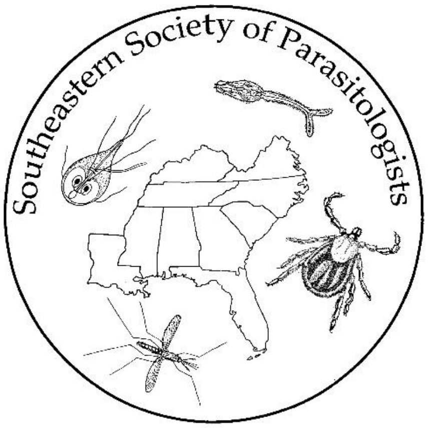
SOUTHEASTERN SOCIETY OF PARASITOLOGISTS

(Affiliate of The American Society of Parasitologists)

PROGRAM & ABSTRACTS



April 20-22, 2023

Hosted by:

Richard A. Gillespie College of Veterinary
Medicine, Lincoln Memorial University
Harrogate, TN

SOUTHEASTERN SOCIETY OF PARASITOLOGISTS

President: Christopher A. Cleveland
President - Elect: Elizabeth R. Gleim
Past-President: Gabriel J. Langford
Vice-President: Kristina M. Hill-Spanik
Council Representative: Gabriel J. Langford
Secretary-Treasurer: Charles T. Faulkner

PAST PRESIDENTS

1969 Elon E. Byrd
1970 Burton J. Bogitsh
1971 Robert B. Short
1972 Felix H. Lauter
1973 James H. Oliver, Jr.
1974 A. B. Weathersby
1975 Reinard Harkema
1976 Gerald W. Esch
1977 John V. Ernst
1978 John McCall
1979 Grover C. Miller
1980 Kenneth C. Corkum
1981 Sharon Patton
1982 Raymond E. Kuhn
1983 John P. Harley
1984 Jeffrey A. Butts
1985 Gayle P. Noblet
1986 John R. Seed
1987 William B Lushbaugh
1988 Leon W. Bone
1989 Robert W. Edwards
1990 Stephen G. Kayes
1991 Michael D. Stuart
1992 William F. Font
1993 Byron L. Blagburn
1994 Larry S. Roberts
1995 Leon Duobinis-Gray
1996 Robin M. Overstreet
1997 John M. Aho
1998 David S. Lindsay
1999 D. Bruce Conn
2000 George W. Benz
2001 Cheryl D. Davis
2002 Oscar Pung
2003 Vincent A. Connors
2004 Charles T. Faulkner
2005 Malcolm E. Powell
2006 Jennifer Spencer
2007 Claire Fuller
2008 Vina D. Faulkner
2009 Michael Yabsley
2010 Alexa Rosypal
2011 Isaure de Buron
2012 Chris Hall
2013 Derek Zelmer
2014 Dennis Kyle
2015 Stephen A. Bullard
2016 Andrea Varela-Stokes
2017 Reginald Blaylock
2018 Reginald Blaylock
2019 Gabriel J. Langford
2020 Gabriel J. Langford
2021 John V. Stokes / Christopher A. Cleveland
2022 Christopher A. Cleveland

PAST VICE-PRESIDENTS

1969 Richard E. Bradley
1970 Gerald W. Benz
1971 Raymond L. Kisner
1972 James S. McDaniel
1973John V. Ernst
1974 Gerald W. Esch
1975 John V. Aliff
1976 Grover C. Miller
1977 Kenneth C. Corkum
1978 Vernon Powders
1979 Raymond E. Kuhn
1980 Jeffrey A. Butts
1981 Larry R. McDougald
1982 William L. Current
1983 Gayle P. Noblet
1984 William C. Grant
1985 William B Lushbaugh
1986 Leon W. Bone
1987 Robert W. Edwards
1988 Michael D. Stuart
1989 Rick L. Tarleton
1990 J. Ed Hall
1991 Byron L. Blagburn
1992 Larry N. Gleason
1993 Robin M. Overstreet
1994 John M. Aho
1995 David S. Lindsay
1996 D. Bruce Conn
1997 George W. Benz
1998 Cheryl D. Davis
1999 Vincent A. Connors
2000 Charles T. Faulkner
2001 Claire A. Fuller
2002 Vina Diderrich-Faulkner
2003 Jennifer Spencer
2004 Isaure de Buron
2005 Edwin C. Rowland
2006 Michael Yabsley
2007 Alexa Rosypal
2008 Heather Stockdale
2009 Shella Mitchell
2010 Derek Zelmer
2011 Andrea Varela-Stokes
2012 Dennis E. Kyle
2013 Stephen A. Bullard
2014 Richard Gerhold
2015 Claire Fuller
2016 Agustín Jiménez
2017 John V. Stokes
2018 John V. Stokes
2019 Elizabeth Gleim
2020 Elizabeth Gleim
2021 Christopher A. Cleveland / Kristina M. Hill-Spanik
2022 Kristina M. Hill-Spanik

