

PROGRAM & ABSTRACTS
for the 2025 meeting of

THE SOUTHEASTERN SOCIETY OF PARASITOLOGISTS

10–12 April 2025

Hosted by...

**The Southeastern Cooperative Fish Parasite and Disease
Laboratory
&
Auburn University**

Auburn, Alabama

We all thank...

THE 2025 LOCAL ORGANIZING COMMITTEE

Brett Warren	SCFPDL, Auburn Univ.	CHAIR
Kamila Cajiao-Mora	SCFPDL, Auburn Univ.	GRAPHICS, LOGISTICS
John Brule	SCFPDL, Auburn Univ.	IT, LOGISTICS
Chrissy Smith	SCFPDL, Auburn Univ.	SPECIAL DIET REQUESTS

and...

THE 2024-25 SSP OFFICERS

Elizabeth Gleim	Hollins Univ.	PRESIDENT
Stephen A. (Ash) Bullard	SCFPDL, Auburn Univ.	PRES-ELECT, PROGRAM CHAIR
Kaitlin Gallagher	Florida Southern College	VICE PRESIDENT
Charles Faulkner	Lincoln Memorial Univ.	SECRETARY TREASURER
Kamila Cajiao-Mora	SCFPDL, Auburn Univ.	STUDENT REPRESENTATIVE

DAY-BY-DAY AGENDA

DAY 1: Thursday 10 April 2025

Arrive in Auburn: Check-in @ TownePlace Suites – 1117 South College St, Auburn, AL, 36832



Drive to ROOFTOP WELCOME RECEPTION held at the Collegiate Hotel (5:00 PM):

Collegiate Hotel; 205 S Gay St., Auburn, AL 36830 (about a 10-minute drive from TownePlace)



Eat, drink, socialize (5:00 PM – 9:00 PM): *We offer baked pimento cheese dip, bruschetta cheese ball, baked phyllo vegetable tarts, assorted fruit, sticky garlic chicken skewers, brisket sliders provided by Wilton's Catering (drink tickets available).*

DAY 2: Friday 11 April 2025

Arrive at meeting site for breakfast (8:00 AM): CASIC Building, 559 Devall Dr, Auburn, AL 36849
(The meeting site [CASIC Building] is across the street from the conference hotel. Breakfast will be served at the CASIC Building, where all talks and posters will be. No session is concurrent. The BBQ catered lunch will also be served at CASIC. Dinner for this night is on your own.)



BREAKFAST 8:00 AM – 8:50 AM

We offer a breakfast burrito bar with flour tortillas, butter scrambled eggs, bacon crumbles, tomato salsa, cheddar cheese, green onions, jalapenos, and diced tomatoes plus gourmet coffee from Wilton's Catering & Well Red AU Coffee Co.

PAPER SESSION #1 9:00 AM – 12:00 PM

LUNCH & POSTERS 12:00 PM – 2:00 PM

We offer a catered BBQ lunch (2 meat plate; chicken on the bone, pulled pork, mac & cheese, seasonal fruit, cheese biscuits) from Jim N' Nick's BBQ.

PAPER SESSION #2 2:00 PM – 4:00 PM

DINNER ON YOUR OWN

DAY 3: Saturday 12 April 2025

Arrive at meeting site for breakfast (8:00 AM): CASIC Building, 559 Devall Dr, Auburn, AL 36849

BREAKFAST 8:00 AM – 8:50 AM

We offer Mini cinnamon rolls, pesto parmesan quiche, breakfast cookies, bacon cheddar biscuits from Well Red AU Coffee Co.

PAPER SESSION #3 9:00 AM – 10:45 AM

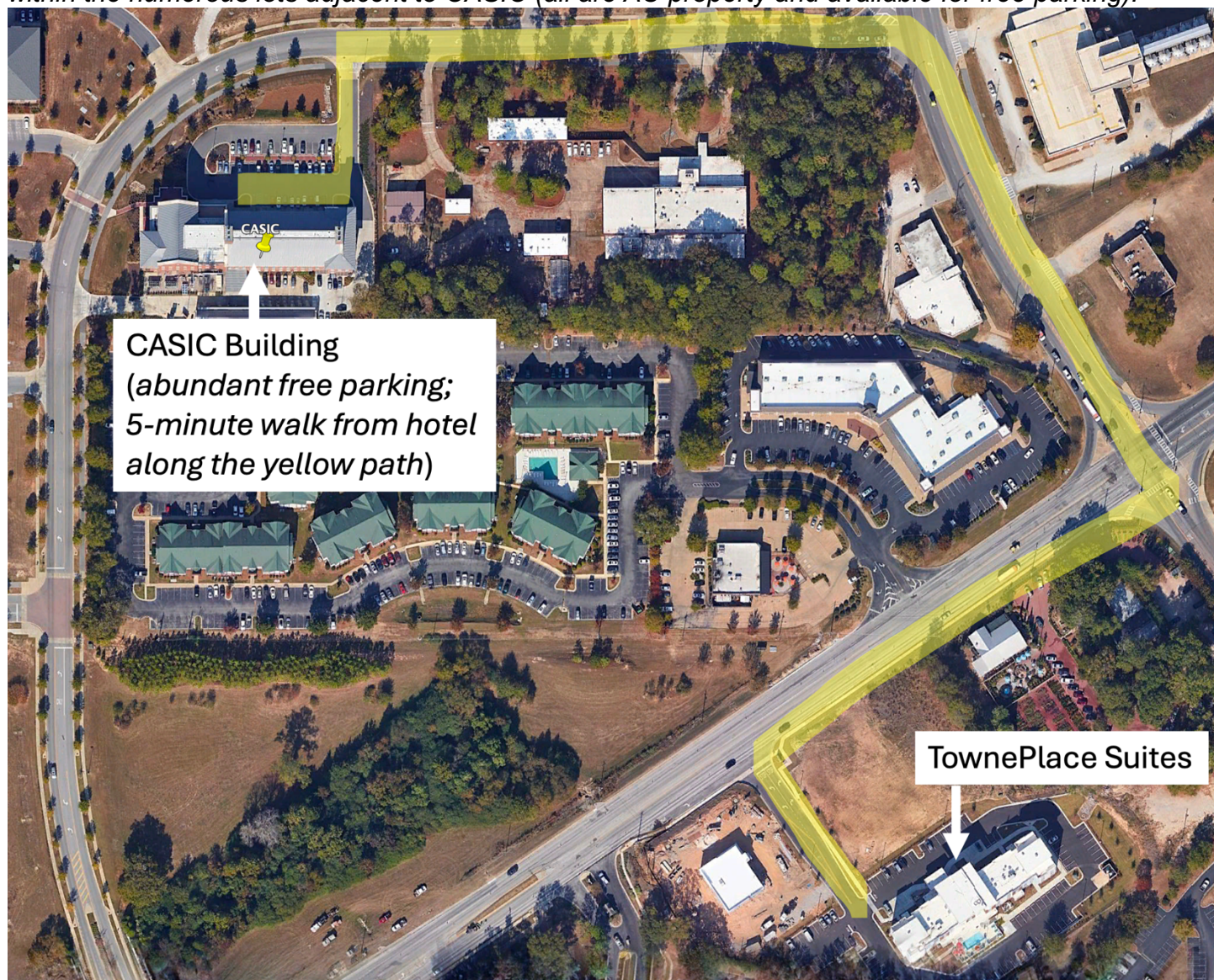
LUNCH & BUSINESS MEETING 11:15 AM – 1:00 PM

We offer a shrimp boil (shrimp, corn, sausage, potatoes, cajun seasoning) provided by Big Blue Crawfish Catering.

The SSP Business Meeting will adjourn at 1:00 pm sharp to respect the fact that everyone wants to get back on the road and get home by a decent hour. It is the responsibility of the SSP ExCom to adjourn the meeting on time. The Student Awards Ceremony is held during the SSP Business Meeting. To be eligible for an award, the student winner must be physically present at the Student Awards Ceremony. The LOC and SSP ExCom pledge to adjourn on time so that we can have all of our outstanding student winners present to receive their award and be photographed.

LEAVE AUBURN 1:00 PM SHARP

Meeting site & parking: See map below. TownePlace Suites is across the street (College Street) from the meeting site (CASIC) where all talks, posters, and meals happen. You can easily walk or drive from TownePlace Suites. Abundant parking is available in front of the CASIC Building as well as within the numerous lots adjacent to CASIC (all are AU property and available for free parking).



Thanks to our vendors and boosters:



PAPER SESSION #1

Friday, April 11th

9:00 AM – 12:00 PM

Location: CASIC Classroom, 1st floor

Moderators: Prof. Isaure de Buron & Prof. Ash Bullard

Presenting Author is first author unless indicated.

(Breaks will be 30 minutes long so that students and researchers can have more time to ask questions of speakers one-on-one and soon after their talk. Hopefully, this time will be used to have one-on-one interactions)

9:00 CIORIDIA-PORTER COMPETITOR

1. Occurrence of pyrantel pamoate resistant strains of the canine hookworm, *Ancylostoma caninum* in the Central Savannah River Area (CSRA)

Lauren E. Strock and Derek A. Zelmer

University South Carolina, Aiken, South Carolina.

9:15 BYRD DUNN COMPETITOR

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

Haley R. Dutton^{*1}, Stephen A. Bullard¹, Louis H. Du Preez^{2,3}, and Anita M. Kelly⁴

¹Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, Alabama; ²African Amphibian Conservation Research Group, Unit for Environmental Sciences and Management, North-West University, Private Bag x6001, Potchefstroom, 2520, South Africa; ³South African Institute for Aquatic Biodiversity, Somerset Street, Makhanda, South Africa; ⁴Alabama Fish Farming Center, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Greensboro, Alabama.

9:30 CIORIDIA-PORTER COMPETITOR

3. You are what you eat: Using molecular tools to study tapeworm life cycles in young-of-the-year bull sharks *Carcharhinus leucas*

Molly A. Kennedy, Melanie Langford, Allison Durland-Donahou, Kaitlin A. Gallagher, and

Gabriel J. Langford

Florida Southern College, Lakeland, Florida.

9:45

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

Chrissy M. Smith, Triet N. Truong, Stephen S. Curran, and Stephen A. Bullard

Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, 559 Devall Drive, Auburn, Alabama.

10:00 BYRD DUNN COMPETITOR

5. Diversity of digeneans parasitizing bats from two regions of Panama

Alex McFarland¹, Jonathan L. Dunnum^{*2}, Blas Armien^{*3}, Joseph A. Cook^{*3}, Jocelyn P. Colella^{*4}, and Stephen E. Greiman^{*1}

¹Biology Department, Georgia Southern University, Statesboro, Georgia; ²Museum of Southwestern Biology and Department of Biology, University of New Mexico, Albuquerque, New Mexico; ³Department of Research in Emerging and Zoonotic Infectious Diseases,

Gorgas Memorial Institute of Health Studies, Panama City, Panama; ⁴Sistema Nacional de Investigación, Secretaría Nacional de Ciencia y Tecnología, Panama City, Panama; ⁵University of Kansas Biodiversity Institute and Ecology Camp; Evolutionary Biology Department, University of Kansas, Lawrence, Kansas.

10:15-10:45 30 MIN BREAK- Time to ask speakers questions one-on-one

10:45 BYRD DUNN COMPETITOR

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

D. Santiago Escobar¹, Haley R. Dutton¹, Frank E. Williams IV², Jim D. Hedrick², and Stephen A. Bullard¹

¹Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, Alabama; ²West Virginia Department of Natural Resources, Elkins, West Virginia.

11:00 CIORIDIA-PORTER COMPETITOR

7. Investigating gastrointestinal nematode dynamics at the wildlife-domestic interface in Alabama

Jordan Crapia, Charlotte Alford, Kayla Alston, and Aniruddha Belsare
College of Forestry, Auburn University, Auburn, Alabama

11:15 BYRD DUNN COMPETITOR

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

Daniel Gordillo-González¹, A. George², B. Kuhajda², Steven P. Ksepka¹, Haley R. Dutton¹, Kamila Cajiao.-Mora¹, John H. Brule¹, & Stephen A. Bullard¹

¹Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, Alabama; ²Tennessee Aquarium Conservation Institute, Tennessee Aquarium, Chattanooga, Tennessee.

11:30 BYRD DUNN COMPETITOR

9. Disease ecology from biorepositories: Patterns in parasite community assembly reveal disparate costs of parasitism across a salamander hybrid zone

Timothy L. Odom^{1,2}

¹Odum School of Ecology, University of Georgia, Athens, Georgia; ²Center for the Ecology of Infectious Diseases, University of Georgia, Athens, Georgia.

11:45 BYRD DUNN COMPETITOR

10. Morphological and molecular characterization of *Pneumatophilus* in aquatic snakes in Louisiana

David A. Ervin¹, Ethan T. Woodyard², Jonah A. Nguyen¹, and T. Graham Rosser¹

¹Department of Comparative Biomedical Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi; ²Department of Pathobiology and Population Medicine, College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi.

12:00 PM - 2:00 PM LUNCH & POSTERS

Location: CASIC Classroom

P1. Helminth survey of Virginia opossums (*Didelphis virginiana*) from central Illinois with temporal and regional comparisons.

Alexa A. Howard and Elliot A. Zieman
Eastern Illinois University, Charleston, Illinois.

P2. Ancient flea diversification and the Gondwanan land bridges

Wade M. Burris and Bryan S. McLean
University of North Carolina, Greensboro, North Carolina.

P3. Investigating pH and serine protease dynamics in the *Ctenocephalides felis* midgut: Implications for pathogen transmission

Piper N. Zellner*¹ and Lisa D. Brown²
Georgia Southern University, Statesboro, Georgia.

P4. Parasite assemblages in bluntnose minnow (*Pimephales notatus*): Patterns, prevalence, and ecological implications in Illinois creeks

Alam Rowshan, Elliott Zieman, and Robert E. Colombo
Eastern Illinois University, Charleston, Illinois.

