. Despite the identified impacts of antibiotics on humans and wildlife, the effect of antibiotics on host-parasite life cycles is relatively unexplored. We utilize the trematode parasite *Schistosoma mansoni*, and its snail intermediate host *Biomphalaria glabrata* to explore the influence of an ecologically relevant antibiotic concentrations on the life history characteristics of both parasite and host. Our results demonstrate that antibiotics not only accelerate parasite development and have a positive effect on parasite reproduction, but also increase the likelihood of host egg laying, and delay parasite-induced host castration. Using a mathematical model, we suggest that life history alterations associated with antibiotics are likely to increase parasite transmission and disease burden.

50. Unidirectional stream drift, dendritic ecological networks and host dispersal: Parasite gene flow in riverine habitats.

Mary J Janecka¹, Jan E Janecka², Charles D Criscione³.

¹University of Pittsburgh, Pittsburgh, PA, USA. ²Duquesne University, Pittsburgh, PA, USA. ³Texas A&M University, College Station, TX, USA.

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 gene flow are largely unknown. We examined the effects unidirectional stream drift, dendritic ecological networks, and host dispersal have 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. There was geographic clustering of populations associated with river branches in the principal coordinate's analysis. The results of the STRUCTURE analysis however yielded no strong evidence of unique genetic clusters, except for the population below the reservoir. Our results demonstrate that host dispersal negates some but not all the generative processes unique to river habitats.

51. Lessons learned from teaching parasitology in the non-traditional classroom.

Jeffrey Bell¹, Nicole Chodkowski², Makedonka Mitreva³, Sarah Orlofske⁴, J Trevor Vannatta⁵.

¹University of North Dakota, Grand Forks, ND, USA. ²Lawrence University, Appleton, WI, USA.

³Washington University in St. Louis, St. Louis, MO, USA. ⁴University of Wisconsin- Stevens Point, Stevens Point, WI, USA. ⁵University of Minnesota, Minneapolis, MN, USA.

The rapid shift to online instruction due to the COVID-19 pandemic required instructors to develop strategies to deliver course material in an online environment. The flexibility in course instruction required during the pandemic, although difficult has provided a unique opportunity to develop new methods of teaching effectively across delivery modes. It is important to build on the lessons learned during this shift to continue to improve instruction in parasitology and related courses. An increasing number of students are looking for flexibility in course offerings and course delivery methods, thus continuous adaptations to meet these needs are required. One goal of the ASP Education Committee is to consider the strategies developed during the pandemic so that instructors can provide quality learning experiences for students in various scenarios and promote diverse educational resources for parasitology and other courses. To aid in this goal, faculty that have developed innovative techniques for teaching aspects of parasitology in traditional, hybrid, and remote learning modalities will present a series of mini-talks with scheduled time for discussion. In addition, tools and techniques that could be used in non-traditional classroom settings will be highlighted and emphasis will be given to various ways

existing teaching resources can be adapted to various delivery methods. The aim of this presentation by the ASP Education Committee is to provide information that will facilitate filling gaps in teaching resources, sharing teaching strategies, and building a sustainable community of educators within the ASP.

52. A parasitological life in the shadow of H. B. Ward and Harold W. Manter.

John Janovy Jr.

University of Nebraska-Lincoln, Lincoln, Nebraska, USA.

My wife Karen's job as secretary to J. Teague Self at the University of Oklahoma forced me to become a parasitologist because we were in constant social and intellectual contact with Dr. Self, his parasitological challenges, and his students, who always seemed to have the most interesting projects. So when it came time to do doctoral work, I asked if I could be his student, and he agreed. He regularly told me that my own students would be my greatest reward in an academic career, and he was certainly correct, although G. Robert Coatney's advice, to get out of their way and let them work, played a major role. Those students demonstrated clearly that a university's most valuable resources walk in the front door every year by the thousands, and not only that, they'll help you recruit others from afar. The most important events in my career were the opening of the Cedar Point Biological Station and the publication of my first book, *Keith County Journal*. Both events provided more opportunities for research, innovative teaching, creative writing, and interactions with the broader community that I could ever have envisioned. How has my outlook on parasitology changed over time? I've become more and more convinced that parasitology is the most rewarding, challenging, and just downright fascinating area of biology, and indeed of science. The opportunities for participation in this discipline are far broader, far more accessible, and far more diverse than in most if not all other areas of science, allowing for a wide range of people and personalities to become engaged regardless of their age, background, and long-term goals. The most important parasitological event of the foreseeable future? That holy grail of an effective, cheap, and easily distributed vaccine against *Plasmodium falciparum* seems tantalizingly within reach, although a vaccine against infective bad ideas would probably do just as much to free humanity from its most destructive inclinations.

53. Looking back and looking ahead.

Timothy G Geary^{1,2}.

¹McGill University, Ste-Anne-de-Bellevue, QC, Canada. ²Queen's University-Belfast, Belfast, NI, UK.

I have been involved in research on parasites for over 40 years, focused primarily on how to treat or prevent infections by protozoan and helminth pathogens. This path has included forays into basic research on parasite biology and the host-parasite interface to drug discovery and development to drug resistance. It includes almost even amounts of time spent in the pharmaceutical industry and academia. My career was more a case of "Things happened" and much less a case of "Just as I planned". What success I had come from making the most of the opportunities that presented themselves. My career witnessed sometimes breathtaking paces of change; for example, experimental paradigms and science communication have changed dramatically. Demands on the time of both industrial and academic scientists have multiplied, sometimes to a ridiculous extent. Competition for academic funding has rarely been more intense, and extreme consolidation and changing priorities in industry limit to some extent career opportunities in parasitology in that sector. I am thus sometimes glad that I was born

when I was. But there are many other times at which I wish I was just starting out. The ability to do revolutionary research on parasites has never been greater; recent technological developments now permit us to approach fundamental questions in parasitology in experimental frameworks – though additional revolutions in methods and systems remain to be achieved. We are nearing the ability to tackle one great unsolved mystery in parasitology: the basis for host-parasite specificity. Parasites and hosts participate in a molecular dialog that leads to infection or its early resolution. New ‘omics platforms allow us to decipher this language to understand why hosts are non-permissive for almost all parasite species. New techniques may soon allow us to validate our interpretation by manipulating gene expression in parasitic helminths. What remains is the daunting challenge of being able to maintain full parasite life cycles in culture, to me the ‘holy grail’ of parasitology research.

54. Parasitology methods looking forward: Genomics, phylogenomics, Iso-Seq, single-cell RNA-Seq, and spacial transcriptomics.