Secretary-Treasurer

1969-86 Mary C. Dunn
1987-08 Sharon Patton
2008-12 Vincent Connors
2014-19 Reneé Carleton

Council Representative

1970-71 GW Hunter III
1972 Harry W. Leigh
1973-74 A.B Weathersby
1975 Richard Harkema
2007 Michael Yabsley
2008-10 Sharon Patton
2010-17 Bruce Conn
2017-19 Stephen A. Bullard
2020 Andrea Varela-Stokes

2020-present Charles T. Faulkner

1976 Gerald W. Esch

1977-80 Robert B. Short
1981-83 Gerald W. Esch
1984-00 Sharon Patton
2001-03 Edwin C Rowland
2004-06 Isaure de Buron

2021 Reginald Blaylock

2022 Reginald Blaylock

Past Award Recipients

Meritorious Service Award
1983 Robert B. Short
1985 James H. Oliver, Jr.
1986 A.B. Weathersby
1990 Grover C. Miller
1991 Burton J. Bogitsh
1996 Sharon Patton
1999 John Richard Seed
2004 Gayle P. Noblet
2013 Charles T. Faulkner

President's Award

1986 Mary C. Dunn

Ciordia-Stewart-Porter Undergraduate Student Award

2012 Zachary Adkins
2013 Frank W . Soveg
2014 Candice Alge
2015 John Doran
2016 Abigale Willemse
2017 Carly Haywood
2018 Katie Brittain
2019 Madison Barshick and Jarvis Strickland
2021 Marisa Fonseca
2022 Julia Legiec

Byrd-Dunn Graduate Student
1975 William F. Font
1976 Hugh M. Turner
1977 Raymond S. Kutzman
1978 Kenneth S. Saladin
1979 Dean S. Cunningham
1980 Gregory F. Mathis
1981 Oliver J. Booker, III
1982 Steve J. Upton
1983 Wesley L. Shoop
1984 Dennis E. Kyle
1986 Cheryl D. Davis
1987 Charles T. Faulkner
1988 Victoria H. Mann
1989 Constance E. Bell
1990 Sheila A. Peel
1991 Sara R. Davis
1992 Fred J. Herndon
1993 Rebecca A. Cole & Chrystal L. Mars
1994 Lance W. Fontenot
1995 Julia S. Jackson
1996 Vina R. Diderrich
1997 Derek A. Zelmer
1998 Chris A. Hall
1999 Kelly Still
2000 Michael Barger & Allison K. Witherow
2001 Megan R. Collins
2002 Deborah M. Lai
2003 Alyssa Kunz
2004 Michael J. Yabsley
2005 Francisco Palomeque
2006 Tiffany G. Baker
2007 Andrew McElwain
2008 Heather Stockdale
2009 Dawn M. Roellig
2010 Rick Gerhold
2011 Carrie Umberger
2012 Elizabeth Gleim
2013 Alice E. Houk
2014 Adonis McQueen & Brigette Brinton
2015 Skylar Hopkins
2016 Raphael Orelis-Ribeiro
2017 Jackson Roberts
2018 Morgan Siebka
2019 Ian Will
2021 Tyler Achatz
2022 Kayla Garrett

