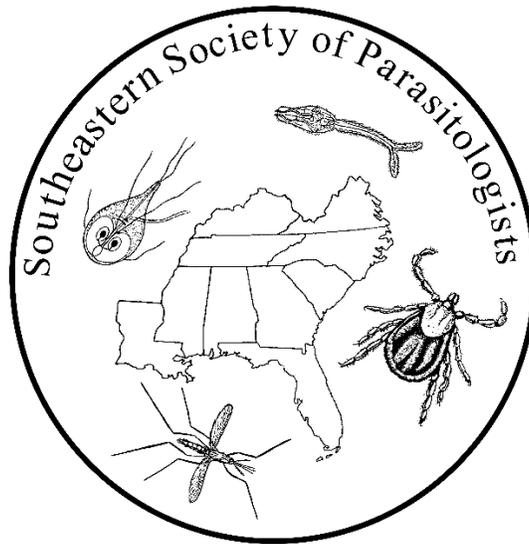


SOUTHEASTERN SOCIETY OF PARASITOLOGISTS

An affiliate of The American Society of Parasitologists

PROGRAM & ABSTRACTS



March 19-21, 2026

Hosted by

The College of Charleston
School of Natural and Environmental Sciences
&
Department of Biology
Charleston, South Carolina

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		1977-80	Robert B. Short	2010-17	Bruce Conn		
		1981-83	Gerald W. Esch	2017-19	Stephen A. Bullard		

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1986	A.B. Weathersby	1996	Sharon Patton	2013	Charles T. Faulkner		

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2019	Madison Barshick & Jarvis Strickland	1982	Steve J. Upton	2000	Michael Barger & Allison K. Witherow	2017	Jackson Roberts
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The SSP 2026 LOC would like to thank:

- Dr. Seth Pritchard, Interim Dean of the School of Natural and Environmental Sciences, College of Charleston
- Dr. Eric McElroy, Chair of the Department of Biology, College of Charleston
- Dr. Tanya Darden, Director of the Marine Resources Research Institute, SC Department of Natural Resources (SCDNR)
- Courtney Wigfall, Kathryn Johnson, and IT staff, SCDNR
- Shelly Brew and Greg Townsley, College of Charleston
- Jack Houk, Julian Houk, and Kevin Spanik for their musical talents!
- Anonymous donors; SC Governor’s Cup Billfishing Series; the Graduate Program in Marine Science, College of Charleston, and our vendors.



2026 Annual Meeting of the Southeastern Society of Parasitologists

March 19-21, 2026

Charleston, SC

PROGRAM SUMMARY

Thursday, March 19

SCDNR Outdoor Classroom

Check-in & late registration	5:00 – 6:00 PM
Social	6:00 – 7:00 PM
Opening remarks and introductions	7:00 – 7:30 PM
Poster session	7:30 – 8:00 PM
Raffle	8:00 PM

Friday, March 20

MRRI Lobby and Auditorium

Light refreshments	7:45 – 8:30 AM
Paper Session I	8:30 – 10:15 AM
Morning Break	10:15 – 10:45 AM
Paper Session II	10:45 AM – 12:15 PM
Lunch (on site)	12:15 – 2:00 PM
Paper Session III	2:00 – 3:45 PM
Afternoon Break	3:45 – 4:15 PM
Paper Session IV	4:15 – 5:45 PM
Student Meet & Greet	5:45 – 6:45 PM

Saturday, March 21

MRRI Lobby and Auditorium

Light refreshments	7:45 – 8:30 AM
Paper Session V	8:30 – 10:00 AM
Morning Break	10:00 – 10:30 AM
Paper Session VI	10:30 – 11:45 AM
SSP Business Meeting	11:45 AM – 12:45 PM
Lunch	12:45 PM

2026 Annual Meeting of the Southeastern Society of Parasitologists

Thursday, March 19, 7:00 – 8:00 PM

SCDNR OUTDOOR CLASSROOM

Presenting author(s) are underlined

OPENING REMARKS, INTRODUCTIONS, AND POSTER SESSION

WELCOME REMARKS AND INTRODUCTIONS

S. Ash Bullard, SSP President

Auburn University, Auburn, AL

P1. GASTROINTESTINAL PARASITES OF GOPHER TORTOISES (*GOPHERUS POLYPHEMUS*) FROM ARCHBOLD BIOLOGICAL STATION, FLORIDA

Barnhill M, Langford GJ

Department of Biology, Florida Southern College, Lakeland, FL, USA

P2. COMPARATIVE ANALYSIS OF ENDOPARASITES IN *OREOCHROMIS AUREUS* AND *LEPOMIS* SPP.: AN INVESTIGATION INTO POTENTIAL SPILLOVER IN LAKE HOLLINGSWORTH, POLK COUNTY, FLORIDA

Delgado C, Gunnison E, Langford GJ

Department of Biology, Florida Southern College, Lakeland, FL, USA

P3. MONOGENEAN PARASITES OF NATIVE BLUEGILL (*LEPOMIS MACHROCHIRUS*) AND INVASIVE BLUE TILAPIA (*OREOCHROMIS AUREUS*) FROM LAKE HOLLINGSWORTH, FLORIDA

Herzberg M, Mays D, Langford GJ

Department of Biology, Florida Southern College, Lakeland, FL, USA

P4. THERE AND BACK AGAIN: DISCOVERING THE COMPLEX LIFE CYCLES OF BULL SHARK (*CARCHARHINUS LEUCAS*) TAPEWORMS

Minton B, Langford ML, Durland-Donahou A, Langford GJ

Department of Biology, Florida Southern College, Lakeland, FL, USA

PAPER SESSION I

Friday, March 20, 8:30 – 10:15 AM

MRRR Auditorium

Moderators: Haley Dutton, Auburn University, and Jill Hudnall, Mississippi State University

Presenting author is underlined

†Byrd-Dunn Graduate Student Paper Competitor

8:30 **1. IDENTICAL LIFE CYCLES IN TWO CLOSELY RELATED AMERICAN ALLIGATOR TREMATODES: *PROCTOCAECUM DIPLOPORUM* AND *PROCTOCAECUM CORONARIUM* (DIGENEA: CRYPTOGONIMIDAE) FROM COASTAL ALABAMA**

Cajiao-Mora K[†], Curran SS, Brule JH, Gordillo-González D, Dutton HR, Warren MB, Bullard SA

Southeastern Cooperative Fish Parasite and Disease Laboratory and Southeastern Cooperative Fish Genetics Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, AL, USA

- 8:45 **2. PATHOLOGIC FINDINGS OF COLD-STRESSED THREADFIN SHAD (*DOROSOMA PETENENSE*) IN EASTERN TENNESSEE**
Correia I¹, Hall S², Lovy J², Gerhold R¹, Dennis M¹
¹Biomedical and Diagnostic Sciences Department, University of Tennessee College of Veterinary Medicine, Knoxville, TN, USA
²USGS Western Fisheries Research Center (WFRC), Seattle, WA, USA
- 9:00 **3. URBAN OWLS AS SENTINELS: NGS DIETARY ANALYSIS REVEALS THE ECOLOGICAL COMPLEXITY OF RAT LUNGWORM TRANSMISSION**
Jones H^{1,2,3}, Castleberry N⁴, Piersma B⁴, Yabsley MJ^{1,2,3,5}
¹Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, University of Georgia, Athens, GA, USA
²Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA
³Center for Ecology of Infectious Diseases, University of Georgia, Athens, GA, USA
⁴Audubon Florida, Marco Island, FL, USA
⁵Odum School of Ecology, University of Georgia, Athens, GA, USA
- 9:15 **4. SURVEY OF PARASITE PRODUCTS OBSERVED DURING ZINC FECAL FLOTATION OF FROZEN BANKED ELK (*CERVUS CANADENSIS*) FECES**
Richards J¹, Braunstein J², Pagett C¹, Davis A¹, Kojima E¹
¹The University of Tennessee College of Veterinary Medicine Biomedical and Diagnostic Sciences, Knoxville, TN, USA
²Tennessee Technological University, Cookeville, TN 38505
- 9:30 **5. ASSESSING SEASONAL TRENDS, DETECTION PATTERNS, AND CO-INFECTION OF *PHOTOBACTERIUM DAMSELAE* SUBSP. *DAMSELAE*, CETACEAN HERPESVIRUS, AND *BRUCELLA CETI* IN STRANDED BOTTLENOSE DOLPHIN (*TURSIOPS EREBENNUS*) LUNG TISSUES**
Trayhan JK¹, Aquilina-Beck A², Greig TW², McFee WE², Janech MG¹
¹Department of Biology, Grice Marine Laboratory, College of Charleston, SC, USA
²National Centers for Coastal Ocean Science, National Oceanic and Atmospheric Administration, Charleston, SC, USA
- 9:45 **6. THERMAL PREFERENCES OF BIVESICULID CERCARIAE**
Zaffiro B¹, Blonar CA¹, Kerstetter DW², Martinez E¹
¹Department of Biology, Nova Southeastern University, Davie, FL, USA
²Department of Marine Science, Nova Southeastern University, Davie, FL, USA
- 10:00 **7. ENVIRONMENTAL DRIVERS OF VIRAL INFECTION IN SALTMARSH BENTHIC DIATOMS**
Glendening GM¹, Byrum CA¹, Hernandez CA², Pinckney JL², Plante CJ¹
¹Department of Biology, Grice Marine Laboratory, College of Charleston, SC
²University of South Carolina, Columbia, SC
- 10:15 – 10:45 **MORNING BREAK**

PAPER SESSION II

Friday, March 20, 10:45 AM – 12:15 PM
MRR Auditorium

Moderators: Dakeishla Díaz-Morales, DePaul University, and Thanveer Aslam, Eastern Illinois University

Presenting author is underlined

*Ciordia-Stewart-Porter Undergraduate Student Paper Competitor

- 10:45 **8. HELMINTH PARASITES OF CRAYFISH IN SOUTH CAROLINA**
Cudahy RD*¹, **Chowansky AN**¹, **Hill-Spanik KM**², **Rothman GK**³, **Kendrick MR**³, **de Buron I**¹
¹Department of Biology, College of Charleston, Charleston, SC, USA
²Department of Biology, Grice Marine Laboratory, College of Charleston, Charleston, SC, USA
³South Carolina Department of Natural Resources, Marine Resources Research Institute, Charleston, SC, USA
- 11:00 **9. IDENTIFICATION AND EXPLORATION OF A PARASITIC TREMATODE (*SACCULARINA MAGNACETABULA*) IN TAMPA BAY LADYFISH**
Walker L* , **Durkin E**
Department of Biology, University of Tampa, Tampa, FL, USA
- 11:15 **10. METACERCARIAE OF *STEPHANOSTOMUM* SP. INFECTING ORBITS AND BRAIN OF SOUTH CAROLINA COASTAL FLATFISHES**
Rothenberger F*¹, **Hill-Spanik KM**², **de Buron I**¹
¹Department of Biology, College of Charleston, Charleston, SC, USA
²Department of Biology, Grice Marine Laboratory, College of Charleston, Charleston, SC, USA
- 11:30 **11. DISTRIBUTION OF *ANCYLOSTOMA CANINUM* EGGS IN CANINE FECAL SAMPLES**
Strock LE, **Zelmer DA**
University of South Carolina Aiken, Aiken, SC, USA
- 11:45 **12. NEW SPECIES OF APOROCOTYLID INFECTING NEWLY EXAMINED TEREHELLID IN SOUTH CAROLINA**
Chowansky A*¹, **Hill-Spanik KM**², **Kyle DE**³, **de Buron I**¹
¹Department of Biology, College of Charleston, Charleston SC, USA
²Department of Biology, Grice Marine Laboratory, College of Charleston, Charleston, SC, USA
³Center for Tropical & Emerging Global Diseases, University of Georgia, Athens GA, USA
- 12:00 **13. HERITABILITY OF HOST RESPONSES TO PARASITES IN MARINE AND ESTUARINE COMMUNITIES**
Sotka E, **Strand A**
Department of Biology and Grice Marine Laboratory, College of Charleston, Charleston, SC, USA