James P Bernot.

Department of Invertebrate Zoology, Smithsonian NMNH, Washington, DC, USA.

Like many fields of science, parasitology is witnessing the rapid development and implementation of new research methods. Largely driven by decreasing sequencing costs, genomic and phylogenomic methods are becoming increasingly affordable and widespread, and some recent developments and standards in genomics and phylogenomics are reviewed here. Meanwhile, other new methods are being developed and deployed, typically first in biomedical research where funding is less scarce, datasets are larger, and informatics infrastructure more abundant (e.g., reference genomes, functional annotations, tissue-specific datasets). The application of these methods in biomedical science, model organism research, and, to a lesser extent, vertebrate biology, offers parasitologists a glimpse into future research directions. Some recently developed methods including isoform and alternative splicing analysis (AS), single cell RNA-Seq (scRNA), and spacial transcriptomics hold great promise for parasite research, and these are briefly reviewed here. Yet classic parasitology research is no less important. Many new methods require substantial informatics infrastructure not available for most parasites. Now, more than ever, it is necessary for parasitologists to identify and described species, resolve phylogenies, produce robust host association data, generate accurately identified reference sequences, and assembly and annotate reference genomes to leverage these methods.

55. Trajectory of parasitology: Looking to the future using environmental DNA detection methods.

Jasmine N Childress.

University of California Santa Barbara, Santa Barbara, CA, USA.

From trichomonads to tapeworms, eukaryotic parasites span the tree of life, requiring a wide variety of detection methods. These methods can be costly (e.g. host tracking and capture), destructive (e.g. necropsies), and require intensive training (e.g. staining and microscopy for taxonomic identification). A noninvasive, nonlethal approach to surveying parasites involves the detection of environmental DNA (eDNA). All eDNA detection methods take advantage of the genetic fragments that organisms naturally shed into the environment. I will present two case studies to highlight the untapped potential of eDNA detection methods to study host-parasite populations and communities. I will also discuss limitations and room for improvement inherent to eDNA detection methods. As eDNA technology becomes faster, cheaper, and more robust, reliable implementation is promising for science in general. With the

incorporation of eDNA technology, the field of parasitology is poised to further enrich conservation, human health, animal welfare, and ecosystem health.

56. The postdoctoral research fellowships in biology: An overview for conference participants.

John Barthell, Daniel R Marenda.

National Science Foundation, Alexandria, VA, USA.

The Postdoctoral Research Fellowships in Biology Program is operated by the Division of Biological Infrastructure within the Directorate of Biological Sciences. Overall, the program is designed to provide the postdoctoral fellow with opportunities to be trained in new areas of inquiry and in practical ways that relate to new scientific methodologies and methods of communication (mentoring, public outreach, etc.). The Program has three “Areas” (1-3) of emphasis that include (1) Broadening Participation of Groups Underrepresented in Biology, (2) Integrative Research Investigating the Rules of Life Governing Interactions Between Genomes, Environment and Phenotypes, and (3) Plant Genome Postdoctoral Research Fellowships. This presentation will briefly overview these components of the Program relevant to the field of parasitology and provide general advice on writing proposals to the NSF. Opportunity will be given for an extensive question and answer session.

57. An outbreak of canine schistosomiasis in Utah: Acquisition of a new snail host (*Galba humilis*) by *Heterobilharzia americana*, a pathogenic parasite on the move.

Martina R Laidemitt¹, Scott Z Dolginow², Suzanne Pape², Colin D Topper³, Pilar Alda⁴, Jean P Pointier⁵, Erika T Ebbs⁶, Melissa C Sanchez¹, Guilherme G Verocai⁷, Randall J DeJong⁸, Sara V Brant¹, Eric S Loker¹.

¹University of New Mexico, Albuquerque, NM, USA. ²Mill Creek Animal Hospital, Moab, Utah, USA. ³610 Dragonfly Trail, Moab, Utah, USA. ⁴Centro de Recursos Naturales Renovables de la Zona Semiárida (CERZOS—CCT—CONICET Bahía Blanca), Bahía Blanca, Argentina. ⁵Université de Perpignan, Perpignan, France. ⁶Purchase College, State University of New York, Purchase, NY, USA. ⁷College of Veterinary Medicine & Biomedical Sciences, Texas A&M University, College Station, TX, USA. ⁸Calvin University, Grand Rapids, MI, USA.

Parasites with complex life cycles engaging multiple host species living among different environments well-exemplify the value of a cross-cutting One Health approach to understanding fundamental concerns like disease emergence or spread. *Heterobilharzia americana* is an endemic North American schistosome, and we found that this parasite has expanded its range from the mesic/wet environments of the southeastern United States to the arid southwest. This parasite was found infecting 12 dogs in 2018 from residential areas near an artificial pond in Moab, Utah. Raccoon scats subsequently collected near the pond were positive for *H. americana* eggs, and snails living near the pond’s water edge identified as *Galba humilis* shed *H. americana* cercariae. This is the first confirmed evidence of natural infections in this widespread North American snail species. The susceptibility of *G. humilis* to *H. americana* was confirmed experimentally from miracidia from raccoon scats collected near the pond. Our phylogenetic studies support the existence of two variants of *H. americana* and emphasize the need for further investigations of lymnaeids and their compatibility with *H. americana*, to better define the future potential for its spread. Capture of a new species of intermediate host snail, the continued movement of raccoons, and the construction of artificial habitats suitable for this snail have created the potential for a much more widespread animal health problem, especially for dogs and horses. *H.*

americana will prove difficult to control because of the role of raccoons in maintaining transmission and the amphibious habits of the snail hosts of this pathogenic schistosome.

58. Revealing identities of digenean metacercariae in fishes in the upper Midwest: some progress and more questions.

Jakson R Martens, Tyler J Achatz, Vasyl V Tkach.

University of North Dakota, Grand Forks, ND, USA.

Fishes serve as intermediate hosts for a variety of digenean groups. Digenean larval stages may localize in various organs and tissues of fish. In this study, we examined fishes from several areas in the upper Midwest of the United States (mainly Minnesota and North Dakota) for digenean metacercariae. Special attention was given to the metacercariae causing "black spots" on fish skin, which can cause health issues ranging from mobility loss, increased predation, and death. Sequences of mitochondrial *cox1* and nuclear ribosomal 28S DNA were generated to match the larval stages with morphologically identified adult stages as well as for phylogenetic inferences and analysis of interspecific variation. Our study allowed us to identify metacercariae belonging to several genera from the Diplostomoidea as well as from the families Opicthorchiidae and Heterophyidae. Adult parasites used in the study were collected from vertebrate hosts in the region.