P5. Improving the systematics of the tick subgenus *Scaphixodes* of the genus *Ixodes* (Acari: Ixodidae)

Laila I. Richards¹, Dmitry A. Apanaskevich^{1,2}, and Stephen E. Greiman¹
¹Georgia Southern University, Statesboro, Georgia; ²United States National Tick Collection, Institute for Coastal Plain Science, Georgia Southern University, Statesboro, Georgia.

P6. Comparative analysis of parasite communities within native and invasive gastropods in central Florida

Mara N. Taylor and Kaitlin A. Gallagher
Florida Southern College, Lakeland, Florida.

P7. Cataloging gastrointestinal Helminths of the Virginia opossum (*Didelphis virginiana*)

Aiden W. Jones and Kathryn Purple
Lincoln Memorial University, Harrogate, Tennessee.

P8. Investigating infection by a recently discovered acanthocephalan, *Heterospinus mccordi* in crayfish of South Carolina

Annie N. Chowansky¹; Riley D. Cudahy¹; Gregory K. Rothman²; Michael R. Kendrick², and Isaure de Buron¹
¹Department of Biology, College of Charleston, Charleston, South Carolina; ²Marine Resources Research Institute, South Carolina Department of Natural resources, Charleston, South Carolina.

P9. Cestode diversity of *Sorex* shrews (Eulipotyphla: Soricidae) from Mongolia

Rokeya Ahmed¹; Bryan S. McLean²; Joseph A. Cook³; Kurt E. Galbreath⁴; Timothy J. Odom⁵; Stephen E. Greiman⁶
¹Department of Environmental Science, Box-30460, Georgia Southern University Statesboro, Georgia; ²Department of Biology, University of North Carolina Greensboro, 321 Mclver St., Greensboro, North Carolina; ³Museum of Southwestern Biology, Department of Biology, MSC03 2020, University of New Mexico, Albuquerque, New Mexico; ⁴Department of Biology, Northern Michigan University, Marquette, Michigan; ⁵Odom School of Ecology, University of Georgia, 140 E. Green St., Athens, Georgia; ⁶Department of Biology, Box-30460, Georgia Southern University Statesboro, Georgia.

P10. Effects of an introduced seaweed on *Vibrio* spp. densities in eastern oysters

Emma M. Mathew and Erik E. Sotka

College of Charleston, Charleston, South Carolina.

P11. Infection induced foraging suppression mediates macroparasite interactions across a salamander hybrid zone

Grace P. Mason¹ and Timothy L. Odom^{1,2}

¹*Odum School of Ecology, University of Georgia, Athens, Georgia;* ²*Center for the Ecology of Infectious Diseases, University of Georgia, Athens, Georgia.*

P12. Diversity and interrelationships of diplostomids (Digenea: Diplostomoidea) parasitic in kingfishers

Maggie A. Young¹; Tyler J. Achatz¹; Jeffrey A. Bell², Stephen E. Greiman³, Eric E. Pulis⁴; Simona Georgieva⁵, and Vasyl V. Tkach²

¹*Middle Georgia State University, Macon, Georgia;* ²*University of North Dakota, Grand Forks, North Dakota;* ³*Georgia Southern University, Statesboro, Georgia;* ⁴*Northern State University, Aberdeen, South Dakota;* ⁵*Bulgarian Academy of Sciences, Sofia, Bulgaria.*

P13. Initial detection of rat lungworm, a human pathogen, in invasive snails in Georgia

Caley H. Chun¹, Maggie A. Young¹, Jim Page², Matthew Rowe², Caroline Cox², Laura Wenk², Vasyl V. Tkach³, and Tyler J. Achatz¹

¹*Middle Georgia State University, Macon, Georgia;* ²*Wildlife Resources Division, Georgia Department of Natural Resources, Atlanta, Georgia;* ³*University of North Dakota, Grand Forks, North Dakota.*

P14. Host size and parasite burden in freshwater fish in Georgia

Cassie Ellenberger, Jade Salis, Nick Tsangarides, Whitney C. Preisser

Kennesaw State University, Kennesaw, Georgia.

P15. Parasite load and body size in three genera of salamanders in Georgia

Evan C. Johnson and Whitney C. Preisser

Kennesaw State University, Kennesaw, Georgia.

P16. Dogs traveling internationally transport *Dirofilaria* spp. from endemic regions

Theresa A. Quintana¹, Breck Aguinaga², Guwin Nilaweera², Jessica Mitchell^{1,2,3}, Grace Schieferecke², Janine Seetahal^{2,3}, and Jeba J.R. Jesudoss Chelladurai¹

¹*Auburn University, Auburn, Alabama;* ²*Kansas State University, Manhattan, Kansas;* ³*Kansas State Veterinary Diagnostic Laboratory (KSVDL), Manhattan, Kansas.*

P17. Parasites across time: The impact of environmental change on monogenean abundance

Imani J. Jones¹, Desmond Boyd², Gabriella Commisso³, Shyanne Christner⁴, Katie L. Leslie³; Jolee Thirtyacre³, Conner Whalen³, Armand A. Kuris⁵; Justin Mann⁶, Hank L. Bart⁶, Daki Diaz-Morales³, Chealsea L. Wood³; M. Egnin¹, and O. Idehen¹

¹*Dep. of Agricultural Sciences and the Plant Biotech & Genomics Research Lab, Tuskegee, Alabama;* ²*University of South Carolina, Columbia, South Carolina;* ³*School of Aquatic and Fishery Sciences, University of Washington, Seattle, Washington;* ⁴*Valdosta State University, Valdosta, Georgia;* ⁵*UC Santa Barbara, Santa Barbara, California;* ⁶*Department of Ecology and Evolutionary Biology, Tulane University, New Orleans, Louisiana.*

PAPER SESSION #2

Friday, April 11th

2:00 – 5:00 PM

Location: CASIC Classroom, 1st floor

Moderators: Haley Dutton & Prof. Derek Zelmer

Presenting Author is senior author unless indicated.

(Breaks will be 30 minutes long so that students and researchers can have more time to ask questions of speakers one-on-one and soon after their talk. Hopefully, this time will be used to have more relaxed and one-on-one interactions)

2:00 BYRD DUNN COMPETITOR

11. An unusual and novel dinoflagellate parasite of freshwater fish

Jonah A. Nguyen¹, Justin M. Stilwell¹, Nicole A. Nietlisbach², Sarah Sanderson³, Elisabeth Hehenberger⁴, Eric Leis⁵, Chip Long², Ethan T. Woodyard¹, Matt J. Griffin¹, T. Graham Rosser¹

¹Mississippi State University College of Veterinary Medicine, Mississippi State, Mississippi;

²Wisconsin Department of Natural Resources, Madison, Wisconsin; ³McGill University, Montreal, Quebec, Canada; ⁴Biology Centre of the Czech Academy of Sciences, České Budějovice, Czechia; ⁵U.S. Fish and Wildlife Service, Onalaska, Wisconsin.

2:15 BYRD DUNN COMPETITOR

12. Redescription of *Benedeniella posterocolpa* with many novel sequences and many novel specimens infecting cownose rays (*Rhinopteridae* spp.) and a giant manta (*Mobula birostris*) and phylogenetic analysis of *Capsalidae*

John H. Brule, Micah B. Warren, and Stephen A. Bullard

Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, 559 Devall Drive, Auburn, Alabama.

2:30 BYRD DUNN COMPETITOR

13. Characterization of a *Posthodiplostomum* sp. parasitizing pond-raised fingerling largemouth bass *Micropterus salmoides*

Ali A. Marchant¹, Adrián López-Porras², Wes A. Baumgartner³, Ethan T. Woodyard⁴, Matt J. Griffin^{4,5}, Lester H. Khoo^{4,5}, and T. Graham Rosser¹

¹Department of Comparative Biomedical Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi; ²Department of Biosciences, University of Oslo, Oslo, Norway; ³Veterinary Diagnostic Laboratory, College of Veterinary Medicine, University of Illinois, Urbana, Illinois; ⁴Department of Pathobiology and Population Medicine, Mississippi State University, Mississippi State, Mississippi; ⁵Thad Cochran National Warmwater Aquaculture Center, Delta Research and Extension Center, Mississippi State University, Stoneville, Mississippi.

2:45 BYRD DUNN COMPETITOR

14. New species of *Acanthostomum* Looss, 1899 (Digenea: Cryptogonimidae) infecting the aquatic coral snake, *Micrurus surinamensis* (Cuvier, 1817) (Serpentes: Elapidae) from the flooded rainforest habitat of the Yahuaraca Lake System (Amazon River, Colombia) with a phylogenetic analysis.

Kamila Cajiao-Mora¹, John H. Brule¹, Haley R. Dutton¹, José R. Caicedo-Portilla², and Stephen A. Bullard¹

¹Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, Alabama; ²Instituto Amazónico de Investigaciones Científicas “SINCHI”, Sede Principal, Leticia, Colombia.

3:00 BYRD DUNN COMPETITOR

15. Mosquito and *Culicoides* vector breeding ecology in wild pig (*Sus scrofa*) wallows in Georgia and South Carolina

Taylor A. Fisher^{1,2}, Lilyanne Callahan³; James C. Beasley^{2,3}, Vienna Brown⁴, Ellen Haynes¹; Erin K. Lipp⁵, Bethany McGregor⁶; Michael J. Yabsley^{1,3}; Daniel A.H. Peach^{2,7,8}; Christopher A. Cleveland^{1,5,9}

¹*Southeastern Cooperative Wildlife Disease Study, University of Georgia, Athens, Georgia;*

²*Savannah River Ecology Laboratory, Aiken, South Carolina;* ³*Warnell School of Forestry and Natural Resources, University of Georgia, Athens, Georgia;* ⁴*USDA APHIS Wildlife Services National Feral Swine Damage Management Program, 4101 Laporte Avenue, Fort Collins, Colorado;* ⁵*Department of Environmental Health Science, University of Georgia, Athens, Georgia;* ⁶*Arthropod-Borne Animal Diseases Research Unit, USDA-ARS, Manhattan, Kansas;* ⁷*Precision One Health Initiative, University of Georgia, Athens, Georgia;* ⁸*Department of Infectious Diseases, University of Georgia, Athens, Georgia;* ⁹*Center for Emerging Infectious Diseases, Athens, Georgia.*

3:15-3:45 30 MIN BREAK- Time to ask speakers questions one-on-one

3:45

16. Black spot disease goes global: revealing even further diversity of *Uvulifer*

Zoe Von Holten¹, Tyler J. Achatz², Stephen E. Greiman¹, Simona Georgieva³, Eric E. Pulis⁴, Vasyly V. Tkach⁵

¹*Georgia Southern University, Statesboro, Georgia;* ²*Middle Georgia State University, Macon, Georgia, USA;* ³*Bulgarian Academy of Sciences, Paterna, Spain;* ⁴*Northern State University, Aberdeen, South Dakota;* ⁵*University of North Dakota, Grand Forks, North Dakota.*

4:00

17. New species of *Baccigeroides* (Digenea: Gymnophalloidea) infecting intestinal mucosa of gulf menhaden, *Brevoortia patronus* Goode, 1878 (Clupeiformes: Alosidae) from the northern Gulf of Mexico

Triet N. Truong and Stephen A. Bullard

Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, 559 Devall Drive, Auburn, Alabama.

4:15 BYRD DUNN COMPETITOR

18. Prevalence and diversity of *Borrelia* species in ixodid ticks, domestic animals, and wildlife from Coastal Georgia

Taylor A. Pearson¹, Bailey Ward¹, Dylan DiNello^{1,2}, Christopher A. Cleveland^{1,3}, and Michael J. Yabsley^{1,2,3}

¹*Southeastern Cooperative Wildlife Disease Study, University of Georgia, Athens, Georgia;*

²*Warnell School of Forestry and Natural Resources, University of Georgia, Athens, Georgia;*

³*Center for the Ecology of Infectious Diseases, University of Georgia, Athens, Georgia.*

4:30

19. Revisiting the taxonomy and classification of *Postporus* Manter, 1949 (Trematoda: Digenea), an enigmatic intestinal parasite of groupers

Stephen S. Curran and Stephen A. Bullard

Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, Alabama.

4:45

20. Prevalence of avian haemosporidian parasites in house sparrows (*Passer domesticus*) from an urban environment in central Kentucky

Erin Gray¹, Becky Fox¹, Benson Otarigho², and Mofolusho Falade^{1*}

¹Biology Program Transylvania University, Lexington, KY, USA. ²Department of Genetics, The University of Texas MD Anderson Cancer Center

PAPER SESSION #3

Saturday, April 12th

9:00 AM – 10:45 AM

Location: CASIC Classroom, 1st floor

Moderators: Kaitlynn Stewart & Prof. Charles Faulkner

9:00

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

Micah B. Warren, Steven P. Ksepka, and Stephen A. Bullard

Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, 559 Devall Drive, Auburn, Alabama.

9:15

22. Patterns of *Echinostoma caproni* infection in sentinel snails in a mesocosm.

Derek A. Zelmer¹ and Thomas R. Platt²

¹University of South Carolina Aiken, Aiken, SC; ²Saint Mary's College, Notre Dame, Indiana.

9:30

23. *Heterospinus mccordi*: a newly described polymorphid acanthocephalan from introduced crayfish *Procambarus clarkii* in South Carolina, USA

Gregory K. Rothman¹, Kristina M. Hill-Spanik², Graham A. Wagner¹, Michael R. Kendrick¹, and Isaure de Buron^{*2}

¹Marine Resources Research Institution, SC Department of Natural Resources, Charleston South Carolina; ²Department of Biology, College of Charleston, Charleston, South Carolina; ^{*}presenting the talk

9:45

24. The diversity and ecology of freshwater snail-helminth relationships in Alabama: a summary of 10-years of data

Lori R. Tolley-Jordan

Department of Biology, College of Arts and Sciences, Jacksonville State University, 700 Pelham Rd. N., Jacksonville, Alabama.