LUNCH AT THE SCDNR OUTDOOR CLASSROOM, 12:15 – 2:00 PM

PAPER SESSION III

Friday, March 20, 2:00 – 3:45 PM

MRRRI Auditorium

Moderators: M. Brett Warren, Auburn University, and Makhali Voss, University of Tennessee

Presenting author is underlined

†Byrd-Dunn Graduate Student Paper Competitor

- 2:00 **14. FIRST REPORT OF A MONOGENOID, *DACTYLOGYRUS NOBILIS* LONG AND YU, 1958 (DACTYLOGYRIDAE) INFECTING BIGHEAD CARP, *HYPOPHTHALMICHTHYS NOBILIS* IN NORTH AMERICA WITH PHYLOGENETIC ANALYSIS AND INVENTORY OF PARASITES INFECTING INVASIVE FISHES IN THE UNITED STATES**
Brule JH¹, Cajiao-Mora K¹, Gordillo-González D¹, Escobar-Alfonso S¹, Horton ML², Winningham K³, Bullard SA^{1,4}
¹Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, AL, USA
²Arkansas Game and Fish Commission, Little Rock, AR, USA
³Arkansas Game and Fish Commission, Hot Springs, AR, USA
⁴Southeastern Cooperative Fish Genetics Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, AL, USA
- 2:15 **15. FURTHER OPTIMIZATION OF *PARELAPHOSTRONGYLUS TENUIS* SEROLOGICAL ASSAY**
Kelley E⁺, Richards J, Gerhold R
Department of Biomedical and Diagnostic Sciences, University of Tennessee, Knoxville, TN, USA
- 2:30 **16. MOLECULAR DETECTION OF WHITE SPOT SYNDROME VIRUS (WSSV) AND YELLOW HEAD VIRUS (YHV) IN WILD-CAUGHT NORTHERN BROWN SHRIMP (*FARFANTEPENAEUS AZTECUS*), NORTHERN WHITE SHRIMP (*LITOPENAEUS SETIFERUS*), AND ROUGH MANTIS SHRIMP (*SQUILLA EMPUSA*) FROM THE GULF OF AMERICA**
Escobar-Alfonso S⁺¹, Brule JH¹, Bullard SA^{1,2}
¹Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, AL, USA
²Southeastern Cooperative Fish Genetics Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, AL, USA
- 2:45 **17. RISK FACTORS, PREVALENCE, AND COMPARISON OF METHODS FOR DIAGNOSING *TOXOPLASMA GONDII* IN VARIOUS WILDLIFE SPECIES OF THE SOUTHEASTERN USA**
Fiedler SE¹, Riese KE¹, Riley J², Su C¹, Dennis M¹, Gerhold RW¹
¹Department of Biomedical and Diagnostic Sciences, College of Veterinary Medicine, University of Tennessee, Knoxville, TN, USA
²Blue Ridge Wildlife Center, Boyce, VA, USA
- 3:00 **18. NOVEL *MANSONELLA OZZARDI*-LIKE NEMATODE IN BLACK BEARS AND RACCOONS OF EAST TENNESSEE**
Riese K, Richards J, Dennis M, Sheldon J, Lee M, Gerhold R
University of Tennessee College of Veterinary Medicine, Knoxville, TN, USA
- 3:15 **19. OPTIMIZING TREATMENT FOR PRIMARY AMOEBIC MENINGOENCEPHALITIS CAUSED BY *NAEGLERIA FOWLERI***
Waller Del Valle A⁺^{1,2}, Kyle DE^{1,2}
¹Department of Cellular Biology, University of Georgia, Athens, GA, USA
²Center of Tropical and Global Emerging Diseases, University of Georgia, Athens, GA, USA
- 3:30 **20. PREVALENCE OF *CYTAUXZON FELIS CYTOCHROME-B* VARIANTS IN DOMESTIC CATS AND BOBCATS**
Aslam T⁺, Zieman EA
Department of Biological Sciences, Eastern Illinois University, Charleston, IL, USA

3:45 – 4:15 PM AFTERNOON BREAK

PAPER SESSION IV

Friday, March 20, 4:15 – 5:45 PM

MRRRI Auditorium

Moderators: Dennis Kyle, University of Georgia, and Jessie Richards, University of Tennessee

Presenting author is underlined

†Byrd-Dunn Graduate Student Paper Competitor

- 4:15 **21. NOT SO RIDLEY-CULOUS: *PLESIOCHORUS* SP. IN AN ADULT KEMP'S RIDLEY *LEPIDOCHELYS KEMPII* IN THE MISSISSIPPI SOUND**
Hudnall JB^{†1,3}, Rosser TG^{2,3}, McNulty K^{1,3}, Woodyard ET^{1,3}, Peterman B^{1,3}, Reichley SR^{1,3}, Lawrence ML^{2,3}
¹Department of Pathobiology and Population Medicine, College of Veterinary Medicine, Mississippi State University, Mississippi State, MS, USA
²Department of Comparative Biomedical Sciences, College of Veterinary Medicine, Mississippi State University, MS, USA
³Global Center for Aquatic Health and Food Security, Mississippi State University, MS, USA
- 4:30 **22. FROM CLAM TO FISH: LIFE CYCLE ECOLOGY OF DIGENEANS *LASIOLOCUS TRACHINOTI* AND *L. CHOANURA* IN COQUINAS *DONAX* SPP.**
Stewart KM^{†1}, de Buron I², Hill-Spanik KM¹, McElroy EJ²
¹Department of Biology, Grice Marine Laboratory, College of Charleston, Charleston, SC, USA
²Department of Biology, College of Charleston, Charleston, SC, USA
- 4:45 **23. TAPING TOGETHER THE PUZZLE OF WILD TURKEY DECLINES: IDENTIFICATION OF THE CESTODE SPECIES INFECTING THE EASTERN WILD TURKEY (*MELEAGRIS GALLOPAVO SILVESTRIS*) IN TENNESSEE**
Perrin GM^{†1}, Horton LK¹, Riese KE¹, Gotez F², Schauble M², Phillips AJ², Gerhold RW¹
¹Department of Biomedical and Diagnostic Sciences, College of Veterinary Medicine, University of Tennessee, Knoxville, TN, USA
²Smithsonian Institution, National Museum of Natural History, Department of Invertebrate Zoology, Washington, DC, USA
- 5:00 **24. BLACK BASS GILL LICE: TAXONOMY AND GENETICS OF *ACHTHERES MICROPTERI* WRIGHT, 1882 (COPEPODA: LERNAEOPODIDAE) INFECTING LARGEMOUTH BASS, *MICROPTERUS SALMOIDES* AND SPOTTED BASS, *MICROPTERUS PUNCTULATUS* IN ALABAMA AND NORTH CAROLINA**
Gordillo-González D¹, Cajiao-Mora K¹, Brule JH¹, Escobar-Alfonso S¹, Warren MB¹, Truong TN¹, Curran SS¹, Dutton HR¹, Smith CM¹, Bullard SA^{1,2}
¹Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, AL, USA
²Southeastern Cooperative Fish Genetics Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, AL, USA
- 5:15 **25. FLIES AS ENVIRONMENTAL DRONES IN WILDLIFE DISEASE ECOLOGY: TRACKING PERSISTENCE OF *HISTOMONAS MELEAGRIDIS* IN THE BLACK BLOW FLY, *PHORMIA REGINA* (MEIGEN)**

Voss MS⁺¹, Gerhold RW², Owings CG¹

¹Department of Entomology and Plant Pathology, University of Tennessee, Knoxville, TN, USA

²Department of Biomedical and Diagnostic Sciences, University of Tennessee, Knoxville, TN, USA

5:30 **26. TEMPORAL CHANGES IN ZOOPLANKTON COMMUNITY STRUCTURE IN RELATION TO INFECTIONS BY *ANGUILLICOLA CRASSUS***

Parish J^{+1,2}, Clajus E², Harrington R², Mitchener G³, de Buron I⁴, Kendrick M²

¹EVSS Graduate Program, School of Natural and Environmental Sciences, College of Charleston, Charleston, SC, USA

²Department of Natural Resources, Marine Resources Research Institute, Charleston, SC, USA

³Department of Mathematics, College of Charleston, Charleston, SC, USA

⁴Department of Biology, College of Charleston, Charleston, SC, USA

PAPER SESSION V

Saturday, March 21, 8:30 – 10:00 AM

MRR Auditorium

Moderators: Derek Zelmer, University of South Carolina–Aiken, and John Brule, University of Auburn

Presenting author is underlined

8:30 **27. A NEW SPECIES OF FISH BLOOD FLUKE INFECTING BLACK BASSES (*MICROPTERUS* SPP.) FROM THE COOSA RIVER, ALABAMA**

Warren MB, Bullard SA

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

8:45 **28. DESCRIPTIONS AND LIFE CYCLES OF THREE NEW SPECIES OF *PROTEROMETRA* HORSFALL, 1933 (DIGENEA: AZYGIIDAE) INFECTING ENDEMIC PLEUROCERIDS AND FISHES FROM THE DUCK RIVER, TENNESSEE**

Truong TN¹, Brule JH¹, Simcox BL², Bybel AP², Bullard SA^{1,3,4}

¹Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, AL, USA

²Tennessee Wildlife Resources Agency, Nashville, TN, USA

³Southeastern Cooperative Fish Parasite and Disease Laboratory and Southeastern Cooperative Fish Genetics Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, AL, USA

⁴Department of Zoology, School for Environmental Sciences and Development, North-West University, Private Bag X6001, Potchefstroom, South Africa

9:00 **29. AN *EX VIVO* ASSAY FOR CHARACTERIZING CHEMICAL INHIBITION OF MYXOZOAN SPORE ATTACHMENT TO THE FISH HOST**

Brubaker LS¹, Lotan T², Atkinson SD¹

¹Department of Microbiology, Oregon State University, Corvallis, OR, USA

²Department of Marine Biology, The Leon H. Charney School of Marine Sciences, University of Haifa, Israel

9:15 **30. REELFOOT LAKE, TENNESSEE, USA: TURTLE BLOOD FLUKE CAPITAL OF THE WORLD. A HISTORY AND UPDATE SINCE BYRD, 1939**

Dutton HR, Brule JH, Curran SS, Cajiao-Mora K, Warren MB, Bullard SA

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

9:30 **31. EDNA METABACORDING AS COMPLEMENTARY TOOL TO TRADITIONAL METHODS FOR CHARACTERIZING AQUATIC PARASITE DIVERSITY**

Díaz-Morales DM¹, Kendrick M², de Buron I³, Atkinson SD⁴, Georgieva S⁵, Sures B⁶, Kmentová N^{7,8}, Vanhove MPM^{7,8}, Hill-Spanik KM³

¹Biological Sciences Department, DePaul University, Chicago, IL, USA

²Marine Resources Research Institute, South Carolina Department of Natural Resources, Charleston, SC, USA

³Department of Biology, Grice Marine Laboratory, College of Charleston, Charleston, SC, USA

⁴Department of Microbiology, Oregon State University, Corvallis, OR, USA

⁵Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, Sofia, Bulgaria

⁶Aquatic Ecology and Centre for Water and Environmental Research (ZWU), University of Duisburg-Essen, Essen, Germany

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9:45 **32. DIGENEANS FROM FISHES SOURCED FROM THE OREGON II SUMMER GROUND FISH SURVEY OFF FLORIDA**

Curran SS, Brule JH, Bullard SA

Southeastern Cooperative Fish Parasite and Disease Laboratory and Southeastern Cooperative Fish Genetics Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, AL, USA

10:00 – 10:30 **MORNING BREAK**

PAPER SESSION VI AND BUSINESS MEETING

Saturday, March 21, 10:30 AM – 12:45 PM

MRRRI Auditorium

Moderators: Graham Rosser, Mississippi State University, and Anissa Waller Del Valle, University of Georgia