PROGRAM SUMMARY

Thursday, April 20th

Angelo's in the Gap,
527 Colwyn St, Cumberland Gap TN

SSP Executive Committee	5:00 – 6:30 PM
Check-in/Late Registration	6:00 – 7:00 PM
Opening Remarks and SSP Reception (hors d'oeuvres & beverages)	7:00 – 10:00 PM
Dinner on Your Own	Anytime

Friday, April 21st

Richard A. Gillespie College of Veterinary Medicine (CVM), Rm 100
Lincoln Memorial University, Harrogate Campus

Continental Breakfast (catered on site)	7:30AM – 10:30AM
Paper Session I	8:00 – 10:00 AM
Break / Poster Session (CVM, 3rd floor mezzanine & hallway)	10:00 – 10:15 AM
Paper Session II	10:15 – 11:30AM
President's Symposium	11:30AM – 12:30PM
Lunch (catered on site) & President's Award Ceremony	12:30 – 1:30 PM
Poster Session (3rd floor, CVM building)	1:00 – 2:00PM
Paper Session III	1:30 – 3:30 PM
Break / Poster Session (CVM, 3rd floor mezzanine & hallway)	3:30 – 3:45 PM
Paper Session IV	3:45 – 5:15 PM
Break	5:15 – 5:30PM
Paper Session V	5:30 – 6:30PM
Dinner On Your Own	Anytime

Saturday, April 22nd

Richard A. Gillespie College of Veterinary Medicine (CVM), Rm 100
Lincoln Memorial University, Harrogate Campus

Continental Breakfast (catered on site)	7:30 – 10:30 AM
Paper Session VI	8:00 – 10:00 AM
Break	10:00 – 10:15 AM
Paper Session VII	10:15AM – 12:30PM
Lunch & SSP Business meeting	12:30 – 1:30 PM

SSP RECEPTION

Thursday, April 20 **7:00 – 10:00 PM**
Location: Angelo’s in the Gap, Cumberland Gap, TN

7:00 **Christopher A. Cleveland**, University of Georgia, Athens, GA. Welcome remarks.

7:10 **Charles T. Faulkner,** Lincoln Memorial University, Harrogate, TN. Meeting announcements.

Hors d’oeuvres & drinks provided

PAPER SESSION I

Friday, April 21 **8:00-10:00AM**
Location: Richard A. Gillespie College of Veterinary Medicine (CVM), Rm 100
Moderators: Kayla Buck & Reece Hughes
* Presenting Author
† Ciordia-Stewart-Porter Undergraduate Paper Competitor
‡ Byrd-Dunn Graduate Student Paper Competitor

Information for speakers & poster presenters: If presenting an oral presentation, *please upload your presentation files before your session. There is time in the morning before the first presentation and during breaks to do this. If presenting a poster, please put your poster up at your assigned location (see your location number below in the poster session section) before 10AM. All easels, etc. will be present on the 3rd floor mezzanine and hallway.*

7:30 – 8:00 Load presentations

7:30 – 10:30 Continental Breakfast

8:00 1‡ **Blanchard, Vanessa R.*, Kerstetter, David W., Blanar, Christopher A.** Nova Southeastern University, Fort Lauderdale, FL, USA. **Parasites of raptorial birds of Southeast Florida.**

8:15 2‡ **Hilber, Alexia*, Kerstetter, David, Blanar, Christopher.** Nova Southeastern University, Fort Lauderdale, FL, USA. **An overview of the helminth endoparasite community of wading birds in southeastern Florida.**

8:30 3‡ **Williams, Stacie D.*, Wisnieski, Lauren, Gruszynski, Karen, Faulkner, Vina, Faulkner, Charles.** Lincoln Memorial University, Harrogate, TN, USA. **A cross-sectional analysis of the knowledge, beliefs, and perceptions of canine heartworm prophylaxis use for prevention of canine heartworm disease.**

8:45 4‡ **Horton, Laura*, Ammar, Sawsan, Bruce, Megan, Gerhold, Richard.** University of Tennessee College of Veterinary Medicine, Knoxville, TN, USA. ***Histomonas meleagridis* outbreak & transmission pathway investigation on a private farm in Tennessee, United States.**