10:00

25. A new species of *Huffmanella* Moravec, 1987 (Nematoda: Trichosomoididae) infecting the buccal cavity of smalltooth sawfish, *Pristis pectinata* Latham, 1794 (Rhinopristiformes: Pristidae) from Cudjoe Key, Florida

Steven P. Ksepka¹, Micah B. Warren¹, Micah D. Bakenhaster², and Stephen A. Bullard¹

¹Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, 559 Devall Drive, Auburn, Alabama; ²Fish and Wildlife Institute, Florida Fish and Wildlife Conservation Commission, 100 8th Ave SE, St. Petersburg, Florida.

10:15-10:45 BREAK- Time to ask speakers questions one-on-one

10:45

26. Shooting for the moon: Using environmental DNA metabarcoding to capture parasite diversity during a ParasiteBlitz

Kristina M. Hill-Spanik¹, Dakeishla M. Díaz-Morales^{2,3}, Stephen D. Atkinson⁴, Simona Georgieva⁵, Nikol Kmentová^{6,7}, Maarten M.P. Vanhove⁶, Bernd Sures², Edward W. Davis, II⁴, Robin Schütz², and Isuare de Buron¹

¹College of Charleston, Charleston, South Carolina; ²University of Duisburg-Essen, Essen, Germany; ³University of Washington, Seattle, Washington; ⁴Oregon State University, Corvallis, Oregon; ⁵Bulgarian Academy of Sciences, Sofia, Bulgaria; ⁶Hasselt University, Diepenbeek, Belgium; ⁷Royal Belgian Institute of Natural Sciences, Brussels, Belgium.

11:00

27. Morphological and molecular evidence of multiple *Orchidasma* spp. in loggerhead and Kemp's ridley sea turtles

T. Graham Rosser^{1,4}, Aiden Meaux^{2,4}, Ethan T. Woodyard², Justin M.² Stilwell, Bradley M. Richardson³, Logan R. S. Robison¹, Jill B. Hudnall^{2,4}, Kaylin McNulty^{2,4}, Jonah A. Nguyen¹, Divya Rose², Debra Moore^{2,4}, Beth Peterman^{2,4}, Stephen R. Reichley^{2,4}, Mark L. Lawrence^{2,4}

¹Department of Comparative Biomedical Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi; ²Department of Pathobiology and Population Medicine, College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi; ³Warmwater Aquaculture Research Unit, United States Department of Agriculture, Agricultural Research Service, Stoneville, Mississippi; ⁴Global Center for Aquatic Health and Food Security, Mississippi State University, Mississippi State, Mississippi.

11:15

28. Preliminary investigation of the relationship between gastrointestinal microbiota and parasitism in the North American raccoon (*Procyon lotor*)

Alivia Elkins¹, Matthew Kolp², and Kathryn E. Purple¹

¹Lincoln Memorial University, Harrogate, Tennessee; ²Lincoln Memorial University College of Veterinary Medicine, Harrogate, Tennessee.

11:30

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

Stephen A. Bullard and Haley R. Dutton

Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, Alabama.

END OF SCIENTIFIC PROGRAM**SSP BUSINESS MEETING & LUNCH**

Saturday, April 11

11:45 – 1:00 PM

Location: CASIC Classroom, 1st floor

ORAL PRESENTATION ABSTRACTS

1. Occurrence of pyrantel pamoate resistant strains of the canine hookworm, *Ancylostoma caninum* in the Central Savannah River Area (CSRA)

Lauren E. Strock* and Derek A. Zelmer

University South Carolina, Aiken, South Carolina.

Ancylostoma caninum, is a common intestinal nematode infecting dogs in the southern United States, with infections ranging from mild to severe. Pyrantel pamoate is a popular anthelmintic treatment used by many veterinarians across the U.S., but its widespread use has raised concern regarding the development of resistance. Multi-drug-resistant (MDR) strains of *A. caninum* have been identified in the U.S., and have also been detected in Canada as the result of the transport of dogs across the border. Analysis of serial fecal samples from weaned puppies dewormed with pyrantel pamoate was used to determine if pyrantel pamoate resistant strains of *A. caninum* are present in the Central Savannah River Area. A modified McMaster technique was used to perform a fecal egg count reduction assay to detect resistance and evaluate the effectiveness of pyrantel pamoate treatment. Thus far, evidence of both pyrantel resistant and MDR strains has been detected in both breeder populations, and household pets. The results of this research will contribute to a better understanding of the geographic extent of anthelmintic resistance in *A. caninum*. Additionally, this may provide valuable information to veterinarians and pet owners that will aid in the development of effective treatment and prevention strategies.

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

Haley R. Dutton*¹, Stephen A. Bullard¹, Louis H. Du Preez^{2,3}, and Anita M. Kelly⁴

¹Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, Alabama; ²African Amphibian Conservation Research Group, Unit for Environmental Sciences and Management, North-West University, Private Bag x6001, Potchefstroom, 2520, South Africa; ³South African Institute for Aquatic Biodiversity, Somerset Street, Makhandla, South Africa; ⁴Alabama Fish Farming Center, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Greensboro, Alabama.

We redescribe *Polystoma nearcticum* Paul, 1935 based on its holotype and vouchers plus new specimens that we collected from the urinary bladder of Cope's gray treefrogs, *Dryophytes chrysoscelis* (Anura: Hylidae) captured from Old Pal Pond, a beaver pond in Wind Creek, Tallapoosa River (Alabama). Our specimens were conspecific with *P. nearcticum* because they matched Paul's original description and were indistinguishable from the holotype and existing vouchers of *P. nearcticum*. Our two new 28S sequences of *P. nearcticum* were identical to each other and nearly identical to that of *P. nearcticum* and *Polystoma cinereum* Du Preez, Verneau and Gross, 2007 (the other congener infecting a North American frog). The 28S phylogenetic analysis recovered the *Polystoma* spp. of North American treefrogs as monophyletic, and all nominal *Polystoma* spp. infecting frogs of the Americas recovered in a clade with monotypic *Wetapolystoma* Gray, 1993. The "*Polystoma*" spp. of North American treefrogs were sister to that of frog polystomatids from Europe and Africa, including the type species *P. integerrimum*. Our new CO1 sequence (446 bp) of *P. nearcticum* was similar to that of *P. nearcticum* and *P. cinereum*. The CO1 phylogenetic analysis recovered the sequence identified as *P. integerrimum* as sister to the North American treefrog *Polystoma* spp. This contrasted starkly with the 28S analysis that recovered that sequence of *P. integerrimum* in relatively unrelated clade (suggesting that the CO1 sequence for *P. integerrimum* was misidentified). This is the first record of a polystomatid from Alabama and only the second record of a species of *Polystoma* (or any frog polystomatid) from the Southeastern United States.

3. You are what you eat: Using molecular tools to study tapeworm life cycles in young-of-the-year bull sharks *Carcharhinus leucas*

Molly A. Kennedy*, Melanie Langford, Allison Durland-Donahou, Kaitlin A. Gallagher, and Gabriel J. Langford

Florida Southern College, Lakeland, Florida.

Unraveling parasite life cycles is challenging under almost all conditions, even when many aspects of the host(s) and parasite can be manipulated in the laboratory. The challenge increases in marine ecosystems when studying host-parasite systems that cannot be maintained in controlled conditions. Given this limitation, it is unsurprising that the life cycles of parasites are unknown for most large marine hosts, such as elasmobranchs (sharks, skates, and rays). Recently, studies have shown the usefulness of molecular tools as an alternative method for linking different organisms that likely serve as hosts for marine parasites. A variety of parasites, including tapeworms, are known to use bull sharks *Carcharhinus leucas* as their definitive host, but we know very little about the remainder of their life cycles. This study uses molecular techniques to link intermediate hosts for *Cathetocephalus* sp., *Paraorygmatobothrium* sp., a species of the order Trypanorhyncha, and a yet to be identified adult cestode that were collected from young-of-the-year Bull Sharks in the Alafia River Estuary from Tampa Bay, Florida. It is hypothesized that these sharks are primarily preying upon small, abundant teleost fishes; we have collected larval tapeworms from these potential intermediate hosts, and common invertebrates in the area, that we will attempt to molecularly match to our adult worms from the Bull Shark. Results from this molecular analysis will be presented at this meeting.

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

Chrissy M. Smith*, Triet N. Truong, Stephen S. Curran, and Stephen A. Bullard
Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, 559 Devall Drive, Auburn, Alabama.

Crepidostomum transmarinum (Nicoll, 1909) Hunninen and Hunter, 1933 (Digenea: Allocreadiidae) has been regarded as a junior subjective synonym of *Crepidostomum farionis* (Müller, 1780) Lühe, 1909 since 1918. We herein resurrect *C. transmarinum* and provide a supplemental description for this species based on light microscopy of adult specimens infecting the intestine of brook trout, *Salvelinus fontinalis* (Mitchill, 1814) (Salmoniformes: Salmonidae) from Gragg Prong, Johns River, North Carolina. *Crepidostomum transmarinum* is morphologically distinct from all congeners by the combination of having a ventral sucker that is wider in diameter than the oral sucker, testes that have irregular margins, a genital pore that opens at or immediately posterior to the intestinal bifurcation, a vitellarium that extends anteriorly into the forebody, and an excretory bladder that extends anteriorly to the posterior margin of the anterior testis. Our new 28S sequence of *C. transmarinum* aligned over 1,151 bases was most similar to those of *Crepidostomum nemachilus* Krotov, 1959, (6 base pairs different, representing 0.5%) and *Crepidostomum brinkmanni* Faltýnková, Pantoja, Skírnisson, and Kudlai, 2020 and *Crepidostomum metoecus* (Braun, 1900) Braun, 1900 (type species) (both 7 bp, 0.6%). Our new ITS2 sequence of *C. transmarinum* spanning the entire ITS2 region was most similar to that of *C. brinkmanni* (397 bases, differing at 3 bases, representing 0.8%). Phylogenetic analyses of the 28S and ITS2 sequences both recovered *Crepidostomum* as polyphyletic within Allocreadiidae Looss, 1902, and *C. transmarinum* was sister to *C. brinkmanni*. This is the first record of *C. transmarinum* from the Johns River or from North Carolina.

5. Diversity of digeneans parasitizing bats from two regions of Panama

Alex McFarland^{*1}, Jonathan L. Dunnum^{*2}, Blas Armién^{*3}, Joseph A. Cook^{*3}, Jocelyn P. Colella^{*4}, and Stephen E. Greiman^{*1}

¹Biology Department, Georgia Southern University, Statesboro, Georgia; ²Museum of Southwestern Biology and Department of Biology, University of New Mexico, Albuquerque, New Mexico; ³Department of Research in Emerging and Zoonotic Infectious Diseases, Gorgas Memorial Institute of Health Studies, Panama City, Panama; ⁴Sistema Nacional de Investigación, Secretaría Nacional de Ciencia y Tecnología, Panama City, Panama; ⁵University of Kansas Biodiversity Institute and Ecology Camp; Evolutionary Biology Department, University of Kansas, Lawrence, Kansas.

Bats (Chiroptera) are highly diverse and serve as excellent hosts of endoparasites due to their diverse diets. There are around 1,100 species of bats worldwide and approximately 120 in Panama. Digeneans (Platyhelminthes: Trematoda) are parasitic flatworms with complex life cycles requiring a mollusk first intermediate host, a second intermediate host that could be an invertebrate or vertebrate, and a vertebrate definitive host. Field collection trips in the Darien (2023) and Kuna Yala (2016) regions of Panama resulted in a sample of 338 small mammals (322 bats, 14 rodents, and 2 opossums). Digeneans were found in 85 bats (20 species) and 1 rodent. The most common bat hosts infected with digeneans were *Myotis nigricans* (n=32 infected, 74.42% prevalence, average species richness 1.63), *Phyllostomus discolor* (n=11, 45.83% 1.17), and *Phyllostomus hastatus* (n=5, 35.71%, 1.0). The average species richness for all infected hosts was 1.43. Using morphological and molecular (28S rDNA and COI mtDNA genes) data we identified 15 unique digenean species from 7 genera, including 2 species from a new genus. Six digenean samples, all of which were identified as the same species of *Ochoterenatrema*, from 5 *Myotis nigricans* bats were found to be infected with a single species of *Neorickettsia*. Our phylogenetic analysis of the 16S rRNA gene and the GroEL gene show our species to be most closely related to *Neorickettsia risticii*.

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

D. Santiago Escobar¹, Haley R. Dutton¹, Frank E. Williams IV², Jim D. Hedrick², and Stephen A. Bullard¹

¹Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, Alabama; ²West Virginia Division of Natural Resources, Elkins, West Virginia.

Infectious Pancreatic Necrosis Virus (IPNV) is a double-stranded RNA (dsRNA) (genus *Aquabirnavirus*; family *Birnaviridae*) that can cause disease and kill cultured salmonids in some cases whereas in other cases the infected fish is an asymptomatic carrier of the virus. The effects of this virus on wild fish populations is indeterminate because viral surveys of wild fish are seldom conducted. The purpose of this study was to surveil for IPNV among wild rainbow trout (*Oncorhynchus mykiss*) and brook trout (*Salvelinus fontinalis*) from streams in West Virginia. A total of 168 young-of-the-year trout were captured from 11 freshwater streams in WV. Kidney and spleen were pooled individually from each fish and a reverse transcription polymerase chain reaction (RT-PCR) protocol targeting the VP2 gene of IPNV was applied to the samples. In parallel, the homogenized kidney+spleen from each fish was plated onto Chinook Salmon Embryo (CHSE) and Epithelioma Papulosum Cyprini (EPC) cell lines. A total of 43 (25.6% overall prevalence) fish were positive (25 brook trout [14.9%]; 18 rainbow trout [10.7%]). No cytopathic effect was observed in cell culture. The study contributes to understanding the epidemiology of IPNV in West Virginia and offers insights into enhancing management practices to mitigate the impact of this pathogen on trout populations.

7. Investigating gastrointestinal nematode dynamics at the wildlife-domestic interface in Alabama

Jordan Crapia^{*}, Charlotte Alford, Kayla Alston, and Aniruddha Belsare

College of Forestry, Auburn University, Auburn, Alabama.