Presenting author is underlined

10:30 **33. TAXONOMY AND PARASITOLOGY OF SOME VIVIPARID SNAILS FROM ALABAMA AND ARKANSAS**
Smith CM¹, Curran SS¹, Dutton HR¹, Brule JH¹, Gordillo-Gonzalez D¹, Escobar-Alfonso S², Truong TN¹, Warren MB¹, Bullard SA^{1,2}

¹Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, AL, USA

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10:45 **34. HIGH THROUGHPUT QUANTITATIVE TRACKING OF *PLASMODIUM FALCIPARUM* CLONAL BLOOD STAGE PARASITE GROWTH**

Cheng Z^{1,2}, Ru L³, Hoang A², Wang M⁴, Ganjikutna S², Maher SP¹, Kyle DE^{1,2,5}

¹Center for Tropical and Emerging Global Diseases, University of Georgia, Athens, GA, USA

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⁴Institute of Bioinformatics, University of Georgia, Athens, GA, USA

⁵Department of Infectious Diseases, University of Georgia, Athens, GA, USA

11:00 **35. A GENETIC AND ECOLOGIC INVESTIGATION INTO ESOPHAGEAL MONOGENOIDS ALONG THE SOUTHEASTERN SEABOARD OF THE UNITED STATES**

Baker TG¹, **Kritsky D**², **Hill-Spanik KM**³, **de Buron I**³

¹Department of Pathology and Laboratory Medicine, Medical University of South Carolina, Charleston, SC, USA

²Division of Health Science, Idaho State University, Pocatello, ID, USA

³Department of Biology, Grice Marine Laboratory, College of Charleston, Charleston SC, USA

11:15 **36. 'SO MANY SPECIES, SO LITTLE TIME:' THE MESSAGE OF DACTYLOGYRIDAE IN BRAZIL**

Boeger, WA

Universidade Federal do Paraná, PR, Brazil

Instituto de Pesquisas do Jardim Botânico, RJ, Brazil

Research Associate, HW Manter Laboratory, University of Nebraska, Lincoln, NE, USA

11:30 **37. RESTABILIZING THE COMMON NAMES FOR LARGEMOUTH BASS, *MICROPTERUS SALMOIDES* (LACÉPÈDE, 1802) HENSHALL, 1881 AND FLORIDA BASS, *MICROPTERUS FLORIDANUS* (LESUEUR, 1822) GOODE, 1876 WITH COMMENTS ON *MICROPTERUS NIGRICANS* (CUVIER, 1828) COPE, 1865**

Bullard SA^{1,2} **Curran SS**¹

¹Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, AL, USA

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11:45 **SSP BUSINESS MEETING**

S. Ash Bullard, Presiding

12:45 **LUNCH IN THE MRRI LOBBY**

THANK YOU FOR SUPPORTING THE SOUTHEASTERN SOCIETY OF PARASITOLOGISTS!

SAFE TRAVELS!

ABSTRACTS OF POSTER PRESENTATIONS

P1. GASTROINTESTINAL PARASITES OF GOPHER TORTOISES (*GOPHERUS POLYPHEMUS*) FROM ARCHBOLD BIOLOGICAL STATION, FLORIDA

Barnhill M, Langford GJ

Department of Biology, Florida Southern College, Lakeland, FL, USA

Archbold Biological Station has the largest natural population of gopher tortoises (*Gopherus polyphemus*) in the world. Recently, individuals within the Archbold Biological Station population have displayed signs of respiratory illness, likely caused by the bacterium *Mycoplasma* spp. The respiratory illness raised awareness and concerns about the overall health of gopher tortoises and the lack of baseline data on their intestinal parasites. In addition, a recently discovered pentastome (*Raillietiella orientalis*) infection in the lungs of a captive, free-ranging tortoise in south Florida raised concerns of transmission to native tortoises. This study provides a baseline assessment of gopher tortoise intestinal parasites at Archbold Biological Station. Fecal samples were collected from most of the tortoises across the field station, which were frozen or preserved in ethanol, processed using fecal flotation and sedimentation techniques, then identified morphologically using species descriptions and other published literature. While this is an on-going study, 6 different parasite eggs have been found from the following families: Ascaridae, Oxyuridae, and Strongylidae. No pentastome eggs have been discovered in the gopher tortoises to date. Establishing a baseline of parasites is beneficial to evaluate host population health, monitoring spatiotemporal changes in parasite diversity, prevalence, and intensity, and proactively establish disease management protocols (if needed in the future) for this population of gopher tortoises that are a federally threatened species.

P2. COMPARATIVE ANALYSIS OF ENDOPARASITES IN *OREOCHROMIS AUREUS* AND *LEPOMIS* SPP.: AN INVESTIGATION INTO POTENTIAL SPILLOVER IN LAKE HOLLINGSWORTH, POLK COUNTY, FLORIDA

Delgado C, Gunnison E, Langford GJ

Department of Biology, Florida Southern College, Lakeland, FL, USA

Despite being some of the most abundant fish in Florida freshwaters, few parasitological studies have been conducted on native sunfish (*Lepomis* spp.) or invasive blue tilapia (*Oreochromis aureus*). It is also unknown if these two hosts share parasites. Parasite spillover occurs when invasive hosts introduce novel parasites to native animals, whereas parasite spillback happens when invasive hosts acquire parasites that typically infect native hosts. In addition, there is a lack of data on *O. aureus* endoparasites outside of its native range. This study aims to document the endoparasite communities of invasive blue tilapia in a freshwater lake and compare them to native sunfish. Starting in September 2025, tilapia and sunfish were captured with cast nets, then dissected for parasite discovery. Parasites were counted and preserved in 70% ethanol for identification with standard keys and species descriptions. Preliminary results show a greater parasite diversity in sunfish compared to tilapia, and the two species of fish host distinct endoparasite assemblages. We have found minimal support for spillover or spillback in these two species of fish, although parasite discovery and identification is on-going.

P3. MONOGENEAN PARASITES OF NATIVE BLUEGILL (*LEPOMIS MACHROCHIRUS*) AND INVASIVE BLUE TILAPIA (*OREOCHROMIS AUREUS*) FROM LAKE HOLLINGSWORTH, FLORIDA

Herzberg M, Mays D, Langford GJ

Department of Biology, Florida Southern College, Lakeland, FL, USA

Monogeneans are primarily ectoparasites that are typically found on the gills of fish. Few studies have explored Florida fish populations for their monogenean parasites. Florida is a hotspot for invasive species, but little is known about the exchange of parasites between native and invasive species. Spillover occurs when invasive hosts introduce novel parasites to native animals, whereas spillback happens when invasive hosts acquire parasites that typically infect native hosts. The introduction of invasive tilapia into Florida's freshwater systems can significantly impact aquatic ecosystem functions. Our study aims to determine if

the native bluegill (*Lepomis macrochirus*) and invasive blue tilapia (*Oreochromis aureus*) have exchanged parasites in Lake Hollingsworth, Florida. Starting in October 2025, we collected bluegill and blue tilapia for parasite exploration (collections are on-going). We separated each gill and searched for monogeneans, then we counted and identified worms using standard keys and original descriptions. While dissections and identifications are incomplete, we have identified 3 species from blue tilapia and 3 species from bluegill. Parasite preference for lobes has been higher on the outer lobes (closest to the operculum) than the inner lobes. To date, we have no evidence of spillover or spillback; the monogeneans adhere to strict host specificity between these fish hosts. Any additional results will be discussed at the meeting.

P4. THERE AND BACK AGAIN: DISCOVERING THE COMPLEX LIFE CYCLES OF BULL SHARK (*CARCHARHINUS LEUCAS*) TAPEWORMS

Minton B, Langford ML, Durland-Donahou A, Langford GJ

Department of Biology, Florida Southern College, Lakeland, FL, USA

Parasites are integral yet often overlooked components of marine ecosystems influencing biodiversity, food web structure, and host population health. Among parasitic taxa, tapeworms (Class Cestoda) are remarkably diverse, with many species exhibiting unique evolutionary relationships with elasmobranchs, the subclass of cartilaginous fishes that includes sharks, rays, and skates. These cestodes display extraordinary morphological adaptations to the spiral valve intestine, reflecting a long coevolutionary history with their hosts. Despite extensive documentation of cestode diversity in elasmobranchs, the complete life cycles of most species remain unresolved. Like other tapeworms, they are believed to pass through multiple intermediate hosts, such as crustaceans and teleost fishes, before reaching maturity in the definitive elasmobranch host. However larval stages are difficult to identify morphologically, and the species of hosts involved in transmission remain largely unknown. This research aims to elucidate the life cycles of elasmobranch cestodes by identifying intermediate hosts and linking larval and adult stages through an integrative approach combining classical parasitology and molecular tools such as PCR and DNA sequencing. Field sampling in the Alafia River and surrounding coastal systems will provide host specimens for morphological and genetic analysis. By reconstructing the developmental pathways of these cestodes, this research will clarify transmission routes, reveal host-specific associations, and improve understanding of how cestodes persist and disperse in marine ecosystems. The results of this ongoing study will be presented at the meeting.

ABSTRACTS OF ORAL PRESENTATIONS

1. IDENTICAL LIFE CYCLES IN TWO CLOSELY RELATED AMERICAN ALLIGATOR TREMATODES: *PROCTOCAECUM DIPLOPORUM* AND *PROCTOCAECUM CORONARIUM* (DIGENEA: CRYPTOGONIMIDAE) FROM COASTAL ALABAMA

Cajiao-Mora K†, Curran SS, Brule JH, Gordillo-González D, Dutton HR, Warren MB, Bullard SA

Southeastern Cooperative Fish Parasite and Disease Laboratory and Southeastern Cooperative Fish Genetics Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences; College of Agriculture, Auburn University, Auburn, AL, USA

We investigated the life cycle of *Proctocaecum diploporum* and *Proctocaecum coronarium* (Digenea: Cryptogonimidae) obtained during a parasitological survey of the cockscomb hydrobe, *Littoridinops monroensis* (Gastropoda: Cochliopidae), saltmarsh fishes, and the American alligator, *Alligator mississippiensis* (Alligatoridae) within a saltmarsh pond in the Bon Secour Bay (Alabama) and other localities. Cercariae were naturally shed from the cockscomb hydrobe. Fish scales of seven estuarine fish species were infected with two metacercarial cyst size classes, a small (<200µm) and a large (>240µm), suggesting the presence of distinct but closely related sympatric cryptogonimids. Morphological and nucleotide evidence demonstrated that *P. diploporum* (small cyst) and *P. coronarium* (large cyst), previously regarded as taxonomic synonyms, share the same first intermediate host (cockscomb hydrobe), are

encysted within the scales of the same fish host species, and mature in the intestine of the same definitive host (American alligator). The taxonomy of these trematodes and that of another similar American alligator trematode, *Caimanicola pavidus* (Digenea: Cryptogonimidae), needed reconsideration. Herein, we describe the first complete and naturally occurring life cycle of a reptile-infecting cryptogonimid, provide the first nucleotide data for a species of *Proctocaeum*, taxonomically reassess both *P. diploporum* and *P. coronarium*, and designate a neotype for *P. coronarium*. We consider *C. pavidus* as a junior subjective synonym of *P. coronarium*. Phylogenetically related and sympatric trematodes that use the same invertebrate and vertebrate hosts such as these *Proctocaeum* spp. could be a good model to further explore the mechanisms of sympatric speciation and host specificity among trematodes with complex life cycles.