59. Filling the flap gap: New "tetraphyllidean" diversity in stingray and guitarfish hosts.

Kara M Heilemann, Janine N Caira.

University of Connecticut, Storrs, CT, USA.

This work focused on expanding our understanding of the cestode taxon provisionally referred to as New genus 9 in earlier molecular work. Examination of material from previous collections of batoids from around the world yielded specimens of this taxon from 14 species of elasmobranchs spanning the batoid families Dasyatidae, Glaucostegidae, Myliobatidae, Pristidae and Rhinidae. Light microscopy and scanning electron microscopy revealed these species to exhibit an unusual suite of key diagnostic features consisting of bothridial pouches with anterior and posterior flap-like structures, bearing an apical sucker and various numbers of marginal loculi, respectively. However, the results of a phylogenetic analysis of sequence data for the D1–D3 region of the 28S rRNA gene, which included 14 undescribed species with this morphology, along with representatives of a variety of other "tetraphyllidean" taxa, led to a surprising result. The undescribed species all grouped robustly with the representative of the genus *Pithophorus* Southwell, 1925 included in the analysis. This suggests that these species would be more appropriately placed in the genus *Pithophorus* than in a new genus. However, the limited work conducted on *Pithophorus* since its erection by Southwell almost a century ago, indicates that the type and only described species, *Pithophorus tetraglobus* (Southwell 1912) Southwell, 1925—reported from hosts identified as *Rhynchobatus djiddensis*—is characterized by its possession of unique pouch-like bothridia that bear dorsal and ventral openings, and are thus hollow. Yet, this is clearly not the case for the 14 undescribed species. Further morphological work yielded specimens of two additional species with hollow bothridia from *Rhynchobatus palpebratus* and *Rhina ancylostoma*. Despite these scolex differences, the proglottid anatomy of species with and without hollow bothridia is remarkably similar. As a consequence, this may be yet another example of a case in which proglottid anatomy is more evolutionarily conserved than scolex morphology.

60. Jumping the continents and major host lineages: A curious case of the Cryptotropidae.

Taylor P Chermak¹, Tran Thi Binh², Vasyl V Tkach¹.

¹University of North Dakota, Grand Forks, North Dakota, USA. ²Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, Hanoi, Vietnam.

Members of several small or monotypical genera of the digenean superfamily Microphalloidea, e.g., *Renschtrema*, *Cryptotropa*, *Pseudocryptotropa*, have an unusual dorsal position of the genital atrium. Phylogenetic relationships among these digeneans (and taxa synonymized with them at different times) have always been unclear and as the result, their systematic position has been highly unstable. They have been placed into a variety of sub-families and families by different authors, which has been invariably argued and changed in subsequent publications. No DNA sequence data are currently available for these genera, which prevented their inclusion into molecular phylogenetic analyses. In the present work, we have studied morphologically and sequenced several species belonging to at least 2 microphallolidean genera with dorsal genital pore, collected from vertebrate hosts in Southeast Asia and South America. We used sequences of the partial nuclear large ribosomal subunit gene to infer a superfamily-level phylogeny and more variable DNA regions (nuclear ITS region and mitochondrial *cox1* gene) for species-level comparisons. Our study revealed a new species of *Renschtrema* (previously known only from bats in Southeast Asia) from a bird on the opposite side of the Pacific, in the Peruvian Amazon. This is not only the first member of the genus in the Western Hemisphere, but also the first species of the genus from avian hosts anywhere. We have also discovered a new species of *Cryptotropa* in a lizard (a highly unusual host) from Southeast Asia. Our molecular phylogenetic analysis, combined with the characteristic morphological features, suggests that the family Cryptotropidae proposed by Khotenovsky (1965) likely needs to be restored.

61. Physiological and behavioral interactions of *Drosophila* and two symbionts: *Spiroplasma* and an ectoparasitic mite.

Collin J Horn, Taekwan Yoon, Monika K Mierzejewski, Lien T Luong.

University of Alberta, Edmonton, Alberta, Canada.

Although many arthropod endosymbionts are vertically transmitted, phylogenetic studies show repeated introductions of hemolymph-dwelling *Spiroplasma* in the genus *Drosophila*. These introductions are often attributed to horizontal transmission via ectoparasitic mite vectors. *Spiroplasma* infection rates can be low; however, if *Spiroplasma* infection impacts fly-mite interactions, mites may play an important role as vectors of the endosymbiont. Here, we investigate if *Spiroplasma* infection 1) affects host preference of mites and 2) impacts the ability of host flies to resist mite infection. In this study we use *Drosophila melanogaster* infected or uninfected with the endosymbiont *Spiroplasma poulsonii* MSRO (henceforth called MSRO), and *Macrocheles subbadius*, a natural ectoparasite of *Drosophila* spp. Experiments were conducted at multiple fly ages (2, 14, and 26 days post-eclosion), as MSRO titres increase over fly lifespan. Experiment 1: We tested if mites prefer *Drosophila melanogaster* harbouring *Spiroplasma poulsonii* over uninfected flies using y-maze preference experiments. We also tested if preferences/aversions are explained by changes in fly physiology, specifically metabolic rate (measured as CO₂ production). We hypothesized elevated metabolism caused by infection would drive mite preference for MSRO+flies. However, mites dispreferred MSRO+ flies, relative to MSRO–flies, at 14 days post-eclosion (31% infection), but preferred MSRO+flies (64% infection) 26 days post-eclosion. Using flow-through respirometry, we found that 14 day-old MSRO+flies had higher CO₂ emissions than MSRO–flies (32% greater), whereas the rate of CO₂ production among MSRO+ was 20% lower than

MSRO–flies at 26 days old. Thus, host preferences varied with MSRO status and fly age, but was not driven by mite preference for higher metabolic rates. Experiment 2: To measure fly resistance separate from mite proclivity to infect, we measured fly endurance in geotaxis assays (a proxy measure of susceptibility). We hypothesized *Spiroplasma* infection would reduce fly endurance (measured by duration of climbing, seconds). Among 14 and 26-day old flies, MSRO+flies had reduced endurance relative to MSRO–flies (45% and 110% difference respectively). These results suggest MSRO+flies are more vulnerable to secondary infection by mites. Altered host resistance and parasitic preference may make horizontal transmission of endosymbionts through mite vectors more likely.