Gastrointestinal nematode (GIN) infections often occur in wild and domestic ruminants and can cause slower growth rates, poor reproduction, and overall compromised animal welfare, which negatively affects livestock industry economics. Anthelmintics are used to control GIN infections; however, the recent increase of anthelmintic resistance poses serious challenges. Wild and domestic ruminants share several GIN species; thus, the role wild ruminants play in the spread and persistence of GINs needs to be investigated. Wild ruminants could also provide refugia, as they are not treated with anthelmintic drugs. In this study, we undertook coproscopy to assess GIN infections in domestic and wild ruminants in Lee and Chambers County in Alabama. We assessed 150 beef cattle, 95 dairy cattle, 69 sheep, 66 goat, and 142 white-tailed deer fecal samples between 2024-2025. Most white-tailed deer samples were collected opportunistically from the ground, therefore individual identification is unknown. Infection intensities for trichostrongyles were estimated using a modified McMaster's egg count technique. Common trichostrongyles infecting ruminants include *Haemonchus* spp., *Trichostrongylus* spp., *Ostertagia* spp., and *Cooperia* spp. Prevalence of trichostrongyle infection was compared between host species and seasons. Prevalence of infection was higher in fall and winter months than spring and summer months for all host species. There was a statistically significant difference between seasonal prevalence of trichostrongyle infection in multiple host species. This study will help to guide better livestock management and strategies for mitigating GIN infections. Here we discuss the significance of white-tailed deer in interspecies transmission at the wild-domestic interface.

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

Daniel Gordillo-González¹, A. George², B. Kuhajda², Steven P. Ksepka¹, Haley R. Dutton¹, Kamila Cajiao.-Mora¹, John H. Brule¹, & Stephen A. Bullard¹

¹*Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, Alabama;* ²*Tennessee Aquarium Conservation Institute, Tennessee Aquarium, Chattanooga, Tennessee.*

A captive-bred cohort of Laurel dace (a federally-endangered fish restricted to 2 streams in eastern Tennessee's Cumberland Plateau) became moribund and experienced trickling mortalities. Herein, those fish were processed for histopathology and molecular diagnostics. The Ziehl-Neelsen (ZN) stain revealed an acid-fast microbe within lesions (necrotic areas and intracellularly) in the swim bladder, ovary, spleen, kidney, eye, and body cavity wall. The swim bladder had an acellular, eosinophilic exudate encasing the acid-fast microbe; its serosa was thickened with abundant connective tissue, lymphocytic infiltrates, and severe infiltration of macrophages and multinucleated giant cells (MGCs) plus mixed lymphocytes around some blood vessels. The ovary (60% changed) had variously-sized granulomatous nodules containing caseous necrosis and extensive, severe areas of macrophages, epithelioid cells, and eosinophilic granular cells (EGCs). The spleen (30%) had myriad macrophages and associated melanin-like residue (MLR). The kidney (20%) had clusters of macrophages and epithelioid cells that displaced hematopoietic components and was haloed by MLR. The body cavity wall (40%) had clusters of macrophages, epithelioid cells, and MGCs (Langhans type) that adhered to the hepatic and intestinal serosa and invaded the adipose tissue near some exocrine pancreatic acini. The eye chambers had an eosinophilic exudate and extensive hemorrhages, and 90% of sections showed a choroid plexus infiltrated by macrophages, epithelioid cells, and MGCs plus perivascular lymphocytes and EGCs. We amplified the Hsp65 gene (439 bp) from the lesioned tissues, and it was identical to that of *Mycobacterium gordonae* (type culture, France). This report is the first report of *M. gordonae* from laurel dace.

9. Disease ecology from biorepositories: Patterns in parasite community assembly reveal disparate costs of parasitism across a salamander hybrid zone

Timothy L. Odom^{*1,2}

¹Odum School of Ecology, University of Georgia, Athens, Georgia; ²Center for the Ecology of Infectious Diseases, University of Georgia, Athens, Georgia.

Animal hybrid zones often form over ecological gradients like elevation, latitude, and landscape use, with hybrids experiencing a diversity of conditions relative to either parent taxa. The gradients along which hybrid zones form also influence the diversity and abundance of communities of parasites to which hybridizing host populations are exposed. We leveraged preserved specimens of two *Plethodon* salamanders, *P. shermani* and *P. teyahalee*, and their hybrids from natural history collections at The University of Georgia to determine if hybridizing *Plethodon* at Coweeta Hydrological Station, Otto, NC, USA are host to distinct parasite communities. We found that *P. shermani*, *P. teyahalee*, and hybrids were host to a common species pool of generalist gastrointestinal parasites, but parasite community assembly operated idiosyncratically between hybrids and parent taxa. Interspecific competition between co-infecting parasites was evident across all three host groups, but the degree to which interspecific parasite interactions shaped parasite community assembly was greatest in *P. teyahalee*. We detected significant antagonistic interactions between the ciliated protozoan parasite, *Cepedietta*, and several other co-infecting parasites. A post-hoc analysis of GI contents and *Cepedietta* infection intensity revealed a strong negative association between gut fullness and infection intensity, where heavy infections were most common in *P. teyahalee* and associated with the absence of prey items and other parasites from the GI tract. This pattern was strongest in *P. teyahalee*, present in *P. shermani*, but absent in hybrid *Plethodon* at this locality, suggesting some degree of hybrid vigor via tolerance to intermediate *Cepedietta* infections.

10. Morphological and molecular characterization of *Pneumatophilus* in aquatic snakes in Louisiana

David A. Ervin^{*1}, Ethan T. Woodyard², Jonah A. Nguyen¹, and T. Graham Rosser¹

¹Department of Comparative Biomedical Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi; ²Department of Pathobiology and Population Medicine, College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi.

Trematodes of the genus *Pneumatophilus* parasitize the lung and trachea of aquatic snakes in North America. Currently four species are considered valid, but to date no molecular data have been provided for the genus. With limited accounts of these enigmatic trematodes, there are still many questions about the taxonomy and phylogenetic placement of the genus. *Pneumatophilus* spp. have been identified classically by the variability in testes morphology, location of the ovary, and morphology of the uterus. Some morphological plasticity within the four described species has stimulated debate on the true species diversity within *Pneumatophilus*. In 2019, gravid adult specimens of *Pneumatophilus* were recovered from *Nerodia erythrogaster*, *Nerodia fasciata*, and *Nerodia rhombifer* hunted during an annual snake rodeo event in Louisiana. Hologenophores were prepared by cutting a section of tegumental tissue, extracting genomic DNA, and staining for morphological identification. From a single specimen, genomic DNA was sequenced using Oxford Nanopore and Illumina platforms to obtain the entire mitochondrial genome and nuclear ribosomal DNA operon. Using morphological, molecular, and phylogenetic approaches, the placement of the genus within the superfamily Plagiorchioidea is discussed. Comparison of molecular data from morphologically identified adult specimens will be helpful in inferring life cycles as intermediate hosts are identified.

11. An unusual and novel dinoflagellate parasite of freshwater fish

Jonah A. Nguyen^{*1}, Justin M. Stilwell¹, Nicole A. Nietlisbach², Sarah Sanderson³, Elisabeth Hehenberger⁴, Eric Leis⁵, Chip Long², Ethan T. Woodyard¹, Matt J. Griffin¹, T. Graham Rosser¹

¹Mississippi State University College of Veterinary Medicine, Mississippi State, Mississippi;

²Wisconsin Department of Natural Resources, Madison, Wisconsin; ³McGill University, Montreal, Quebec, Canada; ⁴Biology Centre of the Czech Academy of Sciences, České Budějovice, Czechia; ⁵U.S. Fish and Wildlife Service, Onalaska, Wisconsin.

A novel dinoflagellate parasite infecting bluegill, *Lepomis macrochirus*, rock bass, *Ambloplites rupestris*, largemouth bass, *Micropterus nigricans*, and yellow perch, *Perca flavescens* is described from two lakes in Wisconsin. Unlike most dinoflagellate parasites of fish, which infect their hosts through a trophont stage, the novel species is characterized by a coccoid vegetative cyst found on most external surfaces. This is characteristic of the monotypic genus *Haidadinium* (Dinophyceae: Suessiaceae). The only previously described species, *Haidadinium ichthyophilum*, predominantly parasitizes three-spined stickleback, *Gasterosteus aculeatus* and has only been reported from a single lake in the Haida Gwaii archipelago, British Columbia, Canada. The most distinguishing morphological difference between the two species is the greater vegetative cyst diameter of the novel species when compared to *H. ichthyophilum*. While both species parasitize nearly the entire external surface of fish, *H. ichthyophilum* primarily infects the epidermis and gill filaments, whereas the novel species resides in the dermis and is absent from the gill filaments. Histopathological analysis revealed minimal host response to the novel species, whereas *H. ichthyophilum* induces epithelial hyperplasia that results in a gelatinous coating on parasitized fish. Additionally, intracellular bacteria are associated with *H. ichthyophilum* vegetative cysts but are absent in the novel species. Small and large ribosomal subunit rDNA sequencing was performed for both species for the first time. Pairwise distance and phylogenetic analyses using these markers supported the distinction between the two species. This discovery expands our understanding of parasitic dinoflagellate diversity.

12. Redescription of *Benedeniella posterocolpa* with many novel sequences and many novel specimens infecting cownose rays (*Rhinopteridae* spp.) and a giant manta (*Mobula birostris*) and phylogenetic analysis of Capsalidae

John H. Brule*, Micah B. Warren, and Stephen A. Bullard

Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, 559 Devall Drive, Auburn, Alabama.

We collected capsalids from cownose rays (*Rhinoptera bonasus*) and Brazilian cownose rays (*Rhinoptera brasiliensis*) from the Gulf of America and from a giant manta (*Mobula birostris*) from a public aquarium. All specimens matched the holotype of *B. posterocolpa* (anterior attachment organs with anterior grooves; a haptoral peduncle with one pair of papillae; and a long, narrow vaginal duct that opens laterally at level of the testes). Fifteen novel sequences were generated in this study (cownose ray and giant manta: 2 capsalids each for *ITS1*, *28S*, *CO1*; Brazilian cownose ray: 1 capsalid for the same genes). No *ITS1* or *CO1* sequence existed for *B. posterocolpa* previously. The GenBank *28S* sequence was identical to our *28S* sequences, and the new *ITS1* sequences were identical. Two morphologically-identical specimens (2 hologenophores) of *B. posterocolpa* from the same patch of skin on the same cownose ray had distinct *CO1* sequences (2 bp; 0.2% difference). The *CO1* sequences from 2 specimens of *B. posterocolpa* from giant manta were identical to each other and differed from the previous sequences by 4 bp (0.5%). The *CO1* sequence from the specimen of *B. posterocolpa* from the Brazilian cownose ray differed from the previous sequences by 5 bp (0.6%). This is the first study of *B. posterocolpa* that combines morphology and nucleotide sequences from multiple infections, first record of *B. posterocolpa* infecting the Brazilian cownose ray, and first taxonomically confirmed record of *B. posterocolpa* infecting the giant manta.

13. Characterization of a *Posthodiplostomum* sp. parasitizing pond-raised fingerling largemouth bass *Micropterus salmoides*

Ali A. Marchant^{*1}, Adrián López-Porras², Wes A. Baumgartner³, Ethan T. Woodyard⁴, Matt J. Griffin^{4,5}, Lester H. Khoo^{4,5}, and T. Graham Rosser¹

¹Department of Comparative Biomedical Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi; ²Department of Biosciences, University of Oslo, Oslo, Norway; ³Veterinary Diagnostic Laboratory, College of Veterinary Medicine, University of Illinois, Urbana, Illinois; ⁴Department of Pathobiology and Population Medicine, Mississippi State University, Mississippi State, Mississippi; ⁵Thad Cochran National Warmwater Aquaculture Center, Delta Research and Extension Center, Mississippi State University, Stoneville, Mississippi.

Freshwater aquaculture is an important agricultural economic commodity, especially in the Southeastern United States. There are a wide range of diseases that affect fish populations and may lead to direct and indirect economic losses for producers. A farm in Arkansas experienced recurring losses in fingerling largemouth bass *Micropterus salmoides* during the summer of 2016. Moribund fish were submitted to the Aquatic Research and Diagnostic Laboratory at the Thad Cochran National Warmwater Aquaculture Center. Fish were heavily infected with the metacercaria of a *Posthodiplostomum* sp., commonly known as “white-grub”.

Posthodiplostomum spp. are trematodes that utilizes a three-host life cycle. *Posthodiplostomum* spp. develop as cercaria in freshwater snails, metacercaria in fish, and adults in piscivorous birds. Metacercaria found in the spleen, liver, and kidneys were stained for morphological characterization. Specimens were molecularly assessed using conventional PCR and Sanger sequencing. A subsample was sequenced using Oxford Nanopore and Illumina platforms to obtain the complete mitochondrial genome and entire nuclear ribosomal DNA. Aquatic snails (*Physa gyrina* and *Galba truncatula*) were collected from affected ponds to determine the snail host. Through DNA sequencing, the isolate in fingerlings and cercaria shed from *P. gyrina* was identified as *Posthodiplostomum* sp. 8. This species has been previously described from wild largemouth bass and smallmouth bass *Micropterus dolomieu* in North America. Future work will focus on identifying the avian host to elucidate the life cycle. By understanding the life cycles of these parasites, fish producers can make informed management decisions to limit their impact.

14. New species of *Acanthostomum* Looss, 1899 (Digenea: Cryptogonimidae) infecting the aquatic coral snake, *Micrurus surinamensis* (Cuvier, 1817) (Serpentes: Elapidae) from the flooded rainforest habitat of the Yahuaraca Lake System (Amazon River, Colombia) with a phylogenetic analysis.

Kamila Cajiao-Mora^{*1}, John H. Brule¹, Haley R. Dutton¹, José R. Caicedo-Portilla², and Stephen A. Bullard¹

¹Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, Alabama; ²Instituto Amazónico de Investigaciones Científicas “SINCHI”, Sede Principal, Leticia, Colombia.