2. PATHOLOGIC FINDINGS OF COLD-STRESSED THREADFIN SHAD (*DOROSOMA PETENENSE*) IN EASTERN TENNESSEE

Correia I⁺¹, Hall S², Lovy J², Gerhold R¹, Dennis M¹

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²USGS Western Fisheries Research Center, Seattle, WA, USA

The threadfin shad (*Dorosoma petenense*) is a small freshwater forage fish inhabiting the southeast, midwest, and west coast of the United States. Outside their historic native range, *Dorosoma* spp. are susceptible to cold stress syndrome. There are no reports describing the pathology of dying fish, and the pathophysiology of cold stress is not well understood. In February 2025 during a mortality event of cold-stressed threadfin shad in Knoxville, Tennessee, deceased fish were collected for comprehensive postmortem investigation, including histology (n = 8) and wet-mounted brain squash preparation (n = 13). Histologically, 4/8 fish had cerebral microsporidiosis; 1 of these had granulomatous encephalitis, and 1 had granulomatous peritonitis. Additional findings were lamellar ichthyophthiriasis (1/8), cutaneous or lamellar oomycetosis (5/8), and visceral granulomas with nematode larvae (1/8). On wet mount, 8/13 fish had mature microsporidial spores present. Genetic sequencing of cerebral spores revealed a 99.3% similarity to an undescribed Microsporidia species that was isolated from a wild swamp guppy (*Micropoecilia picta*) in Grenada, West Indies. In January 2026, a comparative sample of cold-stressed threadfin shad (n = 11) was collected from another location in east Tennessee. Interestingly, only 1 fish had microsporidial spores histologically, presenting as necrogranulomatous pancreatitis. Additional findings included lamellar ichthyophthiriasis (3/11) and hepatocellular atrophy (3/11). To our knowledge, this is the first report of cerebral microsporidiosis in threadfin shad. We hypothesize that cold stress predisposes threadfin shad to a variety of opportunistic infections, some of which may be generalist pathogens with significance to sympatric host species and ecosystem health.

3. URBAN OWLS AS SENTINELS: NGS DIETARY ANALYSIS REVEALS THE ECOLOGICAL COMPLEXITY OF RAT LUNGWORM TRANSMISSION

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Angiostrongylus cantonensis—the rat lungworm and leading cause of eosinophilic meningitis worldwide—exploits a remarkable diversity of intermediate and paratenic hosts, complicating efforts to characterize its transmission ecology. Florida burrowing owls (*Athene cunicularia floridana*) on Marco Island, Florida recently emerged as aberrant hosts with fatal neuroangiostrongyliasis, raising the question

of which prey items deliver infective larvae. Using next-generation sequencing of pellets and fecal samples collected during the 2024 breeding season, we documented exceptional dietary breadth encompassing over 60 families, 80 genera, and 74 species across three primer sets. Confirmed and suspected *A. cantonensis* hosts dominated the diet. Veronicellid slugs (*Veronicella cubensis*, *Sarasinula plebeia*) represent known intermediate hosts, while centipedes (*Rhysida longipes*), Cuban treefrogs (*Osteopilus septentrionalis*), greenhouse frogs (*Eleutherodactylus planirostris*), cane toads (*Rhinella marina*), and house geckos (*Hemidactylus* spp.) are documented paratenic hosts. Decapod crustaceans (*Armases cinereum*, *Aratus pisonii*) and ubiquitous cockroaches (*Periplaneta* spp.) suggest additional, understudied transmission pathways. Non-native species comprised 71% of species-level reads, revealing how invasive fauna may facilitate emerging parasite establishment in novel environments. Incidental detection of *Raillietiella* sp., *Ortleppascaris* sp., and *Physaloptera* sp. further demonstrates the utility of NGS dietary analysis as a biodiversity surveillance tool. The taxonomic breadth of potential transmission routes precludes identification of a single dominant infection source, instead revealing the ecological redundancy that enables *A. cantonensis* to exploit new environments. These urban owls are not merely victims of rat lungworm; they are sentinels illuminating the invasive-species-driven food webs through which this parasite conquers new territory.

4. SURVEY OF PARASITE PRODUCTS OBSERVED DURING ZINC FECAL FLOTATION OF FROZEN BANKED ELK (*CERVUS CANADENSIS*) FECES

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We examined 210 elk feces that were opportunistically collected in western North Carolina in 2020 and 2021 and kept frozen at -20°C until thawed for processing. Approximately 2 grams of feces were used for each Zinc Sulfate (specific gravity = 1.18) fecal flotation with centrifugation at 1800xg for 10 minutes. As expected, we found and photographed many parasite products. Parasite products were observed in 13.3% (28/210) of feces examined. From the positive fecal flotations, we observed Trichostrongyle-type eggs in 14.3% (4/28), *Strongyloides* spp. in 28.6% (8/28), *Capillaria* spp. in 10.7% (3/28), *Trichuris* spp. in 7.1% (2/28), *Moniezia* spp. in 7.1% (2/28), *Eimeria* spp. in 25.0% (7/28). Larvae were noted in 28.6% (8/28) of the samples with dorsal spines identified in at least two parasites from one sample. We also found an incidental carnivore *Sarcocystis*-like sarcocyst in one elk and a *Cystoisospora*-like oocyst in another, likely not representing infection, but ingestion from the environment. Surprisingly, we found some specimens of *Strongyloides* still alive and mobile within their eggs, indicating parasite survival during prolonged freezing. This research is ongoing with over 200 samples yet to be processed and molecular work is ongoing.

5. ASSESSING SEASONAL TRENDS, DETECTION PATTERNS, AND CO-INFECTION OF *PHOTOBACTERIUM DAMSELAE* SUBSP. *DAMSELAE*, CETACEAN HERPESVIRUS, AND *BRUCELLA CETI* IN STRANDED BOTTLENOSE DOLPHIN (*TURSIOPS EREBENNUS*) LUNG TISSUES

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Respiratory disease is a major cause of mortality in stranded bottlenose dolphins (*Tursiops erebennus*) within the Charleston Estuarine System Stock (CESS), a highly contaminated and site-specific population along the southeastern United States. While *Brucella ceti* infection is well documented in this population, additional respiratory pathogens such as *Photobacterium damsela* subsp. *damsela* (Pdd) and cetacean herpesvirus (CeHV) remain poorly characterized. This study assessed the presence, seasonal patterns, and

co-infection dynamics of Pdd and CeHV in lung tissues from stranded CESS dolphins and evaluated their relationship with *Brucella ceti*. A total of 159 lung tissue samples collected between 2004 and 2024 were screened using pathogen-specific PCR assays and gel electrophoresis, with representative products confirmed through Sanger sequencing. Previously determined *Brucella ceti* qPCR results were incorporated to evaluate co-infection patterns. Associations between pathogen detection and metadata variables (season, sex, age class, decomposition code, and *Brucella* status) were assessed using chi-squared tests and logistic regression ($\alpha = 0.05$). Overall, Pdd was detected in 49.1% of lung tissues (78/159), while CeHV was detected in 2.5% of individuals (4/159). Pdd detection varied by season, with the highest prevalence observed in fall (65.9%), and was significantly associated with fall season (OR = 3.57, $p = 0.0075$), male sex (OR = 2.00, $p = 0.033$), and higher decomposition code ($p = 0.011$). No significant associations were observed with age class, year, or *Brucella ceti* status. Co-infection occurred in 55 individuals, with Pdd-*Brucella* representing the most common (~75% of co-infection cases). These findings establish baseline data on the presence of respiratory pathogens in CESS dolphins and highlight seasonal and host-related factors associated with pathogen detection.

6. THERMAL PREFERENCES OF BIVESICULID CERCARIAE

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Rising global temperatures are likely modulating parasite-host interactions, yet the direction and magnitude of these changes remain uncertain. Previous work on digenean cercariae has largely focused on temperature effects on activity and mortality: in most species, activity increases with temperature to a peak, beyond which it declines sharply; increased activity is typically associated with elevated mortality. However, the underlying metabolic effects of rising temperature on metabolic demands are understudied. Clark-type polarographic oxygen microelectrodes were used to quantify oxygen consumption in bivesiculid cercariae. 20 bivesiculid cercariae were placed in a glass syringe with Fetig's Medium (Eagles Minimum Essential Medium, 1 mM HEPES, 200 mM L-Glutamin, Antibiotica Mix, 20 mM Glucose Stock, pH: 7.0 at 20°C), with the microelectrodes, oxygen consumption was measured at five temperatures (20°C, 25°C, 30°C, 35°C, and 40°C). Oxygen consumption increased from 3.3 ± 0.96 nanoL of oxygen consumed per individual to 29.3 ± 8.5 nanoL of oxygen consumed at 35°C and declined to 11.8 ± 2.2 nanoL of oxygen at 40°C, indicating a clear thermal optimum around 35°C. Using the respirometry data and assuming oxycalorific coefficient for mixed substrates, we estimated temperature-specific energetic demand per cercaria, with individuals requiring up to $0.013 \text{ kJ}\cdot\text{mol}^{-1}$ of oxygen per day at 35°C. These estimates allow calculation of both per-parasite energetic demand and the cumulative energetic burden imposed on infected snail hosts. Because snail metabolic rates also increase with temperature, heavily infected snails may be vulnerable to elevated energetic costs under warming conditions.

7. ENVIRONMENTAL DRIVERS OF VIRAL INFECTION IN SALTMARSH BENTHIC DIATOMS

Glendening GM⁺¹, Byrum CA¹, Hernandez CA², Pinckney JL², Plante CJ¹

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²University of South Carolina, Columbia, SC, USA

Viruses are increasingly recognized as key drivers of microbial mortality and nutrient cycling in marine systems, yet their roles in benthic microalgal environments remain relatively understudied. This study investigates intracellular viral infection in benthic diatoms across spatial and temporal gradients in North Inlet Estuary, South Carolina to identify environmental drivers behind diatom infection. Benthic diatoms are foundational to salt marsh function, contributing to primary production, sediment stabilization, and

nutrient cycling. Despite their widely recognized ecological importance, viral regulation of these communities has not been characterized, with viral impacts on benthic diatom abundance, species turnover, and role in nutrient cycling remaining unclear. Using sediment sampling across elevation zones and seasons in conjunction with fluorescence microscopy to colocalize virus-like-particles (VLPs) in diatoms, this project aims to assess how environmental factors such as tidal inundation, temperature, salinity, and nutrient availability shape host–virus dynamics. Thus far, no clear elevational pattern is seen, but a seasonal correlation in VLP infection prevalence has been observed. Findings address a critical gap in understanding of virus–microbe interactions in salt marshes, with implications for carbon cycling, microbial ecology, and the resilience of coastal ecosystems under environmental change.

8. HELMINTH PARASITES OF CRAYFISH IN SOUTH CAROLINA

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Crayfish parasitofauna in South Carolina (SC) is understudied, and baseline data are needed to monitor the potential impact of introduced crayfish *Procambarus clarkii* on native species as it can act as reservoir host for multiple parasites. Crayfish *Cambarus* spp. and *Procambarus* spp. (N = 420), including endemic *P. troglodytes* (N = 358/420), were collected throughout SC from 2019 to 2024 and preserved in ethanol or frozen. Individuals were measured and sexed; the carapace and body cavity were examined for helminths. Metacercariae and cystacanths found were isolated and preserved in 100% ethanol. Digeneans were identified molecularly (28S rRNA gene) as *Crepidostomum* sp. and *Gorgoderina* sp., and both were commonly found throughout the state in multiple crayfish species (51.4% overall prevalence, 216/420). In contrast, acanthocephalan infection occurred only along the coast and in *P. troglodytes* (4.4% prevalence, 16/358); mean abundance: 0.12 ± 0.8 ; mean intensity: 2.6 ± 3.2 (range 1-14). The identification of this acanthocephalan is problematic, as specimens yielded limited usable morphology and no molecular results. Based on a parallel study, we suspect it is *Ibirhynchus dimorpha*, which our results support as it is geographically limited to coastal crayfish, indicating that wading birds may be definitive hosts. The presence of *P. clarkii*, known to be susceptible to two species of acanthocephalans in SC, including *I. dimorpha*, has thus the potential to amplify infection in SC native crayfish. Further investigation should evaluate how patterns of parasitic infection (range, abundance, intensity) in native crayfish may be altered by the presence of invasive *P. clarkii*.