62. Mapping parasitism onto host geographic ranges: Do host populations differ in their levels or types of parasitism between range edges and range centers?

Anaí Novoa, Ryan F Hechinger.

Scripps Institution of Oceanography, UC San Diego, La Jolla, CA, USA.

Although evaluating biogeographical distributions and their determinants is a core objective in ecology and biogeography, many basic patterns concerning parasitism and host biogeography remain poorly understood—or documented in the first place. This knowledge gap is particularly troublesome given the rising numbers of species changing their distributions in response to anthropogenic climate change. 1) Do parasite infracommunities follow predictable patterns along latitudinal gradients? 2) Do host populations have different levels or types of parasites at range edges compared to range centers? 3) Are there differences in parasitism at northern versus southern range boundaries? We seek to address these questions in a hypothesis-driven framework—formulated by drawing on basic principles of biogeography, epidemiology, and ecological parasitology. For data, we quantified parasitism by animal and protozoan parasites of four estuarine fish species throughout their entire geographical ranges along the Pacific coast of North America. In addition to identifying parasites to taxa, we also recognize distinct types of parasitic consumer strategies, which differ in fundamental ecological attributes, including how they impact host fitness. Spatial patterns of parasitism at the infracommunity level—expressed with different currencies and diversity metrics—were then fitted to five competing models representing different geographic range distribution patterns. Our analyses show that, consistent with the hypothesis based on the latitudinal diversity gradient, mean parasite richness per host individual increased at lower latitudes for all fish species. Mean richness of a specific functional group of parasites, trophically transmitted parasites, increased at lower latitudes for three fish species, consistent with the general trend that predation is more intense near southern limits. Parasite biomass load (g parasite/ g host) showed two dominant patterns, being highest at northern or southern edges; however, these patterns were only significant for two fish species, suggesting the factor hypothesized as underlying the strong latitudinal diversity gradient in parasite richness may counter a parallel southern increase in parasite biomass load. We therefore documented novel spatial patterns concerning the functional composition of parasite infracommunities. Understanding how parasitism varies throughout species geographic ranges provides fundamental ecological insight and helps inform predictions concerning impacts of global warming induced range shifts.

63. Parasite transmission in a milkweed patch: How are parasites transmitted in insects specializing on milkweed hosts?

Matthew G Bolek¹, Ryan P Shannon¹, Jillian T Detwiler², David D Berman¹, Kristen A Baum¹.

¹Oklahoma State University, Stillwater, Oklahoma, USA. ²University of Manitoba, Winnipeg, Manitoba, Canada.

Milkweeds in the genus *Asclepius* serve as host plants for a diverse assemblage of insect herbivores that utilize milkweeds as their primary food source. However, because milkweeds are perennials and only a small portion of the plant is ever consumed by its insect herbivore, parasites of these insects face spatial constraints in their transmission from host to host. In this study we examined eleven species of insect specialists on milkweeds from three insect orders (Hemiptera, Coleoptera and Lepidoptera) for their parasites and evaluated the transmission strategies of those parasites. The insects included oleander aphids, *Aphis nerii*, large milkweed bugs, *Oncopeltus fasciatus*, small milkweed bugs, *Lygaeus kalmia*, swamp milkweed beetles, *Labidomera clivicollis*, milkweed longhorn beetles, *Tetraopes mandibularis* and *T. texana*, milkweed stem weevils, *Rhysomatus lineaticollis*, unexpected cynthia moths, *Cynthia inopinatus*, milkweed tussock moths, *Euchaetes egle*, queen butterflies, *Danaus gilippus*, and monarch butterflies, *D. plexippus*. All parasites were identified based on morphology and/or sequence data. Of the 11 species of insects sampled, we found that small and large milkweed bugs shared a generalist kinetoplastid (*Leptomonas wallacei*). In contrast, swamp milkweed beetles, and monarchs and queen butterflies were infected with specialist parasites including a podapolipid mite (*Chrysomelobia labidomerae*), and two species of neogregarines (*Ophryocystis elektroscirrha* and *Ophryocystis* sp. n.), respectively. However, the transmission strategies of the four species of parasites found during this study all shared either maternal transmission, where parasite cyst stages are acquired by newly hatched insects when they ingest eggshell remains after hatching (kinetoplastid and neogregarines) and/or sexual transmission, where infective stages of parasites are transmitted between the opposite sexes during copulation (mite and neogregarines). Our study suggests that the spatial constraints of living on milkweed plants have selected for similar transmission strategies in unrelated species of parasites infecting unrelated species of insect hosts. More broadly our work indicates that parasite transmission strategies can be predicted based on understanding the ecological avenues and constraints parasites life cycles and their hosts operate under.

64. The role of gut microbial diversity in *Heligmosomoides bakeri* infections in mice.

Margaret L Doolin¹, Sara B Weinstein², LeAnn Lindsey¹, W Zac Stephens¹, June L Round¹, M Denise Dearing¹.

¹University of Utah, Salt Lake City, UT, USA. ²University of Utah, Salt Lake City, UT, USA.

The gut microbiome plays an important role in the interaction between the host immune system and parasitic infection. More diverse microbiomes are thought to prime the immune system to respond to infections and be more resistant and resilient to perturbations. However, how microbial diversity impacts gut parasite infection is not well understood. To address this question, we compared parasite establishment and host immune responses in mice with typical and low-diversity microbiomes. To create a reduced gut microbial community for this experiment, we established a lineage of gnotobiotic mice with a phylogenetically diverse but species-poor gut microbial community of 14 mouse-isolated bacterial strains. We then infected these mice, and mice with typical gut microbiota with 200 *Heligmosomoides bakeri* larvae to compare host immune response, total worm burden, and fecal egg output. We hypothesized that mice with depauperate gut microbiomes would host heavier worm

burdens due to a suppressed host inflammatory response from atypical immune development. Patent *H. bakeri* infections established in all treated mice, and quantification (currently underway) of infection intensities, total worm biomass, and fecal egg counts will help assess how microbiome diversity influences parasite fitness. We will also profile host inflammatory state throughout infection by measuring levels of several circulating cytokines. This project advances our knowledge of host-microbiome-parasite interactions by experimentally testing common assumptions about the role of intestinal microbiome diversity with respect to resilience to parasite infection.

65. Phylogenetic patterns of *Posthodiplostomum metacercariae* in Texas.

Josue H Zuniga¹, Isabel Blasco-Costa², Kristin K Herrmann¹.