We herein describe a new species of *Acanthostomum* (Digenea: Cryptogonimidae) based on specimens we collected from the intestine of an aquatic coral snake, *Micrurus surinamensis* (Cuvier, 1817) (Serpentes: Elapidae) from the flooded rainforest habitat of the Yahuaraca Lake System (Amazon River) Leticia, Amazonas, Colombia. We assign the new species to *Acanthostomum* Looss, 1899 because it lacks a gonotyl and has an elongate body, spinose tegument, funnel-shaped oral sucker with circumoral spines, ceca each having a posterolateral and nearly terminal pore, and excretory vesicle arms reaching anteriorly to the pharynx. The new species differs from its 19 congeners by having 24–30 circumoral spines (vs. fewer than 20 or aspinose), vitellarium extension (from ovary to posterior half of body vs. from testis or ovary to anterior half of body), and symmetrical ceca each having an anal pore (vs. asymmetrical ceca, a single cecum, or lacking anal pores). Our 28S phylogenetic analysis recovered a paraphyletic *Acanthostomum* within a clade sister to other cryptogonimids. Regarding advancing the systematics of the family, we discuss oral sucker shape and position, circumoral spine distribution, tegumental spine distribution, ceca symmetry, anal pore presence/absence and

position, and gonotyl presence/absence as useful genus-level features. Many of these features remain indeterminate for several species. This is the first published study of a parasite infecting a tetrapod in the Yahuaracaca Lake System, first to record a parasite infecting a coral snake (*Micrurus* spp.) in Colombia, and only the second trematode species reported from the aquatic coral snake.

15. Mosquito and *Culicoides* vector breeding ecology in wild pig (*Sus scrofa*) wallows in Georgia and South Carolina

Taylor A. Fisher^{*1,2}, Lilyanne Callahan³; James C. Beasley^{2,3}, Vienna Brown⁴, Ellen Haynes¹; Erin K. Lipp⁵, Bethany McGregor⁶; Michael J. Yabsley^{1,3}; Daniel A.H. Peach^{2,7,8}; Christopher A. Cleveland^{1,5,9}

¹*Southeastern Cooperative Wildlife Disease Study, University of Georgia, Athens, Georgia;*

²*Savannah River Ecology Laboratory, Aiken, South Carolina;* ³*Warnell School of Forestry and Natural Resources, University of Georgia, Athens, Georgia;* ⁴*USDA APHIS Wildlife Services National Feral Swine Damage Management Program, 4101 Laporte Avenue, Fort Collins, Colorado;* ⁵*Department of Environmental Health Science, University of Georgia, Athens, Georgia;* ⁶*Arthropod-Borne Animal Diseases Research Unit, USDA-ARS, Manhattan, Kansas;* ⁷*Precision One Health Initiative, University of Georgia, Athens, Georgia;* ⁸*Department of Infectious Diseases, University of Georgia, Athens, Georgia;* ⁹*Center for Emerging Infectious Diseases, Athens, Georgia.*

Wild pigs (*Sus scrofa*), also known as feral swine, function as ecosystem engineers and are a significant invasive species in the United States. They consume agricultural crops, native plants and animals, while their rooting and wallowing behaviors lead to extensive habitat modification. Specifically, wallowing creates ephemeral pools distributed throughout the landscape, which may serve as breeding sites for arthropods requiring aquatic or semi-aquatic conditions during development. This study investigates whether wild pig wallows act as habitats for mosquito (Diptera: Culicidae) and biting midge (*Culicoides* spp.) vector species. Collections were conducted at wild pig wallows across three sites in South Carolina and Georgia from April 2024 to August 2025. Sampling methods include mosquito larval dipping and soil incubation for midge emergence. Preliminary morphological identification has yielded 200 mosquito larvae and 90 adult *Culicoides* midges across all sites. Notable species identified include *Culicoides variipennis*, a sister species of the primary North American bluetongue virus vector *C. sonorensis* as well as mosquitoes from the genera including Anopheles, Culex, Aedes, and Psorophora. Mosquito vectors identified morphologically have the capacity to transmit Plasmodium spp. (causative agents of malaria), *Dirofilaria immitis* (canine heartworm), and various Flaviviruses and Alphaviruses. This study highlights that wild pig-created wallows are used as breeding habitats for medically and veterinary important vectors. Furthermore, our results provide a framework for understanding vector driven pathogen transmission in *Sus scrofa*-modified landscapes and potential effects on population health. This study emphasizes the interconnectedness of invasive species, vector ecology, and pathogen transmission within a One Health framework.

16. Black spot disease goes global: revealing even further diversity of *Uvulifer*

Zoe Von Holtzen ^{*1}, Tyler J. Achatz², Stephen E. Greiman¹, Simona Georgieva³, Eric E. Pulis⁴, Vasyl V. Tkach⁵

¹*Georgia Southern University, Statesboro, Georgia;* ²*Middle Georgia State University, Macon, Georgia, USA;* ³*Bulgarian Academy of Sciences, Paterna, Spain;* ⁴*Northern State University, Aberdeen, South Dakota;* ⁵*University of North Dakota, Grand Forks, North Dakota.*

Uvulifer (Diplostomoidea: Diplostomidae) is a broadly distributed genus of digeneans that parasitize the intestines of kingfisher definitive hosts. The metacercariae of *Uvulifer* spp. are common etiological agents of “black spot disease” in fishes worldwide. Unfortunately, morphology of these metacercariae are not suitable for species identification. Recent studies have demonstrated the genus to be much more diverse than previously known. Few studies

have generated DNA sequences from *Uvulifer* spp. outside of the New World, and only two species/species-level lineages from Old World samples are suitable for phylogenetic study. In the present study, we collected adult *Uvulifer* spp. from multiple kingfisher species from Brazil, Philippines, Korea, Uganda, Ukraine, and the USA. These samples were used for both morphological and molecular study when possible. We sequenced fragments of 28S rDNA and *cox1* mtDNA genes. Newly generated sequences were used for phylogenetic inference and to assess potential further diversity of the genus. Our study identified the presence of several species-level lineages. We are in the process of describing 4 of these species. Unfortunately, no morphological vouchers are available for some species-level lineages from South America. However, all nominal species in South America have been previously sequenced. Thus, all collected species-level lineages from Brazil almost certainly represent new species. This study demonstrates the significant diversity within *Uvulifer* and need for further collection of adults, particularly from the Old World. DNA sequences generated from morphologically identified adults will support future identifications of the larval stages.

17. New species of *Baccigeroides* (Digenea: Gymnophalloidea) infecting intestinal mucosa of gulf menhaden, *Brevoortia patronus* Goode, 1878 (Clupeiformes: Alosidae) from the northern Gulf of America

Triet N. Truong* and Stephen A. Bullard

Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, 559 Devall Drive, Auburn, Alabama.

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

18. Prevalence and diversity of *Borrelia* species in ixodid ticks, domestic animals, and wildlife from Coastal Georgia

Taylor A. Pearson*¹, Bailey Ward¹, Dylan DiNello^{1,2}, Christopher A. Cleveland^{1,3}, and Michael J. Yabsley^{1,2,3}

¹*Southeastern Cooperative Wildlife Disease Study, University of Georgia, Athens, Georgia;*

²*Warnell School of Forestry and Natural Resources, University of Georgia, Athens, Georgia;*

³*Center for the Ecology of Infectious Diseases, University of Georgia, Athens, Georgia.*

Borrelia spirochete bacteria are tick-borne pathogens and causative agents of severe borreliosis infections in domestic animals and humans. Despite the public health importance of *Borrelia*, there are few data on the prevalence and diversity of these pathogens in ticks from coastal Georgia. This study aims to characterize *Borrelia* spp. prevalence and diversity in ixodid ticks collected from coastal Georgia. We are collecting ticks from the environment using tick

drags and from various vertebrate hosts including dogs, cats, raccoons, white-tailed deer, bobwhite, rodents, and wild pigs. To investigate potential *Borrelia* reservoirs, we are opportunistically collecting tissue punches from the ears of trapped wildlife. Additional tick samples are being obtained through public submissions and partnerships with coastal veterinarians and livestock farmers. Our protocol involves morphologically identifying each tick and confirming species through PCR and sequencing of the *COXI* gene. We are testing individual ticks for *Borrelia* spp. using a nested PCR targeting the *flaB* gene with species identification determined using bidirectional Sanger sequencing. To date, 1200 ticks have been collected from 13 coastal counties in Georgia and from 131 vertebrate hosts. Tick species include *Amblyomma americanum* (32%, 381/1200), *A. maculatum* (4%, 52/1200), *Dermacentor variabilis* (3%, 34/1200), and *Ixodes* spp. (4%, 51/1200). Additional identification and pathogen testing for all tick species is currently underway. These preliminary data indicate that coastal Georgia has a high diversity of ticks, several of which are known to transmit *Borrelia* spp. of zoonotic and veterinary concern.

19. Revisiting the taxonomy and classification of *Postporus* Manter, 1949 (Trematoda: Digenea), an enigmatic intestinal parasite of groupers

Stephen S. Curran* and Stephen A. Bullard

Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, Alabama.

Postporus epinepheli (Manter, 1947) Manter, 1949 is an intestinal parasite of groupers in the warm western Atlantic Ocean. No knowledge of larval life history stages exists but the genus is currently classified in Postporinae Yamaguti, 1958, which was recently transferred from the Apocreadiidae Skrjabin, 1954 into the Megaperidae Manter, 1934. A second species in the genus, *P. mycteropercae* (Manter, 1947) Manter, 1945, was synonymized with the first in 1960 and *Postporus* Manter, 1949 has been monotypic and rarely reported ever since. During surveys of grouper parasites in the Gulf of America and the Caribbean Sea between 1998 through 2024 we accumulated worms belonging in *Postporus*. Our morphological observations of these clearly show a muscular lining surrounding the male terminal genital structures (a true cirrus sac), thus indicating the genus is miss-classified in the Megaperidae. Furthermore, our data strongly affirm the presence of two congeneric species, and we therefore resurrect *P. mycteropercae* to accommodate this. We generated new nucleotide data (internal transcribed spacer region 2 and 28S ribosomal RNA) from both species, which corroborate the distinctive species; and we conducted a phylogenetic analysis of the 28S rRNA from *Postporus* spp., which produced a best consensus tree that strongly supports a relationship with species in the Lepocreadiidae Odhner, 1905. Consequently, we propose a new classification for the genus in Lepocreadiidae, and since subfamilies are not recognized we consider Postporinae a junior synonym to Lepocreadiidae.

20. Prevalence of avian haemosporidian parasites in house sparrows (*Passer domesticus*) from an urban environment in central Kentucky

Erin Gray¹, Becky Fox¹, Benson Otarigho², and Mofolusho Falade^{1*}

¹Biology Program Transylvania University, Lexington, KY, USA. ²Department of Genetics, The University of Texas MD Anderson Cancer Center

House sparrows (*Passer domesticus*) are widespread wild birds that may serve as reservoirs for avian haemosporidians, vector-borne blood parasites of *Plasmodium*, *Haemoproteus*, and *Leucocytozoon*. Haemosporidian infections have been increasingly reported in urban house sparrow populations across various regions, with higher infection rates linked to population declines. However, data on haemosporidian infections in urban environments within Central Kentucky remain limited. This study assessed the prevalence of blood parasites in 67 house sparrows sampled from Transylvania University's campus using both microscopic and molecular approaches. PCR analysis detected a *Plasmodium* infection

rate of 1.6%, with only one bird testing positive. No infection by a species of *Haemoproteus* or *Leucocytozoon* was detected. The positive *Plasmodium* sample is currently undergoing sequencing to confirm parasite identity and assess potential genetic diversity. The low prevalence observed in this population may be influenced by factors such as limited vector availability in urban habitats or environmental conditions that reduce parasite transmission. Further research, including vector surveillance and expanded sampling, is necessary to better understand the ecological and epidemiological dynamics of haemosporidian infections in urban house sparrow populations.

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

Micah B. Warren*, Steven P. Ksepka, and Stephen A. Bullard
Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, 559 Devall Drive, Auburn, Alabama.

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

22. Patterns of *Echinostoma caproni* infection in sentinel snails in a mesocosm

Derek A. Zelmer*¹ and Thomas R. Platt²

¹University of South Carolina Aiken, Aiken, SC; ²Saint Mary's College, Notre Dame, Indiana. *Echinostoma caproni* has been a popular model for investigations of cercaria behavior because it is relatively easy to maintain using mice as definitive hosts, and snails of the genus *Biomphalaria* as first intermediate hosts. The free-swimming cercariae are capable of using a broad range of species as second intermediate hosts, including the same snail species that acts as the first intermediate host. Cercariae of *E. caproni* have been shown to vary their distributions in experimental chambers with positive responses to light and negative responses to gravity that have been shown to be repeatable in field experiments. A snail shedding cercariae of *E. caproni* was placed in a single fixed position in a 20 liter aquarium (in one corner, either near the top or near the bottom of the aquarium), with uninfected snails placed in 8 fixed positions throughout the aquaria as sentinels. After a 48-hour period, sentinel snails were examined for metacercariae. The expectation that infections would be concentrated in the sentinel snails located near the top of the aquaria was not realized from data pooled from 12 iterations of each shedding snail position. Approximately equal numbers of metacercariae were recovered from sentinel snails located at the top and at the bottom of the aquaria. The

relationship between metacercaria abundance and distance from the source snail did not follow the monotonic nonincreasing relationship of a null model of cercaria dispersal, but a second null model emphasizing vertical movement of the cercariae exhibited a tendency towards nonmonotonicity. The disagreement between measured responses of cercariae to stimuli and actual patterns of infection may be the result of interpreting kinetic responses as tactic responses.