9. IDENTIFICATION AND EXPLORATION OF A PARASITIC TREMATODE (*SACCULARINA MAGNACETABULA*) IN TAMPA BAY LADYFISH

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Within Florida waters, the species richness of parasitic worms, specifically trematodes, has not been cataloged since the early 20th century. There have been few updates in recent years, leaving space for the question of existing host-parasite relations for the Gulf of Mexico and the Atlantic. In a 2022 study, a new genus and species of parasitic trematode in the family Didymozoidae was discovered in the fins of ladyfish, *Elops hawaiiensis*, and named *Saccularina magnacetabula*. A genetic and anatomical analysis was performed, laying the groundwork for new comparisons to this established species. In the fall of 2024, yellow parasitic worms were discovered within the fins of *Elops saurus*, a species of ladyfish in the Tampa Bay area. Since this initial discovery, we have performed thorough data collection, anatomy comparison, and genetic analysis of our unidentified worm and compared it to *S. magnacetabula*. This project explores the ecological, genetic, and anatomical aspects of this parasitic trematode. Here, we have performed DNA analysis on two specific genes and used an image analysis software for anatomical measurements. With

this knowledge, we contribute to the newly developing list of parasite species inhabiting Florida and the geographical distribution of possible *S. magnacetabula*, which opens the floor for further study on host specificity for this trematode.

10. METACERCARIAE OF *STEPHANOSTOMUM* SP. INFECTING ORBITS AND BRAIN OF SOUTH CAROLINA COASTAL FLATFISHES

Rothenberger F*¹, Hill-Spanik KM², de Buron I¹

¹Department of Biology, College of Charleston, Charleston, SC, USA

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We aimed to determine if flatfishes in coastal South Carolina (SC) were infected by metacercariae in their nervous system, which can affect their behavior. Individuals of four species were collected along the SC coast and provided frozen: hogchoker *Trinectes maculatus* (n = 42), southern flounder *Paralichthys lethostigma* (n = 5), fringed flounder *Etropus crossotus* (n = 5), and blackcheek tonguefish *Symphurus plagiusa* (n = 3). Fish were measured, and their eyes, eye sockets, optical nerves, and brain were examined under a dissecting microscope. Metacercariae were isolated, excysted, and fixed in 100% ethanol for morphological and molecular studies. Only fishes from North Inlet (11/18) and none from other estuaries (0/37) were infected. Fish of all four species had some level of infection (overall mean intensity 2.73 ± 2.10 ; range 1-7). Prevalence was highest in fringed flounder (100.0% [5/5], mc mostly in eyes [8 mc/9 total mc collected in this species]), followed by southern flounder (75.0% [3/4], mc mostly in eye sockets [10/16]), tonguefish (33.3% [1/3], mc in optical nerves [1/1]), and hogchoker (33.3% [2/6], mc in brain [2/4], eyes [1/4], optical nerves [1/4]). DNA sequences (LSU rRNA gene) of 15 metacercariae from various fish and sites of infection were identical and were 90-95% similar to sequences of *Stephanostomum* spp., ruling out species of this genus known from the area. This parasite was previously found to infect mudsnails in Charleston Harbor but remains to be identified to species level, which will require the discovery of its fish definitive host(s).

11. DISTRIBUTION OF *ANCYLOSTOMA CANINUM* EGGS IN CANINE FECAL SAMPLES

Strock LE, Zelmer DA

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The canine hookworm, *Ancylostoma caninum*, is an intestinal nematode that is common in dogs and capable of causing anemia, diarrhea, poor growth, and occasionally death in heavily infected animals. Fecal egg count reduction assays using modified McMaster methods are commonly used to recognize anthelmintic resistance in hookworms. Many applications of the McMaster technique implicitly assume that eggs are evenly distributed within a fecal sample. The present investigation addressed this assumption by partitioning infected canine fecal samples longitudinally into three subsamples, that were further subdivided into inner and outer layers, and conducting fecal egg counts on each portion using a modified McMaster method. Preliminary data indicates no longitudinal differences in egg distribution, but clear differences in egg density between inner and outer layers that varied with infection intensity. These findings suggest that hookworm eggs are not uniformly distributed within canine feces and that homogenization of fecal samples is necessary to obtain unbiased estimates of *A. caninum* egg density and accurate interpretation of fecal egg count reduction assays.

12. NEW SPECIES OF APOROCOTYLID INFECTING NEWLY EXAMINED TEREHELLID IN SOUTH CAROLINA

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Terebellid annelids can serve as intermediate hosts for blood flukes of marine fishes and sea turtles. While scarcity of reports of infected annelids reflects the need for further exploration, terebellids in South

Carolina (SC) have recently revealed a surprisingly high diversity of blood flukes although only a few species are known from the southeastern US coast. Our objective was to further our knowledge of diversity and life cycles of blood flukes in coastal SC. Four species of terebellids (*Enoplobranchus sanguineus*, *Amphitrite ornata*, *Pista palmata*, and *Streblosoma hartmanae*) were collected (N = 265) at low tide from September 2025 to February 2026 in North Inlet and Charleston Harbor. Nine specimens of three of the four terebellid species were infected. Parasites were isolated, photographed, and fixed in 100% ethanol for molecular identification (28S, ITS2 rDNA and COI mtDNA sequencing). Specimens of *E. sanguineus* (5.1% prevalence, 4/79) and *A. ornata* (0.03% prevalence, 2/68) were infected with previously reported spirorchiid *Neospororchis* sp. Neogen14 and aporocotyloid *Cardicola parvus*, respectively. None of the specimens of *S. hartmanae* were infected (0/86). One new aporocotyloid with mature sporocysts containing microcercous cercariae was discovered in newly examined *P. palmata* (17.2% prevalence, 5/29). Phylogenetic analysis revealed that 28S rDNA sequences of the new aporocotyloid were within the problematic “*Cardicola*” clade, with sequences most similar to those of *Braya jexi* and *Cardicola abu* (95.5% and 94.9%, respectively). The fish host of this parasite has yet to be discovered to fully elucidate the life cycle of this new aporocotyloid.

13. HERITABILITY OF HOST RESPONSES TO PARASITES IN MARINE AND ESTUARINE COMMUNITIES

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Variation in the traits that mediate interactions between hosts and their parasites often have an underlying genetic basis. Such adaptive genetic variation can play an important role in the patchy, non-normal distribution of parasites within host populations and is central to co-evolutionary dynamics. We surveyed one metric of adaptive genetic variation for complex traits (i.e., heritability) across marine and estuarine host–parasite interactions. They found 130 estimates of heritability in host-response traits (survivorship, growth, and parasite load) to micro- and macro-parasites for 24 species of hosts. They could find no estimate of heritability within any parasite, nor in any seaweed or vascular plant; these are clear gaps in the literature. Heritability in host-response traits had a mean of 0.297, indicating substantial adaptive genetic variation in host-response traits within populations. Heritability was greater among mollusk hosts relative to fish or crustacean hosts and tended to be greater in response to micro-parasites than to macro-parasites and when parasites were deliberately manipulated versus more natural infections. There were no differences across host-response traits, the environmental context (i.e., in tanks, sea pens, or the field), or studies that incorporated molecular markers into the experimental design or not. Abundant heritability means that marine and coastal host species have capacity to co-evolve with their parasites and that ecological patterns of parasite aggregation have a strong genetic component. This genetic variation also provides some hope for evolutionary resilience in ecosystems that continue to see increases in disease prevalence.

14. FIRST REPORT OF A MONOGENOID, *DACTYLOGYRUS NOBILIS* LONG AND YU, 1958 (DACTYLOGYRIDAE) INFECTING BIGHEAD CARP, *HYPOPHthalmichthys nobilis* IN NORTH AMERICA WITH PHYLOGENETIC ANALYSIS AND INVENTORY OF PARASITES INFECTING INVASIVE FISHES IN THE UNITED STATES

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Exotic parasites of exotic, invasive fishes concern fisheries managers, fish culturists, and fish disease diagnosticians because they comprise potential introduced pathogens that can harm cultured hosts and

could theoretically harm sympatric wild fishes. Despite the concern of invasive fishes and their parasites in North America, few parasites are reported from invasive fishes there. In the US, silver carp, *Hypophthalmichthys molitrix* (Valenciennes, 1844) and bighead carp, *Hypophthalmichthys nobilis* (Richardson, 1845) (both Cypriniformes: Xenocypridae) have been introduced into the Mississippi River Basin. Native to Asia, these carps were originally introduced into the US to control algae in aquaculture ponds and wastewater treatment facilities. Herein, silver carp and bighead carp were gill-netted in the Arkansas and Cache rivers, Arkansas in 2025 and necropsied. We collected two exotic, ectoparasitic flatworm species of *Dactylogyrus* (Monogeneoidea: Dactylogyridae) infecting the gill rakers. Dactylogyrids were removed and treated properly for morphological and molecular analyses. Morphology specimens were illustrated using a compound microscope equipped with DIC optical components and a drawing tube. Preserved specimens were sequenced (28S rRNA gene and *ITS1*) and included in maximum likelihood phylogenetic analyses. Dactylogyrids collected from silver carp and bighead carp were morphologically diagnosed as *Dactylogyrus* cf. *skrjabini* and *Dactylogyrus nobilis* Long and Yu, 1958, respectively; sequences generated for each were identical to those of conspecific, morphologically identified sequences in GenBank. The present study is the first report of a monogenoid infecting bighead carp in North America. This report highlights the under sampling of invasive fishes for parasitic infections in North America.

15. FURTHER OPTIMIZATION OF *PARELAPHOSTRONGYLUS TENUIS* SEROLOGICAL ASSAY

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Parelaphostrongylus tenuis is a parasitic nematode commonly found in the meninges of its definitive host, the white-tailed deer (*Odocoileus virginianus*). In atypical hosts such as elk (*Cervus canadensis*) and moose (*Alces alces*), the parasite migrates abnormally through the central nervous system, often resulting in neurological disease and mortality. Currently, the only definitive diagnostic method for *P. tenuis* infection is postmortem identification of the parasite, limiting the ability to detect and manage infections in populations of live animals. To address this, an antemortem diagnostic assay using enzyme-linked immunosorbent assay (ELISA) technology based on synthetic peptides based by predicted immunogenic epitopes specific to *P. tenuis* was developed. Several peptides were identified as reactive, with peptides 15, 16, and 38 showing the most significance. Peptide cocktails (15/38 and 16/38) are evaluated for serological reactivity using positive and negative sera from moose and elk. The difference of means of the optical density for positive and negative controls and consistency between plates is assessed to determine the performance of each peptide cocktail in each species. This research is ongoing and hopes to identify a consistent difference between peptide cocktails that will allow for increased accuracy of the *P. tenuis* serological assay in moose and elk, improving early detection and informing wildlife management and conservation efforts.

16. MOLECULAR DETECTION OF WHITE SPOT SYNDROME VIRUS (WSSV) AND YELLOW HEAD VIRUS (YHV) IN WILD-CAUGHT NORTHERN BROWN SHRIMP (*FARFANTEPENAEUS AZTECUS*), NORTHERN WHITE SHRIMP (*LITOPENAEUS SETIFERUS*), AND ROUGH MANTIS SHRIMP (*SQUILLA EMPUSA*) FROM THE GULF OF AMERICA

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White Spot Syndrome Virus (WSSV), Yellow Head Virus (YHV), and Infectious Myonecrosis Virus (IMNV) comprise demonstrable pathogens in shrimp aquaculture globally but their distribution in nature and occurrence among wild shrimps is less studied. Herein, we used conventional PCR assays to opportunistically surveil for these viruses among wild shrimp specimens that were captured by trawl in the Gulf of America

during the 2025 Summer Bottom Groundfish Survey conducted by the National Oceanic and Atmospheric Administration's (NOAA) National Marine Fisheries Service (NMFS). A total of 90 shrimp specimens were sampled and processed for virology herein: 56 brown shrimp (*Farfantepenaeus aztecus*), 24 white shrimp (*Litopenaeus setiferus*), and 10 rough mantis shrimp (*Squilla empusa*). Muscle tissue was collected for DNA and RNA extractions and screened for WSSV, YHV, and IMNV. Of 90 shrimp specimens examined, 11 were positive for WSSV (8 northern brown shrimp [9%] + 3 northern white shrimp [3%]) and 4 were positive for YHV (3 northern brown shrimp [3%] + 1 mantis shrimp [1%]). This is the first record of an infection by YHV in a wild Gulf of America shrimp.