¹Tarleton State University, Stephenville, Texas, USA. ²Natural History Museum of Geneva, Geneva, Switzerland.

Species of the genus *Posthodiplostomum* are trematodes that possess a 3-host life cycle and are most frequently encountered in second intermediate hosts—primarily freshwater fish, where they exist as metacercariae. This developmental stage can be detrimental to the health of its second intermediate host, due in part to their forceful entry and migration through the tissues of these fish, often leading to hemorrhaging and bacterial infections, and secondly due to the ability of these metacercariae to form multiple cysts in tissues of vital organs. Given how widespread and common *Posthodiplostomum* infections are in freshwater fishes, it is important to understand the infection dynamics of this genus. However, trematode metacercariae are difficult to identify at the species level, due to the limited number of morphological characteristics distinguishable at this developmental stage. This includes a lack of sexual organs, which are often used to differentiate between adult species. The objective of this study was to determine the phylogenetic diversity of *Posthodiplostomum* metacercariae from various fish host species in Texas. We obtained specimens from the tissues of four fish species collected in other studies which included *Gambusia affinis*, *Cyprinella venusta*, *Lepomis macrochirus*, and *Micropterus salmoides*. We sequenced two molecular markers, internal transcribed spacer (ITS) regions of rDNA and the mitochondrial cytochrome c oxidase 1 gene (COI). Both Maximum Likelihood and Bayesian analyses were conducted, using RAxML and MrBayes, respectively. Preliminary phylogenetic analyses demonstrate a host specific pattern of association, corroborating the high degree of host-specificity reported by studies in northern North America. Further, metacercariae collected from *G. affinis* fall within a single lineage, distinct from other species/lineages in the *Posthodiplostomum*-*Ornithodiplostomum* clade. Additionally, maximum likelihood analyses show several specimens found in *C. venusta* forming a distinct lineage of *Posthodiplostomum*, to be verified through additional phylogenetic analysis of the nuclear 28S gene.

66. The increasing prevalence and intensity of the invasive copepod, *Salmincola californiensis* in salmonids in Lake Ontario.

Brian R Mullin^{1,2}, Florian B Reyda¹.

¹SUNY Oneonta, Oneonta, NY, USA. ²Regeneron Biotechnology Company, Troy, NY, USA.

Salmincola californiensis (Subclass Copepoda) parasitizes the gills of salmonids of the genus *Oncorhynchus*. Three species of *Oncorhynchus* salmon native to the Pacific Northwest, *Oncorhynchus mykiss* (rainbow trout), *Oncorhynchus tshawytscha* (chinook salmon), and *Oncorhynchus kisutch* (coho salmon) have been reported as hosts for *S. californiensis* since 1852. These three salmonids have been

introduced to the Great Lakes intermittently since the mid 1800's. The introduction of these salmonids to the Great Lakes was followed by the introduction of their parasitic gill copepod, *S. californiensis*. Evidence of this invasion dates back to 2014, with anecdotal observations of *S. californiensis* on salmonids. To formally document this problem, we chose to conduct a survey to quantify the occurrence of this invasive species. Our survey took place in 2018, 2019, and 2021 at the south-eastern side of Lake Ontario. Most fish were examined in conjunction with fish hatchery activities at the Salmon River Fish Hatchery, Altmar, New York, but some were obtained via angling, seining, or backpack electrofishing. In most cases, fish gills were examined by eye in order to detect the presence of the rather large-bodied females of *S. californiensis*. Our survey results from 2018 and 2019 indicated the prevalence of *S. californiensis* to be ~70%, with a mean intensity of 2.71 in the 120 rainbow trout examined and a prevalence of 39% with an intensity of 1.56 in the 223 chinook salmon examined. *Salmincola californiensis* was found on only 1 of the 200 coho salmon examined during those 2 yr. We did not sample salmonids in 2020, but in 2021 we examined 60 rainbow trout, 51 of which were infected, for a prevalence of 85% and a mean intensity of 5.14. The increased prevalence and mean intensity of *S. californiensis* in rainbow trout in 2021 is a concern, given that the infection levels encountered in 2018 and 2019 were already nearly double that of its native range (35%).

67. Drought and infection complexity: Insights from over twenty-years of research on a sand fly-transmitted malaria parasite.

Allison T Neal¹, Joshua Sassi¹, Joseph J Schall², Anne M Vardo-Zalik³.

¹Norwich University, Norwich, VT, USA. ²The University Of Vermont, Burlington, VT, USA. ³The Pennsylvania State University, York Campus, York, PA, USA.

Microparasites often exist as a collection of genetic 'clones' within a single host (termed multi-clonal, or complex, infections). Malaria parasites are no exception, with complex infections playing key roles in parasite ecology. Even so, we know little about what factors, whether internal or external to the host, govern the distribution and abundance of complex infections in natural settings. Utilizing a natural dataset that spans more than 20-years, we examined the effects of drought conditions on infection complexity and prevalence in the lizard malaria parasite, *Plasmodium mexicanum*, and its vertebrate host, the western fence lizard, *Sceloporus occidentalis*. A zero-truncated Poisson model (ZTP) standardized for lizard size, site of capture, and sex was used for analysis of infection complexity data. Drought conditions were measured on three timescales: short-term (2010-2012 vs. 2014-2016; categorical: before and after the most recent drought); intermediate (2001-2016; USDM drought index used as drought measure); long-term (1978-2016; rainfall data used as drought measure). Our data for the intermediate and long-term data sets illustrate significant, negative effects of drought-like conditions for infection complexity ($p < 0.0001$). The effect of drought on infection prevalence remains unclear: both the short- and long-term data sets show significant correlations ($p < 0.05$), but they do so in opposing directions. To our knowledge, this is the first reported evidence for environmental factors, such as drought, affecting the abundance and distribution of multi-clonal infections in natural malaria parasites. While the overall effect of reduced rainfall on malaria prevalence remains unclear, identifying changes of parasite diversity at the host scale has implications for infection and transmission dynamics of the parasite.

68. Alpha and beta diversity trends of parasite communities in English Sole (*Parophrys vetulus*) in Salish Sea, Washington, USA over the past nine decades.

Whitney C Preisser¹, Rachel L Welicky¹, Katie L Leslie¹, Natalie Mastick¹, Evan Fiorenza², Katherine Maslenikov¹, Luke Tornabene¹, John M Kinsella³, Chelsea Wood¹.

¹University of Washington, Seattle, Washington, USA. ²University of California, Irvine, California, USA. ³HelmWest Laboratory, Missoula, Montana, USA.