23. *Heterospinus mccordi*: a newly described polymorphid acanthocephalan from introduced crayfish *Procambarus clarkii* in South Carolina, USA

Gregory K. Rothman¹, Kristina M. Hill-Spanik², Graham A. Wagner¹, Michael R. Kendrick¹, and Isaure de Buron^{*2}

¹Marine Resources Research Institution, SC Department of Natural Resources, Charleston South Carolina; ²Department of Biology, College of Charleston, Charleston, South Carolina; ^{*}presenting the talk

Heterospinus mccordi was described to accommodate cystacanths recovered from the mesentery of red swamp crayfish *Procambarus clarkii* collected in 2023 in South Carolina, i.e., outside their native range. Morphological characteristics of the specimens collected placed them in the family Polymorphidae. However, the presence of two fields of markedly different sized spines on the foretrunk, six cement glands, a digitiform and spinose bursa, and absence of genital spines differentiated them from individuals of currently valid genera in the family. This prompted us to erect a new genus and species, which was supported by our sequencing data (portions of the mitochondrial cytochrome c oxidase I (COI) and large subunit ribosomal RNA genes). Phylogenetically, sequences from our specimens appeared in a clade with those of polymorphids *Hexaglandula corynosoma* and *Ibirhynchus dimorpha*, but were 27% divergent from both using the COI marker. This is the first record of polymorphids infecting *P. clarkii* outside of its native range; its definitive host is unknown and whether this acanthocephalan was introduced in South Carolina along with its crayfish host also remains unknown.

24. The diversity and ecology of freshwater snail-helminth relationships in Alabama: a summary of 10-years of data

Lori R. Tolley-Jordan^{*}

Department of Biology, College of Arts and Sciences, Jacksonville State University, 700 Pelham Rd. N., Jacksonville, Alabama.

Although snails are known hosts or associates of a diverse range of helminths, reports on these relationships in freshwater systems of Alabama are rare. Here, I summarize results from surveys and ecological studies of snails and their helminth associates conducted with students over the past 10 years. At least 15 lineages of digenetic trematodes, unidentified nematodes, one group of annelids (Naididae: *Chaetogaster* spp.), and a single specimen of Apistogastridae sp. were recovered from 17 snail species collected from 38 streams in seven river basins. All snail species were infected with at least one trematode taxon, 10 species harbored nematodes, and seven species were found with *Chaetogaster* spp. In general, the co-occurrence of multiple helminth taxa within a single snail was rare. Also, 1 to 4 helminth taxa would infect a single snail species from a single locality with prevalence ranging from 1% to 50 %, although parasite communities and prevalence changed through time. Ecological studies showed that parasitized and non-parasitized snails occupied similar habitats. However, the proportion of infected snails was substantially lower most likely leading to skewed results. Ongoing research using δ^{15} Nitrogen and δ^{13} Carbon stable isotopes to study interactions between trematodes and their snail hosts suggests that both groups occupy similar trophic levels although nutrient uptake differs between uninfected and infected snails. These efforts, combined with inter-institutional collaboration and student engagement, are needed to describe the diversity, distributions, and interactions of helminths and freshwater snails in Alabama.

25. A new species of *Huffmanella* Moravec, 1987 (Nematoda: Trichosomoididae) infecting the buccal cavity of smalltooth sawfish, *Pristis pectinata* Latham, 1794 (Rhinopristiformes: Pristidae) from Cudjoe Key, Florida

Steven P. Ksepka^{*1}, Micah B. Warren¹, Micah D. Bakenhaster², and Stephen A. Bullard¹

¹*Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, 559 Devall Drive, Auburn, Alabama;* ²*Fish and Wildlife Institute, Florida Fish and Wildlife Conservation Commission, 100 8th Ave SE, St. Petersburg, Florida.*

A new species of *Huffmanella* Moravec, 1987 (Nematoda: Trichosomoididae) is described from the buccal cavity of smalltooth sawfish, *Pristis pectinata* Latham, 1794 (Rhinopristiformes: Pristidae) from Cudjoe Key, Florida, United States. We diagnose the new species as: egg ellipsoid, 63.0–68.0 (mean \pm SD = 64.5 ± 1.5 ; N = 30) long with protruding polar plug, 55.0–60.0 (56.8 ± 1.5 ; 30) long without protruding polar plug, 37.0–40.0 (38.6 ± 1.1 ; 30) wide; eggshell 6.0–8.0 (6.4 ± 0.6 ; 30) thick; polar plugs protruding, 6.0–9.0 (8.1 ± 0.9 ; 30) long and 7.0–9.0 (7.9 ± 0.6 ; 30) wide. The new species differs from all congeners by egg size, polar plug size, and eggshell thickness, and is morphologically most similar to *Huffmanella selachii* Al-Sabi, Ibrahim Al-Hazib, Al-Jabr, Al-Shubaythi, and Huffman, 2022, infecting great hammerhead shark, *Sphyrna mokarran* (Ruppel, 1837) (Carcharhiniformes: Sphyrnidae) in the Arabian Gulf. The new species differs from *H. selachii* by having a shorter egg (55.0–60.0 [56.8] vs. 62.8–85.3 [75.2]). A phylogenetic analysis of the small subunit ribosomal DNA recovered the new species sister to *Huffmanella markgracei* Ruiz and Bullard, 2013 and *Huffmanella* sp. ON838246 that infect Atlantic sharpnose shark, *Rhizoprionodon terraenovae* (Richardson, 1836) (Carcharhiniformes: Carcharhinidae) and blacktip shark, *Carcharhinus limbatus* (Valenciennes, 1839) (Carcharhiniformes: Carcharhinidae), respectively. Histological sections of infected skin revealed eggs in the epithelium between denticles. The new species comprises the fifth reported from elasmobranch and the first reported from a rhinopristiform.

26. Shooting for the moon: Using environmental DNA metabarcoding to capture parasite diversity during a ParasiteBlitz

Kristina M. Hill-Spanik^{*1}, Dakeishla M. Díaz-Morales^{2,3}, Stephen D. Atkinson⁴, Simona Georgieva⁵, Nikol Kmentová^{6,7}, Maarten M.P. Vanhove⁶, Bernd Sures², Edward W. Davis, II⁴, Robin Schütz², and Isuare de Buron¹

¹*College of Charleston, Charleston, South Carolina;* ²*University of Duisburg-Essen, Essen, Germany;* ³*University of Washington, Seattle, Washington;* ⁴*Oregon State University, Corvallis, Oregon;* ⁵*Bulgarian Academy of Sciences, Sofia, Bulgaria;* ⁶*Hasselt University, Diepenbeek, Belgium;* ⁷*Royal Belgian Institute of Natural Sciences, Brussels, Belgium.*

Environmental DNA (eDNA) metabarcoding effectively and efficiently assesses biodiversity but has lagged in parasite community assessments, partially because the development of universal parasite primers is precluded as parasites span multiple phyla and often have free-living sister taxa. We implemented eDNA metabarcoding to examine parasite diversity in sediment and water from four habitats (wetland, freshwater pond, brackish impoundment, tidal creek) in coastal South Carolina as part of a ParasiteBlitz in April 2023. Sediment was collected using syringe corers, and water samples using active filtration and passive collection via deployment and recovery of filter membranes. Five amplicon libraries were produced using primers targeting the COI mtDNA of platyhelminthes, and 18S rDNA of nematodes, myxozoans, microsporidians, and protists. We identified >1,000 parasite amplicon sequence variants (ASVs) from six phyla, with each sampling method yielding unique ASVs. Most diversity was observed among the microsporidians (735 ASVs), whose assay demonstrated the highest fidelity. Actively-filtered water samples captured ASVs of all six phyla, whereas sediment only captured four, despite yielding 3 \times as many ASVs; low DNA yields from passive water samples resulted in fewer ASVs representing only three phyla. Some parasite groups known to be present (e.g., leeches) were not detected. Compared to traditional methods also used during this ParasiteBlitz, our results demonstrate the usefulness, productivity, and feasibility of eDNA

metabarcoding for assessing parasite diversity more exhaustively. Results also highlight the critical need for more comprehensive sequence databases, and the development of specific primers for those parasite taxa for which there are no available genetic markers.

27. Morphological and molecular evidence of multiple *Orchidasma* spp. in loggerhead and Kemp's ridley sea turtles

T. Graham Rosser^{*1,4}, Aiden Meaux^{2,4}, Ethan T. Woodyard², Justin M.² Stilwell, Bradley M. Richardson³, Logan R. S. Robison¹, Jill B. Hudnall^{2,4}, Kaylin McNulty^{2,4}, Jonah A. Nguyen¹, Divya Rose², Debra Moore^{2,4}, Beth Peterman^{2,4}, Stephen R. Reichley^{2,4}, Mark L. Lawrence^{2,4}

¹Department of Comparative Biomedical Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi; ²Department of Pathobiology and Population Medicine, College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi; ³Warmwater Aquaculture Research Unit, United States Department of Agriculture, Agricultural Research Service, Stoneville, Mississippi; ⁴Global Center for Aquatic Health and Food Security, Mississippi State University, Mississippi State, Mississippi.

The seven extant sea turtle species span a cosmopolitan distribution in tropical and temperate waters. Parasitological studies of sea turtles are rich and date back almost two centuries! Most are single species taxonomic descriptions, new geographic records, or clinical case studies documenting pathology or associated mortality. Opportunistic sampling of gastrointestinal tissues was performed during the necropsy cold-stunned loggerhead *Caretta caretta*, green *Chelonia mydas*, and Kemp's ridley *Lepidochelys kempii* sea turtles. Gastrointestinal tissues were screened for parasites, helminths were relaxed and preserved in 70% molecular biology grade ethanol for molecular and morphological characterization. *Orchidasma* is a cosmopolitan and monotypic genus of endoparasitic trematode within the family Telorchidae originally described in 1899. Adult *Orchidasma amphiorchis* identified tentatively based on morphology were recovered from the small intestine of loggerhead and Kemp's ridley sea turtles. Molecular data clarified the presence of an overlooked separate species based on pairwise distance comparisons of partial mitochondrial cytochrome c oxidase subunit 1 gene data. Further examination of stained and mounted holocephalophores and subsequent molecular analysis revealed a second *Orchidasma* sp. This novel species has been misattributed to *O. amphiorchis* in published descriptions from the Western hemisphere. Phylogenetic analyses of partial ribosomal 28S rDNA suggests systematic revision of the genus and removal from the family Telorchidae. These data will be useful in the specific identification of trematode larval stages as they are identified in intermediate hosts when encountered and sequenced.

28. Preliminary investigation of the relationship between gastrointestinal microbiota and parasitism in the North American raccoon (*Procyon lotor*)

Alivia Elkins^{*1}, Matthew Kolp², and Kathryn E. Purple¹

¹Lincoln Memorial University, Harrogate, Tennessee; ²Lincoln Memorial University College of Veterinary Medicine, Harrogate, Tennessee.

Microbial symbionts in the gastrointestinal tract, from mutualistic bacteria to parasitic helminths, may have significant impacts on host health and fitness. However, the interactions between parasites and gut microbiome diversity within the host are unknown. We necropsied 4 North American raccoons (*Procyon lotor*) and extracted DNA from ingesta samples, which was then submitted for 16S microbiome sequencing. We also identified the presence of gastrointestinal helminths by gross examination of the GI tract for adult parasites and fecal flotation to observe parasite eggs. Three raccoons tested positive for parasites either by gross necropsy, fecal flotation, or both. No parasites were detected in 1 racoon. We compared species richness and diversity of the gut microbiome in parasitized versus non-parasitized hosts. We found no significant difference between Chao1 species richness, inverse Simpson diversity index, or Shannon diversity index between the parasitized raccoons (n=3) and the non-parasitized raccoon (n=1). Although these preliminary results did not uncover any relationship in

our small sample, parasitism in other animals has been shown to influence gut microbiomes either by affecting the host immune system or through direct interactions in the GI tract. We are expanding sample size with an additional 6 raccoons and 9 Virginia opossums (*Didelphis virginiana*) to further explore this question.

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

Stephen A. Bullard and Haley R. Dutton

Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, Alabama.

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

POSTER PRESENTATION ABSTRACTS

P1. Helminth survey of Virginia opossums (*Didelphis virginiana*) from central Illinois with temporal and regional comparisons.

Alexa A. Howard* and Elliot A. Ziemann

Eastern Illinois University, Charleston, Illinois.

This study aims to update prevalence, diversity, and abundance data on the helminths of the Virginia opossum (*Didelphis virginiana*) in central Illinois and compare findings to past opossum helminth surveys from the region to update the opossum's potential to spread disease and to track changes in their assemblages over time. Twenty-two opossum necropsies included dissection of internal organs, flushing of gastrointestinal contents, and inspection for parasites. The prevalences for each parasite taxa are as follows: acanthocephalans (4.5%), cestodes (22.7%), nematodes (100%), and trematodes (22.7%). Nematodes were the most prominent taxon, with the two most abundant species being *Cruzia americana* (prevalence = 72.7%, intensity = 1-748, mean intensity = 199.11) and *Turgida turgida* (prevalence = 95.4%, intensity = 8-427, mean intensity = 156.9). Chi-square tests for independence indicated significant differences in prevalences between this study and an opossum helminth survey in Illinois from 1995 for *Turgida turgida* in the stomach, *Viannaia* spp. in the small intestines, *Cruzia americana* in the large intestines, and *Brachylaimus virginianum* in the small intestines ($p < 0.05$), while *Oligacanthorhynchus tortuosa* did not significantly differ between studies ($p = 0.089$). Notably, helminths not found in Southern Illinois in 1995 but found in this study included *Viannaia* spp. (prevalence=18.2%), *Trichurus* spp. (prevalence = 9.09%), and a *Diplostomum* spp., (prevalence = 4.54%). Because there is a temporal gap in opossum helminth surveys in the region, this study will be important by documenting changes in helminth assemblages which are already evident based on the significant changes found in helminth prevalences since 1995.

P2. Ancient flea diversification and the Gondwanan land bridges

Wade M. Burris* and Bryan S. McLean

University of North Carolina, Greensboro, North Carolina.