17. RISK FACTORS, PREVALENCE, AND COMPARISON OF METHODS FOR DIAGNOSING *TOXOPLASMA GONDII* IN VARIOUS WILDLIFE SPECIES OF THE SOUTHEASTERN USA

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Toxoplasma gondii is a zoonotic protozoan parasite with a broad host range that infects most endothermic species. Although it is a leading cause of foodborne illness worldwide, it remains a neglected parasite. Increased research on *T. gondii* can better inform the public about risk factors and disease prevention. The goal of this study is to compare three diagnostic methods for detecting *T. gondii* in various avian and mammalian wildlife species. The first method, Modified Agglutination Test (MAT), detects *T. gondii* antibodies in serum samples. The second method was histological screening for tachyzoites and bradyzoites in formalin-fixed tissues. The third method was Polymerase Chain Reaction (PCR) testing frozen tissue samples, with positive samples submitted for sequencing to further identify parasite species. MAT results showed 56/244 (23.0%) samples were seropositive. A total of 234 histology slides were prepared from formalin-fixed heart, brain, spleen, and liver tissues. To date, 168/234 (72.0%) have been evaluated, and only 1/168 (0.6%) showed *T. gondii* histologically. PCR testing was conducted on 228 frozen tissue samples, with 41/228 (18.0%) testing positive. Of these, 1/41 (2.0%) was identified as *T. gondii* or the similar species *Hammondia* spp., while 40/228 (17.5%) were other cyst-forming parasites. Current findings suggest MAT may be more sensitive than histology or PCR alone. Ongoing research will expand serological, histological, and molecular testing, map infection prevalence, and examine transmission patterns, including host diet (carnivore vs. herbivore).

18. NOVEL *MANSONELLA OZZARDI*-LIKE NEMATODE IN BLACK BEARS AND RACCOONS OF EAST TENNESSEE

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Mansonella ozzardi-like nematodes have been reported sporadically in black bears in Japan and the States (U.S.), and, most recently, have been reported in raccoons in the U.S. *Mansonella ozzardi* is a human filariid that can cause mansonelliasis in humans. Little is known about the *M. ozzardi*-like parasite that infects bears and raccoons. We analyzed blood samples from 93 American black bears (*Ursus americanus*) and 47 raccoons (*Procyon lotor*) in eastern Tennessee from 2022 to 2025. A modified Knott's test was performed on all samples. Microfilaria was found on a total of 66 (66/93, 71%) bears and 15 (15/47, 32%) raccoons. For both bears and raccoons, microfilaria sizes ranged from 225 and 275µm long and 2.5 to 5µm wide. Average length and width for microfilaria found in bears was 254.4µm (± 16µm), and 4µm (± 1.2µm). For raccoons, average length and width was 255µm (± 8.5µm), and 2.5µm (± 0µm). Conventional PCR using filarial ITS F (5'- TTCCGTAGGTGAACCTGC-3') and filarial ITS R (5'-ATATGCTTAAGTTCAGCGGG-3') primers was performed on a select number of positive samples. PCR samples sent to sequencing came back as 85.57% to 92.61% similar to *Mansonella ozzardi*. The relatively high prevalence in bear and raccoon populations of this region emphasizes the need to address knowledge gaps about this novel filarial

nematode, including its life cycle, anatomical location of the adult nematodes, its pathologic impact on host species, and its zoonotic potential.

19. OPTIMIZING TREATMENT FOR PRIMARY AMOEBIC MENINGOENCEPHALITIS CAUSED BY *NAEGLERIA FOWLERI*

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Naegleria fowleri is a pathogenic free-living amoeba that causes primary amoebic meningoencephalitis (PAM). PAM is a rare but rapidly progressing central nervous system infection with a fatality rate exceeding 97% and a median time from symptom onset to death of approximately five days. Treatment currently relies on a multidrug regimen comprising up to seven antimicrobial, antifungal, and antiparasitic agents, largely selected empirically based on either survivor data or activity against other pathogens, rather than on systematic evaluation against *N. fowleri*. The current standard of care, informed by the most recent documented survivor in the United States, includes amphotericin B, miltefosine, azithromycin, fluconazole, rifampin, dexamethasone, and nitroxoline. The goal of this study is to characterize the drug-drug interaction profiles of compounds included in this regimen. Using *in vitro* viability-based assays and two-drug checkerboard combination testing, we quantify individual drug toxicity against *N. fowleri* trophozoites and assess combinatorial effects to identify toxic, additive, or synergistic interactions that may enhance or compromise therapeutic safety.

20. PREVALENCE OF *CYTAUXZOOM FELIS* CYTOCHROME-B VARIANTS IN DOMESTIC CATS AND BOBCATS

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Cytauxzoonosis, a highly fatal disease of domestic cats and other felids caused by the apicomplexan *Cytauxzoon felis* is treated with atovaquone and azithromycin (A&A) with 60% (highest) survival rates. Atovaquone, a structural analog of a protozoan mitochondrial protein called ubiquinone, inhibits binding of ubiquinone to cytochrome bc1 in the electron transport chain. Atovaquone resistance has recently been associated with M128 cytochrome-b mutations in *C. felis*, however its prevalence and relationship to clinical disease in natural populations remains poorly defined. This study evaluated cytochrome-b mutations at M128 to determine the prevalence of each mutation in two felid populations, bobcats (*Lynx rufus*) and domestic cats (*Felis catus*). We also evaluated if these mutations were associated with clinical outcomes in domestic cats (clinically ill or subclinical infections). Domestic cat samples included subclinical infections (n=23) and clinical cytauxzoonosis cases (n=20), while the bobcat samples were subclinical. In domestic cats, 87% subclinical cats and 85% clinical cats were associated with M128V mutations. Likewise, M128I mutation was associated with 9% subclinical and 50% clinical cats' "A" point mutations, and 13% subclinical and 45% clinical cats' "T" point mutations. In bobcats (n=69), T was rare (10%), while A (67%) and G (80%) were common with all 3 documenting heteroplasmy. Overall T mutation was observed in 11% subclinical and 45% clinical infections. These outcomes establish enrichment of T mutation in clinical domestic infections and demonstrate a foundational cytochrome-b variant distribution in untreated populations. This supports a need to continue molecular surveillance of *C. felis* for probable resistance-associated variants.

21. NOT SO RIDLEY-CULOUS: *PLESIOCHORUS* SP. IN AN ADULT KEMP'S RIDLEY *LEPIDOCHELYS KEMPII* IN THE MISSISSIPPI SOUND

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The Kemp's ridley sea turtle (*Lepidochelys kempii*, Lk) is a critically endangered species within the Gulf of Mexico and along the Atlantic seaboard. As the most endangered extant sea turtle species, recovery depends on conservation efforts and rehabilitation. MS-LT-005 (005) was an adult male Lk that was reported struggling to swim near Ship Island on April 28, 2025. Repeated CT scans performed throughout rehabilitation showed abnormally increased air-filled spaces within the lungs. Multiple comorbidities ultimately lead to euthanasia on February 10, 2026. On necropsy, 005 had severe musculoskeletal, pulmonary, and hepatobiliary disease. Thirty grossly visible adult trematodes were present within the urinary bladder. Live worms had a narrow fore body and foliate hind body with oral and ventral suckers in the fore body. Twenty-seven specimens were heat-killed and preserved in 70% molecular-grade ethanol while two intact worms and associated bladder tissue were fixed in 10% neutral-buffered formalin for histopathological examination. Based on morphology and anatomic location being the urinary bladder, a presumptive diagnosis of *Plesiochorus* sp. was made. *Plesiochorus* has been described in four of the seven sea turtles: green, hawksbill, loggerhead, and olive ridley. Genomic DNA was extracted from a whole worm and sequenced using Oxford Nanopore and Illumina sequencing to generate a complete mitogenome and complete nuclear ribosomal operon. Comparative morphology of stained and mounted worms, molecular data and phylogenetic analyses using mitochondrial data and 28S rDNA will be presented. To our knowledge, this case represents the first report of a *Plesiochorus* sp. in an Lk sea turtle.

22. FROM CLAM TO FISH: LIFE CYCLE ECOLOGY OF DIGENEANS *LASIOTOCUS TRACHINOTI* AND *L. CHOANURA* IN COQUINAS *DONAX* SPP.

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Bivalves play integral roles within coastal food webs, and often serve as intermediate hosts for parasites, which can have significant impacts on their hosts' fitness, and consequently on ecosystem dynamics. Along the US eastern coast, coquina clams *Donax fossor* and *D. variabilis* are important prey for fish, crabs, and birds and are commonly infected by metacercariae of two digeneans, *Lasiotocus trachinoti* and *L. choanura*, which infect their inhalant siphon and foot, respectively. The siphon and foot are essential to the coquinas' survival. The musculature of these structures allows for siphon retraction and rapid burrowing that facilitates predator avoidance and impediment of these functions may increase clams' exposure to predators and the likelihood of siphon nipping. We thus hypothesized that the presence of metacercariae alters these structures. Histological observations show some tissue alterations, but no strong evidence of severe damage nor host reaction. To further investigate the potential impacts of metacercarial infection on these coquinas, we studied siphon nipping as a possible non-lethal transmission pathway of *L. trachinoti* to its definitive host, the Florida pompano, *Trachinotus carolinus*. Using paired predator-present and predator-absent experiments, we exposed coquinas to fish for 48 hours and quantified nipped siphons, whole-clam consumption, and infection intensity in clam inhalant siphon and foot. Preliminary results show a higher percentage of siphons nipped in coquinas in predator-present aquaria. Examining parasite effects on host tissues and alternative transmission mechanisms will help resolve key aspects of the life cycles of these digeneans and their interactions with their bivalve hosts.

23. TAPING TOGETHER THE PUZZLE OF WILD TURKEY DECLINES: IDENTIFICATION OF THE CESTODE SPECIES INFECTING THE EASTERN WILD TURKEY (*MELEAGRIS GALLOPAVO SILVESTRIS*) IN TENNESSEE

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In the past two decades, 15% of Eastern wild turkey (*Meleagris gallopavo silvestris*) populations have been lost. One way to track stressors affecting populations is by monitoring indicator parasite species. Because of their intricate relationship with their host and environment, cestode parasites may act as an indicator of ecological balance as well as flock health. The most recent report on the prevalence of cestode species in wild turkeys in Tennessee was in 1984. The aim of this study is to establish updated baseline morphological and genetic reference of cestode species infecting wild turkey populations in Tennessee. Post-mortem complete gastrointestinal tract flushes were collected from 200 turkeys at hunter harvest check stations across the state of Tennessee during the 2020-2022 seasons. All visible helminths were isolated from the flushes and stored in 70% ethanol. Cestodes will be identified in May 2025 at the Smithsonian Museum of Natural History using morphological techniques: slide mounting, scanning electron microscopy, and comparison to historical samples in the US National Parasite Collection. This will be paired with molecular identification and phylogeny through PCR and DNA sequencing. By creating a cestode species reference for the Eastern wild turkey, we hope to identify differences in infection distribution across the state of Tennessee, providing insight into regional flock health. This work will build a parasite-based model for population health surveillance that may be applied to other wild and declining species.