Even though up to 40% of species are parasitic, we know much less about the diversity of parasites than we do about their free-living counterparts. Most studies describe and monitor parasite diversity through surveys: hosts are collected and sampled for their parasites. However, surveys represent snapshots in time and cannot provide information on past communities. To gain insight on long-term diversity patterns, we can turn to fluid-preserved host specimens, which preserve parasite tissues alongside host tissues. We described temporal patterns of alpha and beta diversity of the parasite communities from fluid-preserved English sole (*Parophrys vetulus*) from Salish Sea (Washington, USA). As this area has experienced several anthropogenic pressures (e.g., pollution and fishing) over the past century, these temporal trends can reveal much about community level responses to stressors. We were thus able to answer three key questions: 1) What parasite species are present in English sole in this ecosystem? 2) Has parasite diversity in this host changed over the past nine decades? 3) How have community composition and community heterogeneity varied over time? We found that while parasite species richness remained consistent over time, community composition did not. Species composition varied across time, with both balanced variation (the substitution of individuals of one species with individuals of another species between sites) and unidirectional gradients (when individuals are lost between sites without replacement) contributing to the observed change. This knowledge can serve as a baseline for future comparisons as environmental change continues. Our research highlights the importance of using multiple measures of diversity to monitor and describe changes in communities over time, as species richness alone did not capture the community changes. To better understand the mechanisms that are driving changes in species richness and composition, our next line of inquiry will examine how diversity changed with host fish abundance and in response to environmental factors.

69. Parasites of the Gulf wedge clam, *Rangia cuneata*, from the tidal reaches of the Pascagoula River, Mississippi.

Stephen S Curran, Micah B Warren, Stephen A Bullard.

Aquatic Parasitology Laboratory and Southeastern Cooperative Fish Parasite and Disease Project, School of Fisheries, Aquaculture, and Aquatic Sciences, Auburn, Alabama, USA.

The Gulf wedge clam or Atlantic rangia (*Rangia cuneata*) is a common clam in the coastal and intertidal rivers of the northern Gulf of Mexico. The species has colonized the east coast of the United States during the last 70 years and is now found as far north as New York. We collected *R. cuneata* from Moon Lake, an oxbow of the Pascagoula River in Jackson County, Mississippi on several occasions and examined clams for internal parasites. Larval stages of 2 species of digeneans represented by sporocysts containing cercariae infected the digestive gland and gonad of clams. The more common form had an ox-head shaped cercariae and represented a species in the Bucephalidae, and the other was a species with a non-oculate trichocercous cercaria belonging in the Fellodistomidae and representing *Cercaria rangiae* Wardle, 1983. We attempted to elucidate the life cycles for both species by comparing ribosomal RNA sequences from the sporocysts and various metacercariae and adult digeneans we collected from the same area of the river. Those results will be presented in the oral presentation.

70. Freeze tolerance of the dinoflagellate *Amyloodinium ocellatum*.

Robert D Gonzales¹, Haley Dutton², Reginald B Blaylock¹, Stephen A Bullard².

¹The University of Southern Mississippi, School of Ocean Science and Engineering, Thad Cochran Marine Aquaculture Center, Ocean Springs, MS, USA. ²Auburn University, School of Fisheries, Aquaculture, and Aquatic Sciences, Auburn, AL, USA.

The obligate parasitic dinoflagellate *Amyloodinium ocellatum* causes amyloodiniosis, a virulent and deadly disease of warm water marine fishes, particularly in aquaculture systems. The life cycle comprises three stages – a parasitic stage (trophont) on the gills and skin, a reproductive stage (tomont) that encapsulates after detachment from the host, and a dispersal stage (dinospore) that hatches from tomonts following asexual division. Because each tomont can produce up to 256 infectious dinospores, the disease can spread quickly and cause losses in cultured fish stocks. Infections often remain undiagnosed until mortalities occur, therefore, prevention and biosecurity is the key to control. Frozen, wild fishes are often used as food in aquaculture yet can act as a potential vector for the disease. We investigated the ability of the tomonts to survive freezing, reproduce, and cause infections. Infected gills were frozen for either 0 hr, 24 hr, 36 hr, 48 hr, or 72 hr and assessed for viability both *in vitro* and *in vivo*. For *in vivo*, gills were thawed and placed into tanks with naïve fish. Gills of naïve fish were examined on day 0 to ensure no prior infection and on days 4 and 7 post-exposure to determine the presence of an infection. For *in vitro*, eight tomonts from each freeze duration were placed in 5 ml of artificial seawater at room temperature in eight separate wells of a 12-well plate. Tomonts were observed for several days, and sporulation rates and the number of dinospores produced were assessed. In the *in vitro* experiment, 100% of the tomonts across all freeze durations sporulated; however, there was a decrease in the number of viable dinospores produced as freeze duration increased. In the *in vivo* experiment, heavy infections were produced from tomonts in all freeze durations. Tomonts from the 72 hr freeze duration took longer to establish a heavy infection than those from the other freeze durations. Although tomonts survived, successfully reproduced, and infected fish from all freeze durations, viability decreased as freeze duration increased suggesting that longer-term freezing could prove to prevent infections.

71. Unraveling the role of ostracod and snail hosts in turtle acanthocephalan life cycles.

Ryan W Koch, Matthew G Bolek.

Oklahoma State University, Stillwater, OK, USA.

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. In addition, *Neoechinorhynchus emydis* has been reported from ostracod, turtle, and snail hosts. However, it is currently unclear what species of ostracods serve as intermediate hosts for most species of turtle acanthocephalans and how snail hosts become infected with *N. emydis*. To better understand these life cycles, we first surveyed red-eared slider turtles, as well as four species of ostracods and two species of freshwater snails for acanthocephalans and used molecular barcoding to identify juvenile acanthocephalans from ostracod and snail hosts to the species level. Second, we 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 acanthella and/or the cystacanth (infective stage) only occurred in *Physocypria* sp. In contrast, eggs of the four species of acanthocephalans never developed in

laboratory exposed snails, strongly suggesting that snails become infected with *N. emydis* by ingesting infected ostracods. These laboratory observations support our field surveys in that only a single species of ostracod (*Physocypria* sp.) was infected with multiple species of juvenile turtle acanthocephalans; whereas both species of freshwater snails were infected with juvenile *N. emydis*.

72. The occurrence of mesomycetozoon (Dermocystida) infecting American toads (*Anaxyrus americanus*) from central Illinois.