9:00 5‡ **Grunert, Ryan K. A.[1], Howard, Amanda[2], Beaudry, Megan[2], Frederick, Julia[2], Howard, Marrisa[2], Kieran, Troy[5], Glenn, Travis C.[2,3], Brown, Justin[6], Hammond, Adam[4], Francisco, Raquel[1,4]*, Yabsley, Michael J.[1,4]** [1]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [2]Department of Environmental Health Science, University of Georgia, Athens, GA, USA; [3]Institute of Bioinformatics, University of Georgia, Athens, GA, USA; [4]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA; [5]Centers for Disease Control and Prevention, Influenza Division, Atlanta, GA, USA; [6]Department of Veterinary and Biomedical Sciences, The Pennsylvania State University, University Park, PA, USA. **Cracking the genetic code of *Sarcoptes scabiei* in American bears (*Ursus americanus*): Full mitochondrial genome reveals two distinct lineages.**

9:15 6 **Bullard, Stephen A.*, Warren, Micah B., Brule, John J.** Southeastern Cooperative Fish Parasite and Disease Project, College of Agriculture, Auburn University, Auburn, AL USA. **The surprising (or not so surprising) discovery of a new lineage of Cathariotrematinae Bullard, 2021 (Monogenoidea: Monocotylidae) infecting the olfactory lamellae of deepwater gulper sharks, *Centrophorus granulosus* (Squaliformes: Centrophoridae) in the Gulf of Mexico.**

9:30 7‡ **Shurba, Jacob A.[1]*, Horton, Matthew L.[2], Johnson, Paul D.[3], Warren, Micah B.[1], Brule, John H.[1], Truong, Triet N.[1], Curran, Stephen S.[1], Dutton, Haley R.[1], Ksepka, Steven P.[1], Krol, Justin D.[1], Bullard, Stephen A.[1]** [1]Aquatic Parasitology Laboratory and Southeastern Cooperative Fish Parasite and Disease Laboratory, Auburn University, Auburn, AL, USA; [2]Arkansas Game and Fish Commission, Little Rock, AR, USA; [3]Alabama Department of Conservation and Natural Resources, Marion, AL, USA. **Parasitological survey of two newly-discovered populations of exotic invasive mystery snails (*Cipangopaludina*: Viviparidae: Bellamyinae) in Alabama and Arkansas.**

9:45 8‡ **Brule, John H.*, Warren, Micah B., Dutton, Haley R., Truong, Triet N., Ksepka, Steven P.' Curran, Stephen S., Shurba, Jacob A., Krol, Justin D., Bullard, Stephen A.** Aquatic Parasitology Laboratory and Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, & Aquatic Sciences, College of Agriculture, Auburn University, Auburn, Alabama, USA. **First taxonomically confirmed record of a gyrodactylid, *Gyrodactylus cichlidarum*, Paperna, 1968 (Monogenoidea) infecting farmed Nile tilapia, *Oreochromis niloticus* (Linnaeus, 1758) (Cichliformes: Cichlidae) in the United States.**

BREAK & POSTER SESSION

Friday, April 21 **10:00 – 10:15AM**

Location: CVM, 3rd Floor Mezzanine & Hallway

* Presenting Author

**Poster Award Competitor

Information for Poster Presenters: *If presenting a poster, please put your poster up at your assigned location (see your location number below) before 10AM. All easels, etc. will be present on the 3rd floor mezzanine and hallway.*

1 **Garrett, Kayla, B.[1,2]*, Murray, Lance[3], Wolff, Peregrine, L.[3,4], LaHue, Nate [3], Yabsley, Michael, J.[1,2]** [1]Southeastern Cooperative Wildlife Disease Study, University of Georgia, Athens, GA, USA; [2]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA; [3]Nevada Department of Wildlife, Reno, NV, USA; [4]Wildlife Disease Association, Moorepark, CA, USA. **Free-ranging ungulates in Nevada, USA are infected with a high diversity of piroplasm parasites.**

2** **Karl, Kaitlin M.[1]*, Catenazzi, Alessandro M.[2], Jiménez, F Agustín.[3]** [1]Southern Illinois University, Carbondale, IL, USA; [2]Florida International University, Miami, FL, USA; [3]Southern Illinois University, Carbondale, IL, USA. **Documentation of helminth diversity in Peruvian anurans.**