24. BLACK BASS GILL LICE: TAXONOMY AND GENETICS OF *ACHTHERES MICROPTERI* WRIGHT, 1882 (COPEPODA: LERNAEPODIDAE) INFECTING LARGEMOUTH BASS, *MICROPTERUS SALMOIDES* AND SPOTTED BASS, *MICROPTERUS PUNCTULATUS* IN ALABAMA AND NORTH CAROLINA

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The “gill lice” *Achtheres micropteri* Wright, 1882 and *Achtheres pimelodi* Krøyer, 1863 (Copepoda: Lernaepodidae) reportedly infect buccal cavity and “gill” of several species of black basses (Centrarchiformes) and catfishes (Siluriformes), respectively. Both of these lernaepodids need to be reassessed morphologically and genetically: their original descriptions are incomplete, their type hosts ambiguously assigned or indeterminate, type specimens not deposited or never assigned, existing vouchers at Smithsonian are not available for dissection (making species-level identification impossible as the original description is based on morphology only), the synonymy that collapsed these species was unjustified and over-generalized, no useful nucleotide sequences exist for either species, and nucleotide sequences representing the diversity of accepted species of *Achtheres* are few (none represented a North American species of *Achtheres* previously). Herein, we provide a supplemental description of *A. micropteri* based on newly-collected specimens from largemouth bass, *Micropterus salmoides* and spotted bass, *Micropterus punctulatus* from reservoirs in Alabama and North Carolina. Females of *A. micropteri* differed from those of *A. pimelodi* by having five (vs. one) sickle-shaped (vs. conical) denticles on the second antennae exopod distally and having three setae (ventral, central, dorsal) on the endopod maxillules (vs. two; dorsal and ventral). *Achtheres micropteri* males have three maxillular endopod setae (vs. two) and an armed (vs. corrugated pad) maxilla myxal area. We also add character states associated with the maxillular exopod, maxilliped myxal area, vestigial legs, oviduct, and caudal ramus to taxonomically differentiate *A. micropteri*. Our COI sequences of *A. micropteri* were recovered sister to other *Achtheres* spp.

25. FLIES AS ENVIRONMENTAL DRONES IN WILDLIFE DISEASE ECOLOGY: TRACKING PERSISTENCE OF *HISTOMONAS MELEAGRIDIS* IN THE BLACK BLOW FLY, *PHORMIA REGINA* (MEIGEN)

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Histomonas meleagridis is the protozoal causative agent of blackhead disease, a highly lethal disease of poultry, causing 80-100% mortality in infected domestic turkey flocks. Outbreaks in wild turkey populations often go undetected due to difficulty in locating turkey carcasses for diagnostic screening. However, there is one insect that has evolved to locate carcasses quickly after death: the blow fly (Diptera: Calliphoridae). Blow flies are cosmopolitan decomposers that naturally sample DNA while interacting with carrion and can thus be used to non-invasively monitor vertebrate populations and vertebrate associated microbes. This study aimed to investigate the acquisition and persistence of *H. meleagridis* DNA in the guts of the black blow fly, *Phormia regina*. Three-day old lab-reared adult flies were individually exposed for four hours at consistent conditions to *H. meleagridis*-infected turkey liver, store-bought turkey fillet (=uninfected), or water. Three females and three males were then freeze-killed at 0, 24, 72, 96, and 120 hours. Flies underwent gut dissection, DNA extraction, PCR with *Histomonas*-specific primers, and Sanger sequencing. Results demonstrate that *H. meleagridis* DNA can be detected in blow flies up to 96 hours post-exposure and in the excrement of infected flies immediately after feeding. Field collections and rapid molecular methods will be deployed to evaluate the feasibility of wild caught flies as *H. meleagridis* sentinels in eastern Tennessee, enabling detection of *Histomonas*-positive carcasses allowing for rapid response and mitigation. This work establishes a foundation for utilizing blow flies as environmental sentinels, bridging parasitology, entomology, and wildlife disease ecology.

26. TEMPORAL CHANGES IN ZOOPLANKTON COMMUNITY STRUCTURE IN RELATION TO INFECTIONS BY *ANGUILLICOLA CRASSUS*

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The introduced swimbladder nematode *Anguillicola crassus* is pathogenic and negatively impacts eel hosts, including juvenile American eels (*Anguilla rostrata*), a species of ecological and economic importance along the U.S. Atlantic coast. Although it is known that *A. crassus* relies on zooplankton for transmission, local intermediate hosts of this parasite are yet to be identified. Thus, understanding local zooplankton community composition, identifying infection in particular species, and determining the temporal variation of both are essential to our assessment of recruiting juvenile eel exposure risk to this parasite. Our goal is to integrate parasite detection with observed zooplankton community patterns, which will allow the identification of candidate intermediate hosts and clarify how changes in zooplankton communities shape transmission of this parasite. We collected monthly triplicate zooplankton samples over one year in one locality where recruiting eels are known to become infected, and we quantified the zooplankton community composition to the morphospecies level. Ongoing work includes DNA extraction and RT-qPCR assays to screen infection of morphospecies by *A. crassus*. Preliminary analyses reveal clear temporal shifts in morphospecies abundances, with several morphospecies exhibiting distinct seasonal patterns. These fluctuations indicate that putative intermediate host availability changes seasonally, potentially influencing opportunities for parasite transmission. This study will provide a temporal assessment of zooplankton community composition in relation to *A. crassus* exposure risk in South Carolina estuaries and will advance our understanding of host–parasite interactions in a vulnerable native eel species.

27. A NEW SPECIES OF FISH BLOOD FLUKE INFECTING BLACK BASSES (*MICROPTERUS* SPP.) FROM THE COOSA RIVER, ALABAMA

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Fish blood flukes (Digenea: Chimaerohemecidae; Acipensericolidae; Sanguinicolidae; Elopicolidae; Aporocotylidae) are vectored by snails, bivalves, or polychaetes and can kill or debilitate cultured freshwater, marine and estuarine fishes. Freshwater fish blood flukes from North America (Sanguinicolidae) infect trouts (Salmoniformes), basses (Centrarchiformes), minnows (Cypriniformes), and walleye (Perciformes). *Sanguinicola huronis* infects largemouth bass, *Micropterus salmoides* and smallmouth bass, *Micropterus dolomieu* in Wisconsin. However, its morphological description is poor and incomplete, and the single type specimen is damaged making confirmation or comparison impossible. During 2022–2023, the heart/gill of 15 of 381 largemouth bass and 16 of 368 spotted bass, *Micropterus punctulatus* from Neely-Henry Lake (Coosa River) were infected with 13 adults and several juvenile specimens of a new species representing a new genus. Specimens were fixed in 10% formalin for morphology and preserved in 95% ethanol for DNA extraction and phylogenetic analysis. The new species differs from the other blood flukes by having lateral tegumental spines with a recurved distal tip, a vasa efferentia lacking obvious coalesced efferentia along midline, a triangular ovary, and an oviduct that curves around the terminal portion of the ovary. The 28S phylogeny recovered sequences of the new species as a lineage sister to all sequences representing species of *Sanguinicola*, *Pseudosanguinicola occidentalis*, and related cercarial sequences from Poland and Australia. This is the first fish blood fluke infecting a spotted bass and the second report from largemouth bass. Understanding this group of parasites biodiversity, life cycle, and pathogenicity in black basses is important regarding management of the resource.

28. DESCRIPTIONS AND LIFE CYCLES OF THREE NEW SPECIES OF *PROTEROMETRA* HORSFALL, 1933 (DIGENEA: AZYGIIDAE) INFECTING ENDEMIC PLEUROCERIDS AND FISHES FROM THE DUCK RIVER, TENNESSEE

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Azygiidae (Platyhelminthes: Digenea) comprises marine and freshwater trematodes that infect mainly freshwater fishes in Eurasia, North America, and Africa. Most azygiids are macroscopic and are either ectoparasitic (infecting the buccal cavity and pharyngeal esophagus) or endoparasitic (infecting the stomach and intestine). Unlike vast majority of trematodes, however, azygiids exceptionally have a truncated life cycle (lacking an encysted metacercaria): a macroscopic furcocystocercous cercaria asexually reproduces in a gastropod intermediate host and matures in the gut of a fish. The naturally shed cercariae flamboyantly swim (presumably to mimic the appearance and behaviors of the prey of the fish host and thereby to lure the fish to eat them) and are morphologically distinctive, whereas their respective adults are reportedly morphologically similar. Species of *Proterometra* Horsfall, 1933 primarily ectoparasitic and infect endemic pleurocerids and centrarchids. They are distinct from other azygiids by having a progenetic cercaria (having eggs) and a vitellarium that extends anteriorly into the forebody. Our recent work on the parasites of Southeastern freshwater fishes and snails that vector infections has revealed several new species and interesting life cycle adaptations. We herein describe and elucidate life cycles of 3 new species of *Proterometra* infecting endemic snails (pleurocerids of *Lithasia* Haldeman, 1840) and fishes (green sunfish,

Lepomis cyanellus Rafinesque, 1819 and percids of *Percina* Haldeman 1842) in the Duck River (Tennessee). This is the first report of an azygiid from the Duck River, which is known as the most biodiverse river in North America, and only the second species of *Proterometra* from Tennessee.

29. AN EX VIVO ASSAY FOR CHARACTERIZING CHEMICAL INHIBITION OF MYXOZOAN SPORE ATTACHMENT TO THE FISH HOST

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Myxozoans are spore forming endoparasites, responsible for fish diseases including whirling disease, enteronecrosis and proliferative gill disease. Like their free-living cnidarian relatives, myxozoans have nematocysts, which contain tubules that discharge explosively when triggered by specific stimuli. In free-living cnidarians, nematocysts are used for capturing prey and deterring predators, but in myxozoans they are used for attaching to their hosts, as the essential first step of the infection process. The specific mechanism of myxozoan nematocyst discharge remains largely unknown, but previous work suggests that salts, voltage gated calcium channels, P2X and TRPA receptors are involved. In this study, we used *Myxobolus cerebralis*, the cause of salmonid Whirling Disease, and whose life cycle we maintain in the laboratory. First, we demonstrated that the parasite spores could attach *ex vivo* to pieces of gill tissue, using scanning electron microscopy to visualize firing and attachment. Then, we developed a benchtop apparatus to assess the effects of compounds known to interfere with cell signaling mechanisms. In this pilot study, we found that metal salts (NaCl, CaCl₂, MgCl₂, GdCl₃), camphor oil, and 2-Methylthio-ATP inhibited spore attachment, while other chemicals were confounded by initial dissolution in dimethylsulfoxide (DMSO), which enhanced spore attachment. This assay will allow us to screen a wide range of compounds *ex vivo*, prior to testing only a shortlist of targets using live fish. Our goal is to understand myxozoan host sensing and signaling, to ultimately prevent parasite infections in fish.

30. REELFOOT LAKE, TENNESSEE, USA: TURTLE BLOOD FLUKE CAPITAL OF THE WORLD. A HISTORY AND UPDATE SINCE BYRD, 1939

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Reelfoot Lake (National Natural Landmark) is an ~18,000-acre natural lake in northwestern Tennessee formed by earthquakes in the New Madrid Seismic Zone during Winter of 1811. It comprises a relatively unique biological community (supporting >30 rare or endangered plants and animals) occupying a unique geological feature (recently-formed tectonic lake). Locally called "Turtle Capital of the World," Reelfoot Lake is the type locality for 12 species (of four genera) of turtle blood flukes (TBFs; Platyhelminthes: Digenea: Schistosomatoidea) that collectively infect seven Reelfoot Lake turtle species: snapping turtle, *Chelydra serpentina* (Chelydridae); common musk turtle, *Sternotherus odoratus* (Kinosternidae); southern painted turtle, *Chrysemys dorsalis* (Emydidae); river cooter, *Pseudemys concinna* (Emydidae); Cumberland slider, *Trachemys scripta troostii* (Emydidae); false map turtle, *Graptemys pseudogeographica* (Emydidae); and spiny softshell, *Apalone spinifera* (Trionychidae). Herein, we provide a taxonomic summary of the TBFs we collected from these and additional turtle species during a 2023 parasitological survey of Reelfoot Lake fishes, reptiles, amphibians, and invertebrates. Reelfoot Lake is important to the taxonomy of TBFs *sensu lato* as the type locality for several taxonomically diverse and morphologically highly divergent TBF lineages. Several important TBF taxa there needed to be recollected and redescribed, and no taxonomically verifiable nucleotide sequences existed for these species previously. We collected species of *Spirorchis* MacCallum, 1918, *Vasotrema* (Stunkard, 1928) Roberts and Bullard, 2017, and *Unicaecum* Stunkard, 1928 and provide updated morphological appraisals of those species combined with a new phylogenetic analysis using all available nucleotide sequences.