Fleas (Order Siphonaptera) are believed to have originated in the southern half of Pangea (Gondwana), diverging from their free-living arthropod ancestors during the late Cretaceous period. Subsequent diversification of the major groups of fleas during the breakup of Gondwana are thought to have followed the movements and diversification of their early mammalian hosts, specifically marsupials. One major unanswered question in flea evolution surrounds the superfamily Pygiopsylloidea, which is represented by a single Neotropical genus (*Ctenidiosomus*) and 39 other genera confined to the Australian, Oriental, and Ethiopian faunal regions. The position of *Ctenidiosomus* within Pygiopsylloidea is based on shared morphological homologies considered to be diagnostic of this group but has never been supported using genetic data. This project leverages genome sequencing and phylogenetic analyses to reconstruct the evolutionary lineage of pygiopsyllid fleas and infer the relationship between Old and New World members of this group. It also tests the biogeographical hypothesis that some ancestral pygiopsyllid fleas dispersed between Australia and South America across the Gondwanan land bridge around the time of the K-Pg extinction event, effectively hitching a ride on their marsupial hosts. Dating analyses will be used to establish a chronology for isolation in South America and subsequent diversification into the nine extant species that form the modern genus *Ctenidiosomus*.

P3. Investigating pH and serine protease dynamics in the *Ctenocephalides felis* midgut: Implications for pathogen transmission

Piper N. Zellner*¹ and Lisa D. Brown²

Georgia Southern University, Statesboro, Georgia.

Cat fleas (*Ctenocephalides felis*) are holometabolous insect vectors that contribute to pathogen transmission from animals to humans. During ingestion, the gut environment acts as

the first location of pathogen-vector interactions, which influences the outcome of the infection. Serine proteases, enzymes that play a crucial role in the digestive process, are essential for breaking down proteins and other nutrients in the bloodmeal. This enzymatic activity significantly impacts the pH levels in the gut, as the breakdown of blood releases various acidic or basic byproducts. Given that these proteases are a key component of digestion, understanding their concentration and the pH dynamics within the midgut is essential for assessing how digestion occurs in this species. It has been observed that a pH of 6.0-7.0 is the typical range in an unfed flea gut; however, digestion of blood meal is achieved by serine proteases, which have a pH optimum in the alkaline range. Thus, we aimed to measure the pH and the concentration of serine proteases (trypsin and chymotrypsin) over 48 hours after blood meal ingestion. We hypothesize that the pH will become more alkaline, and the highest concentration of trypsin and chymotrypsin will be present during the first 24 hours post-feeding. After three hours, flea guts were dissected at hours 0, 6, 24, 30, and 48 post-feeding. At each time point, we measured the pH and concentration of trypsin and chymotrypsin using colorimetric and fluorometric kits, respectively. In summary, the results of this project provide a better understanding of how flea gut pH and the enzymes responsible for digesting blood change over time after feeding, which may influence the transmission of flea-borne pathogens.

P4. Parasite assemblages in bluntnose minnow (*Pimephales notatus*): Patterns, prevalence, and ecological implications in Illinois creeks

Alam Rowshan *, Elliott Zieman, and Robert E. Colombo
Eastern Illinois University, Charleston, Illinois.

Freshwater environments, particularly creeks, support a rich community of fish, intermediate hosts, and parasites. This study examined the diversity, incidence, and distribution of parasites infecting bluntnose minnows (*Pimephales notatus*) in various creeks in Illinois, USA. A total of 520 fish from 16 sites were dissected, and the body surface, gills, and internal organs were examined for parasites using a stereomicroscope. The parasites were identified to major taxonomic groups (Nematode, Cestode, Trematode). Microscopy and molecular analysis will be conducted in the future for more specific identification. Preliminary data showed that parasite prevalence differed across the creeks. The highest prevalence (100%) was found in Kickapoo, and the lowest was from BPJ A (48%). The parasite prevalence in external, gills, stomach, and intestine were 93.52%, 1.8%, 65.6%, and 47.11%, respectively. Furthermore, the parasite prevalence is also influenced by other physical parameters such as sex, length, and body weight. This demonstrates that these factors confound fish parasite community assemblages. The correlation analysis indicates that sex does not significantly affect parasite prevalence in different organs ($r=0.086$). Total length is positively correlated with parasite prevalence ($r=0.253$). The length and weight of fish significantly affect parasite prevalence ($P<0.001$), but the sex has no significant effect ($P>0.05$) on the total parasite prevalence of bluntnose minnows. This study sheds light on the ecology of fish parasites in Illinois creek ecosystems, explaining their variety, distribution patterns, and ecological interactions. Understanding the dynamics of fish-parasite interactions is critical for effective fisheries management, conservation, and ecological integrity in Illinois creek systems.

P5. Improving the systematics of the tick subgenus *Scaphixodes* of the genus *Ixodes* (Acari: Ixodidae)

Laila I. Richards^{*1}, Dmitry A. Apanaskevich^{1,2}, and Stephen E. Greiman¹

¹Georgia Southern University, Statesboro, Georgia; ²United States National Tick Collection, Institute for Coastal Plain Science, Georgia Southern University, Statesboro, Georgia.

Despite parasites' interactions with virtually all organisms and their role as vectors for disease transmission they are widely understudied. Ticks are ectoparasites of terrestrial vertebrates that mostly live outside their host and have wide geographic ranges. Understanding the phylogeny of this group of organisms is a critical step in bridging the current gap in knowledge about tick systematics. Species of the subgenus *Scaphixodes* in the genus *Ixodes*

are primarily found on various birds in the Palearctic and Nearctic Regions. Ticks categorized as *Scaphixodes* are especially unknown given that their ranges are relatively remote and there are very limited studies on the subgenus as a whole. This study aims to find the phylogenetic position of this subgenus and identify synapomorphies that define it. This was achieved through morphological assessments of the features of adult female ticks currently classified as *Scaphixodes*. Morphological assessment was supplemented with genetic sequence data to determine phylogenetic relationships between the tick species. This study found clear morphological synapomorphies that in conjunction with genomic data provide us with the evidence that two species currently categorized as *Scaphixodes* are misplaced and belong outside of the subgenus.

P6. Comparative analysis of parasite communities within native and invasive gastropods in central Florida

Mara N. Taylor* and Kaitlin A. Gallagher

Florida Southern College, Lakeland, Florida.

Pomacea maculata is an invasive gastropod species that has spread across the Southeastern United States within the last 40 years. While great efforts have gone into determining the snail's impacts on free-living ecosystems, little has been done to examine the potential impacts on parasite communities. We are currently attempting to fill this gap by characterizing the internal parasite communities of *Pomacea maculata* and several native snail species, including *Pomacea paludosa*. We hypothesized that the native snails would have a more abundant and diverse parasite community compared to their invasive counterparts. We have collected 118 snails to date: 61 *Pomacea maculata*, 9 *Pomacea paludosa*, 34 *Planorbella trivolvis*, and 12 snails of indeterminate species. Of these, 22 snails (18.6%) contained one or more parasites, and all 22 snails were native *Planorbella* species. This both affirms and contradicts our hypothesis since there is increased prevalence within native snails, but the entirety of this prevalence is within *Planorbella*. This may indicate a resistance within *Pomacea* against the parasites in this area. Among the members of *P. trivolvis*, 20 (58%) were found to be infected with one or more parasites. Approximately 75% of infected individuals were infected with trematodes and 5.8% were infected by nematodes. For the remainder of this project, we aim to use genetic analysis to determine exact species identities of hosts and parasites, and gather more samples for necropsy to ensure the statistical significance of our work.

P7. Cataloging gastrointestinal Helminths of the Virginia opossum (*Didelphis virginiana*)

Aiden W. Jones* and Kathryn Purple

Lincoln Memorial University, Harrogate, Tennessee.

The Virginia opossum (*Didelphis virginiana*) is a widespread North American marsupial that helps control pests. However, their proximity to human and domestic animal populations increases the potential for parasite transmission. While opossums host various helminths, a comprehensive catalogue of their gastrointestinal parasites is lacking. This study aims to identify species present, determine their prevalence, and develop an identification key for future parasitological research. We necropsied 11 roadkilled opossums collected along a 50-mile route from suburban Knoxville to rural Harrogate, Tennessee. Helminths were preserved in 70–80% ethanol for morphological identification, and fecal flotations were conducted to detect ova and parasites. All opossums (11/11) harbored parasites distal to the duodenum, and 63.6% (7/11) had stomach worms. Microscopic analysis identified at least five helminth species, including zoonotic *Ancylostoma caninum*, the canid whipworm *Trichuris vulpis*, and opossum-specific *Turgida turgida* and *Cruzia americana*. While most were host-specific, some could impact domestic animals and humans. The absence of resources on opossum parasites hinders research and diagnostics. Understanding these parasites' ecological roles and health effects will enhance identification and management efforts. Our findings contribute to a One Health perspective, emphasizing the importance of studying wildlife parasites to assess their broader ecological and public health impacts.

P8. Investigating infection by a recently discovered acanthocephalan, *Heterospinus mccordi* in crayfish of South Carolina

Annie N. Chowansky*¹; Riley D. Cudahy¹; Gregory K. Rothman²; Michael R. Kendrick², and Isaure de Buron¹

¹Department of Biology, College of Charleston, Charleston, South Carolina; ²Marine Resources Research Institute, South Carolina Department of Natural resources, Charleston, South Carolina.

South Carolina (SC) is home to 38 native crayfish species across six genera and two non-native species including the Louisiana red swamp crayfish, *Procambarus clarkii*. Native to the gulf coastal plain, *P. clarkii* was introduced to SC in the 1970's and has since established populations across the state. While *P. clarkii* is known to host acanthocephalans in its native range, SC individuals have been found infected by cystacanths of *Heterospinus mccordi*; a recently described species only reported from *P. clarkii* in SC, making the origin of this parasite unclear. The goal of this project was to investigate if native species of crayfish from SC were also infected with this acanthocephalan, which could then illustrate a case of spillover into *P. clarkii*. Crayfish specimens across several species of the genera *Cambarus* and *Procambarus* were collected from localities across the state of SC from May 2019 to September 2024 and stored at -20C. Individuals were thawed, sexed, measured and weighed, and a piece of their gills was fixed in ethanol for later molecular identification. Over 50 crayfish were examined. Overall, very few crayfish (~5%) showed any parasitic infection. Several types of parasites were encountered in the gills (ostracods), muscle (nematodes, digenean metacercariae, *Psorospermium* sp.), and/or the intestine (nematodes). However, no acanthocephalan was encountered in any individual, suggesting that *Heterospinus mccordi* is specific for *P. clarkii* and that it was potentially introduced to South Carolina along with its non-native host. Further investigation of other native crayfish species is needed to verify this hypothesis.

P9. Cestode diversity of *Sorex* shrews (Eulipotyphla: Soricidae) from Mongolia

Rokeya Ahmed*¹; Bryan S. McLean²; Joseph A. Cook³; Kurt E. Galbreath⁴; Timothy J. Odom⁵; Stephen E. Greiman⁶

¹Department of Environmental Science, Box-30460, Georgia Southern University Statesboro, Georgia; ²Department of Biology, University of North Carolina Greensboro, 321 McIver St., Greensboro, North Carolina; ³Museum of Southwestern Biology, Department of Biology, MSC03 2020, University of New Mexico, Albuquerque, New Mexico; ⁴Department of Biology, Northern Michigan University, Marquette, Michigan; ⁵Odum School of Ecology, University of Georgia, 140 E. Green St., Athens, Georgia; ⁶Department of Biology, Box-30460, Georgia Southern University Statesboro, Georgia.

Shrews (Eulipotyphla: Soricidae), insectivorous small mammals, serve as definitive hosts for a diversity of cestode species, yet soricid parasites remain understudied. Mongolia is currently facing extensive anthropogenic change, which threatens its distinctive ecosystems. To establish foundational data regarding shrew parasite diversity, we collected a total of 121 shrews (55 *Sorex roboratus* and 66 *Sorex tundrensis*) in the summers of 2015, 2016, and 2022 from 7 major sites distributed across Mongolia and identified 16 unique cestode species within 12 genera. Phylogenies based on complete mitochondrial genomes of each cestode species provide new insights into their evolutionary histories. Elements of metacommunity structure (EMS) revealed coherent, dynamic cestode metacommunities with parasite species replacement occurring between localities as well as host species. Boosted regression trees indicate that locality and host (shrew) weight have the greatest relative influence on parasite community structure, likely attributable to differences in host species occupancy and average body size of infected shrews.

P10. Effects of an introduced seaweed on *Vibrio* spp. densities in eastern oysters

Emma M. Mathew* and Erik E. Sotka

College of Charleston, Charleston, South Carolina.

Invasive species are often studied with focus on their impact on macro-organisms, but less is known about their impacts on microbial communities and dynamics. *Gracilaria vermiculophylla* is an invasive red seaweed that has thrived in South Carolina's intertidal mudflats since the early 2000s. Previous work found that bacterial densities found in sediment directly under live *Gracilaria* patches (approximately 300 WM per m²) were almost double relative to densities on bare sediment approximately 50cm away. Considering this recorded relationship, our focus shifted to densities of the gram-negative bacteria *Vibrio* spp. found in Eastern Oyster (*Crassostrea virginica*) tissue as they are often found within the same intertidal habitat as this invasive seaweed. Utilizing a week-long field manipulative experiment during the summer of 2024, when bacterial growth is historically at its peak, we measured 1) total *Vibrio* density and 2) Specific *Vibrio* species density within oyster tissue in presence and absence of *Gracilaria* at two sites on the Ft. Johnson intertidal mudflat. For each sample, bacteria densities and species identification was measured with use of TCBS and CHROMagar culture media in-lab with specific focus on identifying epithets known to cause concern for human health when consumed at high densities. We found no significant effect of *G. vermiculophylla* presence on *Vibrio* density. However, a site specific difference was recorded which allows us to consider alternative factors that may drive bacteria growth. With this conclusion, water quality, environmental differences, and a broader analysis of microbial dynamics may be a focus of future related research.

P11. Infection induced foraging suppression mediates macroparasite interactions across a salamander hybrid zone

Grace P. Mason^{*1} and Timothy L. Odom^{1,2}

¹Odum School of Ecology, University of Georgia, Athens, Georgia; ²Center for the Ecology of Infectious Diseases, University of Georgia, Athens, Georgia.