3 **de Buron, Isaure*, Hill-Spanik, Kristina.** College of Charleston, Charleston, SC, USA. **Using SSP meeting sites and participants' expertise to increase global and local parasite diversity via the BioBlitz approach.**

4** **Francisco, Raquel[1,3]*, Hui Teo, Xuan[1,2], Hammond, Adam[3,4], Nemeth, Nicole M.[1,2], Yabsley, Michael J.[1,3]** [1]Southeastern Cooperative Wildlife Disease Study (SCWDS), Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [2]Department of Pathology, College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [3]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA; [4]Georgia Department of Natural Resources (GADNR), Wildlife Resources Division, Social Circle, GA, USA. ***Ursicoptes americanus*: A case report in an American black bear (*Ursus americanus*).**

5 **Georgieva, Simona*, Choe, Seongjun.** Chungbuk National University, Cheongju, Republic of Korea. **Helminth diversity in freshwater fishes in Korea.**

6** **Grey, Kayla*, Amspacher, Katelyn, Nielsen, Clayton, Jiménez, F. Agustín.** Southern Illinois University, Carbondale, Carbondale, IL USA. **Of intestinal helminths and *Mephitis mephitis*: The importance of DNA barcoding**.

7** **Smith, Catherine A.*, Yabsley, Michael J., Kurimo-Beechuk, Elizabeth, Ruder, Mark G., Garrett, Kayla B., Barton, Ethan P.** University of Georgia, Athens, GA, USA. **Abomasal parasites in white-tailed deer (*Odocoileus virginianus*) in West Virginia.**

8** **Von Holten, Zoe S.[1]*, Achatz, Tyler J.[1], LaFond, Lynda R.[2], Martens, Jakson R.[2], Tkach, Vasyl V.[2]** [1]Middle Georgia State University, Macon, Georgia, USA; [2]University of North Dakota, Grand Forks, North Dakota, USA. **Improving diagnostics of *Crassiphiala bulboglossa*, the type-species of *Crassiphiala* and a common causative agent for black spot disease in fishes.**

PAPER SESSION II

Friday, April 21 **10:15AM-11:30AM**

Location: CVM, Rm 100
Moderator: Simona Georgieva
* Presenting Author
† Ciordia-Stewart-Porter Undergraduate Paper Competitor
‡ Byrd-Dunn Graduate Student Paper Competitor

10:15 9‡ **Rayburn, Alexander U.*, Kerstetter, David W., Blanar, Christopher A.** Nova Southeastern University, Davie, FL, USA. **The parasites of the unwanted: endoparasite fauna of mesopredatory teleost pelagic longline bycatch.**

10:30 10‡ **Hazelrig, Corinna M.[1]*, Farrell, Terence M.[2], Palmisano, Jenna N.[3], Ortega, Jason[2], Haynes, Ellen[1], Cleveland, Christopher A.[1], Nemeth, Nicole M.[1]** [1]University of Georgia, Athens, GA, USA; [2]Stetson University, DeLand, FL, USA; [3]University of Central Florida, Orlando, FL, USA. **Snake mortalities in Florida, USA associated with *Raillietiella orientalis*.**

10:45 11‡ **Ahmed, Rokeya [1]*, McLean, Bryan S. [2], Cook, Joseph A. [3], Galbreath, Kurt E. [4], Greiman, Stephen E.[1]** [1]Georgia Southern University, Statesboro, GA, USA; [2]University of North Carolina Greensboro, Greensboro, NC, USA; [3]University of New Mexico, Albuquerque, NM, USA; [4]Northern Michigan University, Marquette, MI, USA. **Diversity of cestode species within the shrew *Sorex roboratus* (Eulipotyphla: Soricidae) collected from Mongolia.**

11:00 12‡ **Dutton, Haley R.*, Bullard, Stephen A., Kelly, Anita M.** Auburn University, Auburn, AL, USA. **Supplemental description and phylogenetics of *Dracovermis occidentalis* (Digenea: Liolopidae) infecting the intestine of an American alligator, *Alligator mississippiensis* from the Mobile–Tensaw River Delta, Alabama, USA.**