31. EDNA METABACORDING AS COMPLEMENTARY TOOL TO TRADITIONAL METHODS FOR CHARACTERIZING AQUATIC PARASITE DIVERSITY

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Traditional parasite survey methods have been and remain essential for parasite diversity characterization. However, these methods are often invasive, time-intensive, and require extensive taxonomic expertise. Adapting metabarcoding and high-throughput sequencing (HTS) of environmental DNA (eDNA) to complement traditional methods offers several benefits, including expediting parasite biodiversity surveys and reducing direct impact on host species. As such, this study aimed to compare traditional and eDNA methods in their capacity to characterize parasite diversity in terms of richness, community dissimilarity, and taxonomic resolution. The traditional sampling campaign targeted fish and invertebrate hosts, whereas the eDNA sampling campaign included sediment and water samples. Four habitats were sampled – an intermittent wetland, an estuarine tidal creek, a brackish impoundment, and a freshwater pond – within a natural preserve in South Carolina, USA. Preliminary results suggest that the degree to which traditional methods versus eDNA metabarcoding and HTS could capture parasite diversity is dependent on the habitat in question. In the wetland and pond, parasite richness was better captured through eDNA metabarcoding and HTS, while in the tidal creek and the impoundment, more taxa were detected by traditional methods. These results indicate that eDNA metabarcoding with HTS is particularly effective in apparently depleted habitats. It is certainly a promising technique to capture and characterize parasite diversity, but it is limited to the availability of reference sequences in databases, which lags behind especially in parasitology. At this stage, both methods are best used concurrently in explorative studies as they complement each other.

32. DIGENEANS FROM FISHES SOURCED FROM THE OREGON II SUMMER GROUND FISH SURVEY OFF FLORIDA **Curran SS, Brule JH, Bullard SA**

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One of us (JHB) collected fish parasites while aboard NOAA's *Oregon II* (R 332) during the 2025 Summer groundfish survey in the Gulf of America, largely off southern and western Florida (1-15 June 2025). We report on 16 species of digeneans he collected (infecting the stomachs, intestines, and washed from gills) from 15 species of trawled fishes. These comprised: Acanthocolpidae (*Stephanostomum interruptum*); Bucephalidae (*Bucephalus* cf. *brevitentaculatus*); Didimozoidae (1 sp.); Gymnophalloidea, *incertae sedis* (possible n. gen., n. sp.); Hemiuridae (*Genolinea* sp., *Lecithochirium floridense*, *Myosaccium* cf. *opisthonemae*, *Parahemiurus* cf. *anchoviae*, *Parahemiurus* sp.); Lepocreadiidae (*Bianium plicatum*); Monorchidae (*Alloinfundiburictus* sp.); Opicoelidae (*Opicoelina* cf. *helicoleni*, *Opicoelina* cf. *scorpaenae*, 2

Opecoeloides spp), and Zoogonidae (*Glaucivermis spinosus*). Vouchers of each species were prepared and 28S rRNA sequences from most were generated and compared with available sequence libraries. Our results revealed widespread identification errors in GenBank and some past and recent literature, which will be detailed in our presentation.

33. TAXONOMY AND PARASITOLOGY OF SOME VIVIPARID SNAILS FROM ALABAMA AND ARKANSAS

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We investigated the taxonomy of viviparid snails (Gastropoda: Viviparidae) collected from Garland County, Arkansas and Cullman County, Alabama and examined them for parasitic infections. Using provisional morphological sources (photos, general accounts) and by comparing our newly-generated 18S, 28S, and COI nucleotide sequences with those in GenBank (which includes many misidentified sequences and therefore must be used with extreme caution in the realm of taxonomy), we identified the Arkansas viviparid as a species of *Cipangopaludina* Hannibal, 1912 and the Alabama viviparid as a species morphologically and genetically similar to or conspecific with the Japanese mystery snail, *Cipangopaludina japonica* (E. von Martens, 1861) Hannibal, 1912. Most assuredly, the number of available experts to morphologically identify snails is clearly deficient in the Southeastern United States, and we struggled to find useful taxonomic keys and species accounts of the snails we collected. Based on that, we consider these identifications provisional. The collected parasites were observed alive during dissection or heat killed, fixed in formalin or preserved in 95% EtOH for morphology and nucleotide sequencing, respectively, and ultimately whole-mounted on glass slides in Canada balsam. We collected several larval specimens of *Spiroxys* sp. (Nematoda: Gnathostomatidae) in Arkansas only; metacercariae of *Polylekithum ictalurid* (Gorgoderioidea) in Alabama only; and encysted metacercariae of two species of *Alloglossidium* (Plagiorchioidea) in both Alabama and Arkansas collectively. The overall results of the study indicate that these (probably exotic) viviparid snails are becoming infected with parasites that are native to the area and mature in sympatric, native aquatic vertebrate species.

34. HIGH THROUGHPUT QUANTITATIVE TRACKING OF *PLASMODIUM FALCIPARUM* CLONAL BLOOD STAGE PARASITE GROWTH

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New systematic profiling of drug effects is in demand due to limitations in existing approaches to evaluate comprehensive drug effects and distinguish heterogeneity in mixed populations. One challenge is the underdeveloped methods for investigation of causal association between artemisinin induced dormancy and recrudescence in *Plasmodium falciparum*. We developed quantitative Tracking After Chemotherapy Exposure (qTRACE) and an artificial intelligence (AI) mode to evaluate cytotoxic and cytostatic effects simultaneously at single parasite resolution in a high throughput platform. qTRACE is based upon the observation that individual parasites grow into colonies that can be quantified for numbers of viability and growth rate. Applying qTRACE, we revealed parasite-drug killing dynamics after artemisinin exposure, finding up to 50% of viable parasites arise directly from recovery of artemisinin induced dormancy. We further developed next generation qTRACE integrated with deep learning-based

segmentation and analysis, thereby directly linking continuous, time-lapse phenotypes of label-free live *P. falciparum*. Our results confirmed the viability of dormant ring stages and that recovery rates differ between artemisinin-susceptible and -resistant *P. falciparum*.

35. A GENETIC AND ECOLOGIC INVESTIGATION INTO ESOPHAGEAL MONOGENOIDS ALONG THE SOUTHEASTERN SEABOARD OF THE UNITED STATES

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Esophageal monogenoids have only rarely been studied. A total of 493 individuals of 12 fish species were collected along the US southeastern seaboard from latitudes 29°14'N to 35°19'N from June to October 2024 and May to October 2025. The esophagus of each fish was examined for the presence of monogenoids, which were tallied for each host. At least one representative monogenoid from each host species was preserved for gene sequencing (LSU, COI), while the remainder were fixed for the purpose of morphologic examination. No individual of six of the 12 fish species were found infected (*Balistes capriscus*, n=50; *Caranx crysos*, n=26; *Caranx hippos*, n=9; *Rachycentron canadum*, n=11; *Seriola rivirolana*, n=3, and *Seriola dumerili*, n=1). Infected fish were *Chloroscombrus chrysurus* (1.2%, 1/86), *Micropogonias undulatus* (34.4%, 11/32), *Selene setapinnis* (17.9%, 19/106), *Selene vomer* (18.6%, 8/43), *Trachinotus carolinus* (6.4%, 3/47), and *Trichiurus lepturus* (40.5%, 32/79). DNA sequencing indicated three genetically distinct species of monogenoid (LSU p-distances = 5.7-7.7% (755 nucleotides), COI p-distances = 13.7-18.9% (540 nucleotides)), two of which infected multiple host species and one only *T. lepturus*. Multi-monogenoid species infection occurred in all fish species except *M. undulatus*, which harbored a single species with infra-intensity up to 37 worms. No infections occurred north of latitude 33°89'N. Morphological identification of these genetically distinct monogenoids is currently under evaluation. These data demonstrate the presence of multiple species of esophageal monogenoids along the southeast US coast, possibly supporting an opportunistic nature of esophageal monogenoids with nevertheless potential for relative host specificity.

36. 'SO MANY SPECIES, SO LITTLE TIME:' THE MESSAGE OF DACTYLOGYRIDAE IN BRAZIL

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The Neotropical realm is recognized as the most species-rich region globally, encompassing diverse biomes ranging from high-altitude grasslands to extensive rainforests. Within this realm, Brazil is the most biologically diverse country, harboring an estimated 10-12-% of the world's biodiversity. Although 135,470 valid animal species-level taxa have been documented in Brazil by 2026, many remain undescribed. This study focuses on Monogenoidea Neodermata, a group of exclusively parasitic Platyhelminthes that accounts to over 5,000-6,000 species described worldwide. The current level of knowledge of Monogenoidea diversity in Brazil is estimated by the total species richness of freshwater Dactylogyridae using Bayesian modeling techniques. Analyzing the species records of this family and its host group (Actinopterygii) from the *Catálogo Taxonômico da Fauna do Brasil* (CTFB) - comprising 647 valid species – the model estimates the total richness of freshwater Actinopterygii, all putative hosts of the family, in approximately 7,991 species. Based on this estimate, the potential richness of freshwater *Dactylogyridae* in Brazil was projected as 23,575 species (median estimate), which suggests that current records represent less than 3% of the actual diversity. These findings are compatible with evidence derived from the richness of potential host groups, the percentage of these putative hosts already scrutinized, the host-parasite

network, and the spatial distribution of records of parasites. Hence, the results strongly suggested that the diversity of Brazilian Monogeneoidea is vastly underestimated, highlighting a profound taxonomic impediment that necessitates aggressive inventory strategies, enhanced taxonomic training, and increased support for biological sampling and collections to unveil the region's hidden parasitic fauna.

37. RESTABILIZING THE COMMON NAMES FOR LARGEMOUTH BASS, *MICROPTERUS SALMOIDES* (LACÉPÈDE, 1802) HENSHALL, 1881 AND FLORIDA BASS, *MICROPTERUS FLORIDANUS* (LESUEUR, 1822) GOODE, 1876 WITH COMMENTS ON *MICROPTERUS NIGRICANS* (CUVIER, 1828) COPE, 1865

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We advocate that Largemouth Bass is the common name for *Micropterus salmoides* (Lacépède, 1802) Henshall, 1881 and that Florida Bass is the common name for *Micropterus floridanus* (Lesueur, 1822) Goode, 1876. We criticize four specific “naming actions” in Kim et al (2022) that we regard collectively as unwarranted, erroneous, and needlessly confusing. These “naming actions” ignored many foundational recommendations of the ICZN, do not promote new taxonomic or evolutionary understanding, are not justified by a phylogenomic result, and are (expectedly) inherently confusing to the expert taxonomist, fisheries biologist, natural resource manager, and angler alike. We detail our taxonomic and nomenclatural rationale for restabilizing the names for these Black Basses and propose the following remedies based on standard and widely-accepted practices in taxonomy and nomenclature: 1) *Micropterus salmoides* (Lacépède, 1802) Henshall, 1881 is the Largemouth Bass; 2) *Micropterus floridanus* (Lesueur, 1822) Goode, 1876 and *Micropterus nigricans* (Cuvier, 1828) Cope, 1865 remain accepted as junior subjective synonyms of *Micropterus salmoides* (Lacépède, 1802) Henshall, 1881; 3) the common name “Florida Bass” should be abandoned unless and until *Micropterus floridanus* (Lesueur, 1822) Goode, 1876 can be morphologically differentiated from congeners and thereby resurrected from junior subjective synonymy with *Micropterus salmoides* (Lacépède, 1802) Henshall, 1881 (Largemouth Bass), and, if phylogenetic evidence is used to resurrect *Micropterus floridanus* (Lesueur, 1822) Goode, 1876, the work should follow ICZN recommendations; and, 4) if *Micropterus nigricans* (Cuvier, 1828) Cope, 1865 is resurrected, it requires a new common name and must follow ICZN recommendations.