Elliott A Zieman¹, Mathew G Bolek².

¹Eastern Illinois University, Charleston, IL, USA. ²Oklahoma State University, Stillwater, Oklahoma, USA.

The mesomycetozoans are fungal-like unicellular eukaryote parasites, in the order Dermocystida (Ichthyosporea) and the sister clade to the lineage that includes all metazoans. The mesomycetozoans infect a variety of aquatic or semi-aquatic invertebrate and vertebrate hosts, but they have also been reported to infect humans. In amphibians, they cause a granulomatous condition primarily targeting the skin and mucous membranes and occasionally have been reported to be lethal to their amphibian hosts. However, compared to other amphibian fungal pathogens, such as the chytrid fungus (*Batrachochytrium dendrobatidis* and *B. salamandrivorans*), reports of mesomycetozoans in North American anurans are scarce with only five records in the literature. These include three species of toads (*Anaxyrus americanus*, *Anaxyrus canorus*, and *Anaxyrus fowleri*) infected with *Amphibiothecum penneri* and one species of true frogs (*Rana catesbeiana*) infected with *Histocystidium ranae*. All previous infections of North American anuran mesomycetozoans have been documented from Atlantic coastal states with one report from California, United States. Here we report the first case of mesomycetozoans in the American toad from the Midwest region of the United States. A single American toad was found infected with numerous subcutaneous skin nodules (sporangia) located predominantly on the ventral side of the animal. Shortly after capture (>1 hour) the toad perished. An additional 37 breeding American toads were examined over a 4-week period from the same general location and were free of gross lesions. The sporangia were clumped in groups on the abdomen and embedded within the dermis of the infected toad. Sporangia contained hundreds of spores varying in maturity. Spores were located within distinct chambers and each spore contained distinct granules. Granules were more numerous in the largest spores assumed to be fully mature. We will present our *microscopy*, histological and molecular findings of these infections and attempt to place these organisms in the most recent phylogenetic hypothesis of the Dermocystida.

73. Mediterranean and African parasites in North America: Coccidia from introduced populations of the Mediterranean house gecko, *Hemidactylus turcicus* and the tropical house gecko, *H. mabouia*.

Allison Bryant¹, Matthew Bolek¹, Gabriel Langford².

¹Oklahoma State University, Stillwater, Oklahoma, USA. ²Florida Southern College, Lakeland, Florida, USA.

The Mediterranean house gecko, *Hemidactylus turcicus*, is native to the Mediterranean region of Africa, Asia, and Europe. However, it has been widely introduced across the world including the United States, and in Oklahoma. Although a number of studies have documented parasites of *H. turcicus* throughout its introduced range, little information exists on the coccidian parasites of this gecko. We sampled geckos from Oklahoma and examined their fecal samples for coccidian oocysts. Twenty percent of

geckos shed ellipsoid polysporocystid oocysts with a smooth bi-layered wall. Numerous granules were present within oocysts, but a micropyle was absent. The number of sporocysts per oocyst ranged from 8 to 12. Sporocysts were subspherical and contained a residuum composed of scattered granules. These oocysts were most similar to species of *Adelina* which infect invertebrate hosts and should be considered pseudoparasites of geckos. In addition, 31% of geckos shed ellipsoid tetrasporocystid oocysts with a smooth bi-layered wall. Oocysts, contained a polar granule, but a micropyle and residuum were absent. Sporocysts were ellipsoid and without stiedal or substiedal bodies. Sporocysts contained a residuum composed of numerous granules in a spherical mass and 2 sporozoites. These oocysts were most similar to the description of *Acroeimeria lineri* previously reported from *H. turcicus* in the United States, Egypt, Israel and Turkey and from *H. mabouia*, from South Africa. However, a recent study on coccidia of *H. turcicus* from Egypt suggested that *A. lineri* may represent a complex of cryptic species. As a result, we are expanding our coccidian survey and examining Mediterranean house geckos at other locations across the United States and the introduced tropical house gecko, *H. mabouia*, from Florida. This is the first report of *Acroeimeria lineri* from Oklahoma. In addition, we document the first reports of *Acroeimeria lineri*, *Eimeria dixoni*, and *Isospora hamidactyli* from an introduced population of *H. mabouia* from the United States. In the future, and to get a better understanding of potential cryptic species of coccidian parasites in species of *Hemidactylus*, we will utilize DIC microscopy techniques for oocyst morphology, histological techniques for coccidian development in geckos, and molecular techniques for barcoding coccidians.

74. Immune-related thioester-containing proteins (TEPs) in the *Biomphalaria glabrata* embryonic (Bge) cell line.

Deblina Misra, Maria G Castillo.

New Mexico State University, Las Cruces, New Mexico, USA.

Schistosomiasis is a neglected tropical disease caused by trematode parasites including *Schistosoma mansoni*. *Biomphalaria glabrata* is a freshwater snail that serves as an intermediate host for this parasite. Presently, the *B. glabrata* embryonic (Bge) cell line is the only molluscan cell line available, established over 40 years ago from embryos of a susceptible snail strain. Since then, Bge cells have been used in numerous studies aiming at a better understanding of snail host-schistosome parasite interactions and as an *in vitro* model for snail immunity. In addition to hemocytes, several humoral immune components are known to have an important role in the snail host's response to schistosome invasion, including thioester-containing proteins (TEPs). TEPs are a diverse family of proteins most of them characterized by the presence of an active thioester domain that is used to bind and target foreign molecules. To define the role of TEPs in snail defense we tested the expression of these genes in Bge cells and their modulation in response to microbial products using real-time quantitative PCR. Furthermore, utilizing the Bge cells we are studying transcription factors that could potentially be associated with these TEP responses including Rel/DIF (dorsal-related immunity factor), Relish, STAT (signal transducer and activator of transcription (STAT)), and CREB (cAMP response element-binding protein). In preliminary results we confirmed the presence of all *B. glabrata* TEPs in Bge cells, as well as upregulation in transcript expression for some of the molecules like CD109, TEP-1, and CPAMD-8; whereas A2M-1, C3-1, C3-2 appeared downregulated in Bge cells upon microbial exposure. Also, the transcription factors NF-kappa B, CREB, STAT showed to be modulated upon immune stress. These studies aim to better characterize the role of TEPs in *B. glabrata* immune sensing and the associated signaling pathways playing a role in snail-pathogen interactions.

75. The heart-associated immune response is conserved across insect evolution.

Yan Yan, Julián F Hillyer.

Vanderbilt University, Nashville, TN, USA.