11:15 13 **Dukes, Casey G.[1]*, Coker, Sarah M.[1], Yabsley, Michael J.[1,2] and Cleveland, Christopher A.[1]** [1]Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, UGA, Athens, GA, USA; [2]Warnell School of Forestry and Natural Resources, UGA, Athens, GA, USA. **Finding needles in the haystack: the development of a rapid, field-based RT-PCR for Guinea worm detection and confirmation.**

SSP PRESIDENTIAL KEYNOTE TALK

Friday, April 21 **11:30 AM – 12:30 PM**

Location: CVM, Rm 100

11:30 **Vanhove, Maarten P.M.[1,2]** [1]Research Group Zoology: Biodiversity & Toxicology, Centre for Environmental Sciences, Hasselt University, Belgium; [2]Department of Morphology and Pathology, Faculty of Veterinary Medicine, University of Liège, Belgium, **Fish parasitology in the African Great Lakes: From discovering species to proposing markers for fisheries and ecosystem health.**

12:30 – 1:30 Lunch & Presentation of the President's Award

PAPER SESSION III

Friday, April 21 **1:30-3:30PM**
Location: CVM, Rm 100
Moderator: Haley Dutton
* Presenting Author
† Ciordia-Stewart-Porter Undergraduate Paper Competitor
‡ Byrd-Dunn Graduate Student Paper Competitor

1:30 14† **Cunningham, Abigail J.[1,2]*, Garrett, Kayla B.[1,2], Nemeth, Nicole M.[2,3], Barron, Heather[4,5], Stasiak, Iga[6], Groves, Bethany[7], Gibbs, Samantha[8], Ruder, Mark G.[2], Kunkel, Melanie R.[1], Weyna, Alisia[1,3], Teo, Xuan H.[1,3], Goodwin, Chloe[1,3], Radisic, Rebecca[1], O'Reilly, Aidan[1], Yabsley, Michael J.[1,2,9]** [1]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA; [2]Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [3]Department of Pathology, College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [4]Clinic for the Rehabilitation of Wildlife (CROW), Sanibel Island, FL, USA; [5]Loggerhead Marinelife Center, Juno Beach, FL, USA; [6]Strategic Conservation Ministry of Environment, Saskatoon, SK S7N 3K3 Canada; [7]Progressive Animal Welfare Society (PAWS), Lynnwood, WA, USA; [8]United States Fish and Wildlife Service, Chiefland, FL, USA; [9]Center for Emerging Infectious Diseases, Athens, GA, USA. **Surveillance for *Trichomonas* infections in Bald Eagles (*Haliaeetus leucocephalus*) and Golden Eagles (*Aquila chrysaetos*) indicates that subclinical *T. gypaetinii* infections are common in Bald Eagles.**

1:45 15† **Hammond, Kimberly A.*, Gallagher, Kaitlin A.** Christian Brother's University, Memphis, TN, USA. **Parasite diversity among Sunfish species in relation to pollution.**

2:00 16† **Holt, Anna [1]*, Hamilton, Benjamin, Holt[1], Purple, Kathryn[2], Faulkner, Charles[3], Kolp, Matthew[3].** [1]University of Lincoln Memorial, Department of Veterinary Biomedical Science, Harrogate, TN USA; [2]University of Lincoln Memorial, Department of Biology and Microbiology, Harrogate, TN USA; [3]University of Lincoln Memorial - Richard A. Gillespie College of Veterinary Medicine, Harrogate, TN, USA. **Pilot study investigating the prevalence of parasites in abandoned piles of feces collected at dog parks in East Tennessee.**

2:15 17† **Simpson, Morgan D.[1], Ammar, Sawsan[3], Gerhold, Richard.[2],** Purple, Kathryn E.[1], [1]Lincoln Memorial University, Harrogate, TN, USA; [2]University of Tennessee College of Veterinary Medicine, Knoxville, TN, USA; [3]University of Calgary Faculty of Veterinary Medicine, Calgary, Alberta, Canada. **Investigation of the prevalence of the "Trichy" protozoan parasite, *Trichomonas gallinae*, in hunter-harvested mourning doves (*Zenaida macroura*) from East Tennessee.**