Macroparasite infections can trigger neurochemical changes that influence host behavior. Specifically, co-infection may alter foraging efforts depending on parasite species richness and infection intensity. We hypothesized that high intensity of *Cepedietta* found in the gastrointestinal tract results in lower foraging rates due to lethargy, anemia, or host stress among *Plethodon* salamanders. To test this, we dissected a total of 139 *Plethodon* salamanders from natural history collections at The University of Georgia, including *P. teyahalee*, *P. shermani*, and hybrid individuals of the two species. Within these hosts, we quantified gut fullness and categorized guts as being either "full", "half full", or "empty". In addition, we identified the parasite genera that were found in the gastrointestinal tract and recorded the infection intensity. Our analysis revealed that a higher *Cepedietta* infection is correlated with reduced volumes of prey items in the GI tract of infected salamanders, suggesting reduced foraging success. However, this pattern was not present in hybrid *Plethodon*. These hosts experience ecologically distinct habitats associated with differences in precipitation and temperature that transform along an elevational gradient. This may result in idiosyncratic parasite interactions between the nematode *Cosmocercoides* and *Cepedietta* across the hybrid zone. Our findings suggest that *Cepedietta* may benefit from enemy release from competitor parasites through reducing foraging success, and consequently parasite exposure, in *P. teyahalee*. Future work should seek to tease apart the interconnectedness of host and environmental traits as they relate to parasite co-infection patterns in this study system.

P12. Diversity and interrelationships of diplostomids (Digenea: Diplostomoidea) parasitic in kingfishers

Maggie A. Young^{1*}, Tyler J. Achatz¹, Jeffrey A. Bell², Stephen E. Greiman³, Eric E. Pulis⁴, Simona Georgieva⁵, and Vasyl V. Tkach²

¹Middle Georgia State University, Macon, Georgia; ²University of North Dakota, Grand Forks, North Dakota; ³Georgia Southern University, Statesboro, Georgia; ⁴Northern State University, Aberdeen, South Dakota; ⁵Bulgarian Academy of Sciences, Sofia, Bulgaria.

Kingfishers are definitive hosts to a diversity of digeneans that use fish as second intermediate hosts. Many of these digeneans belong to the family Diplostomidae. Their larvae are a well-known cause of fish health problems throughout the world, including "black spot disease". While most prior studies have focused on larval stages, a few have examined adult stages from kingfishers. We provide a summary of recent taxonomic and systematic discoveries based primarily on adult stages of these kingfisher digeneans. The material discussed includes members of 11 genera (9 exclusively in kingfishers) from 5 continents. The combination of morphological and molecular data allowed the description of several new genera and species from around the world. Molecular phylogenies suggest multiple evolutionary host switches of diplostomids from other hosts to kingfishers, including the formation of one highly diverse clade, as well as multiple dispersal events between continents.

P13. Initial detection of rat lungworm, a human pathogen, in invasive snails in Georgia

Caley H. Chun ^{*1}, Maggie A. Young¹, Jim Page², Matthew Rowe², Caroline Cox², Laura Wenk², Vasyi V. Tkach³, and Tyler J. Achatz¹

¹Middle Georgia State University, Macon, Georgia; ²Wildlife Resources Division, Georgia Department of Natural Resources, Atlanta, Georgia; ³University of North Dakota, Grand Forks, North Dakota.

Rat lungworm, *Angiostrongylus cantonensis*, is an invasive nematode that naturally parasitizes rodents, primarily rats. A variety of gastropod mollusks act as the required intermediate host of rat lungworm, including invasive apple snails (*Pomacea maculata*) and mystery snails (*Heterogen japonica*). Freshwater crustaceans may serve as paratenic hosts. In some cases, infective nematode larvae may be found on vegetation exposed to water with infected snails. When infected snails or paratenic hosts are ingested by rats, the larvae reach brain where they mature into adults and then migrate to the lungs. Other mammals, as well as some bird species, may be accidentally infected if they ingest the nematode larvae. In humans, rat lungworm can cause severe pathology (including meningitis) or death. Only one study previously reported rat lungworm in Georgia only in rats collected in the Atlanta Zoo. In the present study, we collected invasive apple and mystery snails from 8 sites across the state of Georgia. Snails were euthanized, necropsied and examined for rat lungworm. Collected nematodes were used for molecular screening. Based on data in GenBank, we sequenced a fragment of the cytochrome c oxidase subunit I (cox1) mtDNA gene. We identified rat lungworm from 5 sites, however, prevalence of these nematodes was extremely low (0.5–18.9% of snails per site). Based on our data, it is clear that rat lungworm is already broadly distributed throughout Georgia. Efforts should be taken to help mitigate potential public health risks associated with this invasive pathogen.

P14. Host size and parasite burden in freshwater fish in Georgia

Cassie Ellenberger*, Jade Salis, Nick Tsangarides, Whitney C. Preisser
Kennesaw State University, Kennesaw, Georgia.

Parasite burdens vary due to a variety of factors, including both host- (e.g., age, size, and immunocompetency) and environmental-related factors (e.g., precipitation, temperature, and human disturbance). While previous studies have found that, in general, parasite burdens tend to increase with body size, we do not know if this holds true for every fish species or only for certain fish species (e.g., species that can attain larger body sizes, etc.). To address these gaps in our knowledge, we investigated how parasite burdens varied with host size in freshwater fish in Georgia. Using ~400 fluid-preserved fish specimens from Kennesaw State University's Mountains-to-Metro Biodiversity collection, we measured and dissected each fish and collected their parasites. Using linear models, we correlated fish length with parasite abundance for multiple species. Preliminary results will be discussed.

P15. Parasite load and body size in three genera of salamanders in Georgia

Evan C. Johnson* and Whitney C. Preisser

Kennesaw State University, Kennesaw, Georgia.

Salamanders are extremely diverse in the southeastern United States, and Georgia is home to over 55 species of salamanders. However, we know very little about their parasites. In this study, we necropsied 106 fluid-preserved salamanders from 13 species from the KSU and UGA herpetology collections and collected their parasites. We used a generalized linear model to analyze the relationship between standard length and parasite abundance. We found that different salamander genera demonstrated different relationships between length and abundance. With this research, we can shed light on the biodiversity of parasites and elucidate some of the factors influencing host-parasite interactions and the distribution of parasitic diseases across salamander species.

P16. Dogs traveling internationally transport *Dirofilaria* spp. from endemic regions

Theresa A. Quintana^{*1}, Breck Aguinaga², Guwin Nilaweera², Jessica Mitchell^{1,2,3}, Grace Schieferecke², Janine Seetahal^{2,3}, and Jeba J.R. Jesudoss Chelladurai¹

¹Auburn University, Auburn, Alabama; ²Kansas State University, Manhattan, Kansas; ³Kansas State Veterinary Diagnostic Laboratory (KSVDL), Manhattan, Kansas.

Dirofilaria spp. are parasitic filarial nematodes endemic worldwide that infect dogs but also cause human dirofilariasis. Traveling dogs serve as carriers of *Dirofilaria* spp. and other zoonotic parasites, introducing them to new regions, but the risk of importation from known endemic areas, is unknown. In this study, we aimed to determine if traveling dogs are infected with *Dirofilaria* spp. from Central & South American countries. Canine sera were obtained from 34 Central and South America countries between September 2022 and December 2023 from the KSVDL biobank. Samples were sorted by country and pooled. Pool sizes were optimized based on recorded prevalence in each country using EPITOOLS. We validated the accuracy of the DiroCHEK ELISA assay (Zoetis) for pooled sampling. Pooled samples were tested for *D. immitis* and cross-reactive nematodes, with and without heat treatment to disassociate immune complexes. Spectrophotometry was used to quantify the ELISA reactions colorimetrically. We determined the ELISA-cutoff for different spectrophotometric wavelengths (490, 620, or 650 nm) with ROC curves. We observed that 50 heat-treated pools and 11 unheated pools were positive. Individuals in positive pools were then re-tested. Pooled and individual prevalence estimates were calculated for each country. These findings provide evidence that traveling dogs are carrying *D. immitis* across the globe, increasing the risk of introduction to new areas or new parasite genetics to endemic areas. Our study supports re-evaluating current U.S. and global canine importation laws to address the gap in controlling the entry and spread of *Dirofilaria* spp. and cross-reactive parasitic nematodes.

P17. Parasites across time: The impact of environmental change on monogenean abundance.

Imani J. Jones^{*1}, Desmond Boyd², Gabriella Commisso³, Shyanne Christner⁴, Katie L. Leslie³, Jolee Thirtyacre³, Conner Whalen³, Armand A. Kuris⁵, Justin Mann⁶, Hank L. Bart⁶, Daki Diaz-Morales³, Chealsea L. Wood³, M. Egnin¹, and O. Idehen¹

¹Dep. of Agricultural Sciences and the Plant Biotech & Genomics Research Lab, Tuskegee, Alabama; ²University of South Carolina, Columbia, South Carolina; ³School of Aquatic and Fishery Sciences, University of Washington, Seattle, Washington; ⁴Valdosta State University, Valdosta, Georgia; ⁵UC Santa Barbara, Santa Barbara, California; ⁶Department of Ecology and Evolutionary Biology, Tulane University, New Orleans, Louisiana.

The Pearl River in Louisiana has been historically influenced by multiple stressors like warming and pulp-mill effluent, potentially impacting parasite abundance. Monogeneans are ectoparasitic on fish gills and have a direct life cycle placing them as ideal models to understand biological responses to environmental change. Thus, we aimed to address whether environmental change influences monogenean abundance over time. We expected monogenean abundance to change linearly or in a downward bell-shaped curve with time, and pollution to interact synergistically or antagonistically with time. To answer this, fish species

including *Ictalurus punctatus*, *Pimephales vigilax*, and *Notropis atherinoides* were seined annually throughout five decades (1963-2005) and preserved at the Tulane University Biodiversity Research Institute. Fish were dissected and examined for monogeneans. Monogeneans were identified to the lowest possible taxonomic level, and their abundance was analyzed in response to time, pollution, and their interaction using generalized linear mixed models. Three different monogenean genera were identified: *Dactylogyrus* spp. infecting *Pimephales vigilax* and *Notropis atherinoides*; *Gyrodactylus* spp. infecting *P. vigilax*, and *Ligictaluridus pricei* infecting *Ictalurus punctatus*. The abundance of *Dactylogyrus* spp. infecting *P. vigilax* increased linearly with time. *L. pricei* infecting *I. punctatus* had a non-linear change in abundance over time. Pollution did not have a single or interactive effect on parasite abundance. The historical genus-specific change of monogenean abundance offers insights relevant to fish health and aquatic ecology in a changing world.

SSP CONDUCT POLICY

Statement of Policy

The Southeastern Society of Parasitologists (SSP) will afford an environment free from discrimination, harassment, and retaliation. The SSP will not tolerate actions, statements, or contacts that discourage the free expression and exchange of 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, political affiliation, veteran status, or any other identity. Harassment, sexual or otherwise, shall be considered as a form of misconduct and violators will be subject to disciplinary actions, including, but not limited to, 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 that are not consensual. It refers to behavior that is not welcome, is personally offensive, creates an unsafe environment, 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. Individuals may be reluctant to outwardly express objections or discomfort regarding unwelcome behavior or language; therefore, it is recommended that all members maintain a high standard of professionalism where peers are treated with respect.

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 officially sanctioned SSP meetings and functions, including social functions, tours, or off-site activities, 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 SSP President or President-Elect (hereon, the Society's designated individuals). This initial contact would not constitute a formal complaint unless the complainant explicitly stated otherwise in writing. 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/s, 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 Society's designated individuals and all involved in the investigation with the exception that the Society designated individual that was initially contacted may confidentially consult with the other Society designated individual and/or SSP Council if deemed necessary by the Society designated individual that was initially contacted. In the event that one of the

society designated individuals is the complainant or respondent, the other society designated individual may confidentially consult with another officer of the Society. Regardless, a complainant may speak in confidence with the Society's designated individuals without involving the respondent, an official report to the Society or investigation by the Society. All complaints that are received will be treated seriously and will be addressed promptly if that is the wish of the complainant. Complainants will be encouraged to report to the police any incidents of sexual assault. Note, however, that many local and regional governments consider a variety of behaviors to be reportable crimes regardless of the wishes of the complainant, respondent, or of the Society and that the Society and its officers will comply, to the best of their knowledge, with any reporting laws.

Should the complainant wish for the Society to initiate a formal investigation into the alleged discrimination, harassment, or misconduct, the complainant should e-mail the society's designated individual and state that they would like to officially report an incident and have the Society launch a formal investigation. The Executive Committee of SSP will be notified by the society's designated individual that a formal complaint has been received and that an investigation will be launched but no additional information, such as the names of complainants or respondents or details of the event, will be disclosed.

Investigation

Following the official report of an incident and the official request of an investigation, the Society's designated individual/s, in consultation with SSP 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 form which the investigator will provide. 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 and/or the investigator 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. Officers would be deemed to have a conflict of interest if they worked at or attended the same institution as the complainant or respondent, were in a romantic relationship with the complainant or respondent, or any other instance in which the majority of the officers or SSP Council agreed that there was a conflict of interest.

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 as such, can be reported (see Reporting an Incident). Offenders found to have retaliated will be subject to disciplinary action, up to and including ejection from the Society.

Disciplinary Action

If an individual is found to have harassed, retaliated, or knowingly made a false claim, they will be subject to disciplinary action. These actions might include a verbal warning, a request to leave the meeting or function without refund of fees, and/or ejected from the SSP.

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 SSP officer or the SSP

designated individual.

Expected Behavior

- Treat all participants with respect and consideration.
- Be considerate, respectful, and collaborative.
- Communicate openly with respect for others, critiquing ideas rather than individuals.
- Avoid personal attacks directed toward others.
- Be mindful of your surroundings and of your fellow participants.
- Respect the rules, policies, and property of the meeting venue and SSP.

Unacceptable Behavior

- Harassment, intimidation or discrimination in any form.
- Physical or verbal abuse.
- Disruption of talks at oral or poster sessions.
- Examples of unacceptable behavior include, but are not limited to, verbal comments related to gender, sexual orientation, disability, physical appearance, body size, race, religion, national origin, inappropriate use of nudity and/or sexual images in public spaces or in presentations, threatening or stalking.