The immune and circulatory systems are functionally integrated in the African malaria mosquito, *Anopheles gambiae*. Some of their immune cells – called hemocytes – reside around the valves of the heart and actively phagocytose pathogens. Infection further increases the aggregation of hemocytes on the heart, enhancing heart-associated immunity. It was unclear whether this heart-associated immune response was specific to *A. gambiae*, so we asked whether this is a general characteristic of insects. To answer this question, we tested whether this response was present in two ectoparasites, the Asian tiger mosquito *Aedes aegypti* and the bed bug *Cimex lectularius*. The heart-associated hemocytes are immunologically activated by infection in both insects, and infection further increases the aggregation of hemocytes on their hearts. Following this, we surveyed 68 species of insects from 51 families in 16 orders and discovered that hemocytes and pathogens aggregate on the heart of insects from all major lineages. Therefore, the integration between the immune and circulatory systems is conserved throughout insect evolution.

76. Conserved immune signaling pathways drive heart-associated immune responses in mosquitoes

Julian F Hillyer¹, Yan Yan¹, Tania Y Estévez-Lao¹, David C Rinker¹, John A Capra².

¹Vanderbilt University, Nashville, TN, USA. ²University of California San Francisco, San Francisco, CA, USA

When a mosquito becomes infected, a series of immune responses are deployed. One of these responses is the aggregation of hemocytes around the valves of the heart, where they phagocytose and kill pathogens. This aggregation of specialized hemocytes, called periostial hemocytes, is beneficial to the insect because it places immune cells in areas of high circulatory flow, increasing the probability that they will encounter circulating microbes. The present study aimed to identify molecular drivers of hemocyte aggregation on the heart of the malaria mosquito, *Anopheles gambiae*. Initial experiments utilized RNAseq to identify genes whose transcription is preferentially upregulated in the periostial hemocytes relative to the circulating hemocytes and the rest of the body. Then, we utilized RNAi and organismal manipulations to test candidate genes identified in the RNAseq dataset, and uncovered that the IMD and JNK signaling pathways drive periostial hemocyte aggregation. In summary, this research uncovered that conserved immune signaling pathways drive heart-associated immune responses in a societally important mosquito.

77. The hirudin superfamily

Christian H Mueller¹, Phil Lukas^{1,2}, Jan-Peter Hildebrandt¹.

¹University of Greifswald, Greifswald, Germany. ²Cheplapharm Arzneimittel GmbH, Greifswald, Germany.

Of all bioactive factors that are secreted by (medicinal) leeches during feeding on their vertebrate hosts, hirudin is the best studied. Originally it was purified from and described in members of the genus *Hirudo*, but since then it has been identified in a range of hematophagous leeches from several taxonomic groups. Hirudin is the one and only leech-derived factor that has found its way from bench to bedside. In *Hirudo medicinalis* three variants of hirudin (HV1:VV; HV2: IT and HV3:PA) have been

described. They are encoded by different genes and can be expressed in parallel within one individual leech. The term hirudin, however, rather describes a concept than a unique entity. In this sense, hirudin is defined by both its activity (the inhibition of thrombin) and a combination of structural (e.g. presence of six cysteine residues) and physico-chemical (e.g. pI value of about 4.1) properties. The essential structural features of hirudin do not belong to this particular protein exclusively, but can be found in other leech-derived factors as well: haemadin (a thrombin-inhibitor of the land-living leech genus *Haemadipsa*), decorsin and ornatin (inhibitors of platelet aggregation found in the North American leeches *Macrobdella decora* and *Placobdella ornata*) and the hirudin-like factors (factors of yet unknown function derived from members of the genera *Hirudo* and *Hirudinaria*). All these factors considerably differ in length (39 - 66 amino acids) and their respective pI value (3.1 - 9.2). Nevertheless, growing evidence clearly indicates that they share a common ancestor and hence form the hirudin superfamily.

78. DNA metabarcoding methods for parasite surveillance and diet analyses of San Miguel Island foxes.

Ana E Garcia Vedrenne¹, Jasmine N Childress², Kevin D Lafferty².

¹UC Los Angeles, Los Angeles, CA, USA. ²UC Santa Barbara, Santa Barbara, CA, USA.

The island fox (*Urocyon littoralis*) is an iconic species endemic to 6 of the 8 Channel Islands off the coast of Southern California. The island fox was removed from the endangered list in 2015, but it was a success story told too soon for San Miguel Island. Since then, the San Miguel fox population has been in decline, and necropsies reveal substantial parasitism by an unidentified acanthocephalan. High acanthocephalan burdens are associated with colitis, enteritis and emaciation- likely contributing to increased fox mortality. Management of these parasites is necessary to prevent further population declines and possible extirpation of the San Miguel Island fox, but little is known about the acanthocephalan's life cycle. Here we develop and apply DNA metabarcoding methods to i) detect infection by the acanthocephalan parasite, ii) characterize the fox diet and identify possible intermediate hosts, and iii) surveil fox feces for other parasites of interest. Fox fecal samples were collected during the Channel Islands National Park's monitoring activities. Libraries were prepared from fecal DNA extracts using CO1 and 18S markers to evaluate fox diet and infection status. Each fecal sample was analyzed simultaneously using DNA metabarcoding methods and fecal egg counts to evaluate infection with the following parasites: the acanthocephalan *Prosthenorchis* sp., hookworm *Uncinaria stenocephala*, lungworm *Angiocaulus gubernaculatus*, nematode *Spirocerca* sp., and tapeworm *Mesocestoides* sp. Together, these methods produce data that can inform the park about the scale of the problem and guide potential management interventions.

AMERICAN SOCIETY OF PARASITOLOGISTS 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 include 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 [whose name will be posted in meeting programs, and the society website with names and emails included]. 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 the society 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.

Netiquette

Netiquette are common courtesies and informal rules that participants follow when communicating in an online setting.

Netiquette expectations for this meeting include:

1. Avoid inflammatory or offensive comments (a.k.a. flaming). It is possible to disagree with an idea without flaming the person espousing the idea.
2. Use emoticons and acronyms to avoid misunderstandings.
3. Remember to be polite and aware of personal and cultural diversity.
4. Listen actively and avoid multitasking.
5. Think critically, seek clarity of meaning and understanding.
6. Question ideas, not people.
7. Mute your microphone by default.
8. Be aware of your surroundings when camera is on.
9. Offensive language is prohibited.
10. Avoid using all caps in comments. (All caps is considered to be shouting).