2:30 18† **Rivera, Odette L.*, Gallagher, Kaitlin A.** Christian Brothers University, Memphis, TN, USA. **Detection of canine gastrointestinal nematodes between stray and non-stray populations.**

2:45 19† **Zaffiro, Briana K.[1]*, Kerstetter, David W.[2], Blanar, Christopher.[3]** [1]Halmos College of Arts and Sciences, Nova Southeastern University, Dania Beach, FL, USA; [2]Halmos College of Arts and Sciences, Nova Southeastern University, Dania Beach, FL, USA; [3]Halmos College of Arts and Sciences, Nova Southeastern University, Dania Beach, FL, USA. **Endoparasites in family Caprimulgidae birds in southeastern Florida (USA).**

3:00 20† **Von Holten, Zoe S.[1]*, Achatz, Tyler J.[1], Fecchio, Alan[2], Greiman, Stephen E.[3], Tkach, Vasyl V.[4]** [1]Middle Georgia State University, Macon, Georgia, USA; [2]Universidad Nacional de la Patagonia San Juan Bosco, Esquel, Chubut, Argentina; [3]Georgia Southern University, Statesboro, Georgia, USA; [4]University of North Dakota, Grand Forks, North Dakota, USA. **Revealing diversity of the Diplostomidae (Digenea) parasites in kingfishers.**

3:15 21† **Blevins, Hannah F.*, Shock, Barbara C., Faulkner, Vina.** Lincoln Memorial University, Harrogate, TN, USA. **Prevalence and diversity of *Ehrlichia* spp. from ixodid ticks in the Cumberland Gap Region of Tennessee, Kentucky, and Virginia.**

BREAK & POSTER SESSION

Friday, April 21 **3:30 – 3:45PM**
Location: CVM, 3rd Floor Mezzanine & Hallway

Same posters as the 10:00-10:15AM session.

PAPER SESSION IV

Friday, April 21 **3:45-5:15PM**
Location: CVM, 100
Moderator: Corinna Hazelrig
* Presenting Author
† Ciordia-Stewart-Porter Undergraduate Paper Competitor
‡ Byrd-Dunn Graduate Student Paper Competitor

3:45 22† **Torres, J.[1]*, Tolliver, E. Morgan[2], Salinas, Nubia[2], Triana, Nicolas[2], Bondo, Kristin J.[3], Grisham, Blake A.[3], Sullins, D.S.[4], Kistler, Whitney M.[1]** [1]School of Mathematics and Sciences, Lincoln Memorial University, Harrogate, TN; [2]College of Veterinary Medicine, Lincoln Memorial University, Harrogate, TN; [3]Llano River Field Station and Department of Natural Resources Management, Texas Tech University, Lubbock, TX; [4]Department of Horticulture and Natural Resources, Kansas State University, Manhattan, KS. **Survey of haemosporidian parasites from Lesser Prairie Chickens (*Tympanuchus pallidicinctus*) from Texas and Kansas.**

4:00 23† **Gomez Perez, Diego A.*, Gallagher, Kaitlin A.** Christian Brothers University, Memphis, TN, USA. **Canada Geese as vectors of waterfowl and zoonotic pathogens.**

4:15 24† **Hughes, Reece[1,2]*, Francisco, Raquel[1,2], Garrett, Kayla B.[1,2], Willitts, Kevin[3], Munk, Brandon[4], Brown, Justin D.[5], Rodriguez, Carlos[6], Dohlen, Alexa Von[7], Hamer, Sarah[8], Yabsley, Michael J.[1,2,9]** [1]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, Georgia USA; [2]Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, University of Georgia, Athens, Georgia USA; [3]Lake Tahoe Wildlife Care, South Lake Tahoe, California USA; [4]California Department of Fish and Wildlife, Rancho Cordovo, California USA; [5]Department of Veterinary and Biomedical Sciences, The Pennsylvania State University, University Park, PA USA; [6]Texas A&M Veterinary Medical Diagnostic Laboratory, College Station, TX USA; [7]Department of Natural and Behavioral Sciences, College of STEM, Johnson C. Smith University, Charlotte, North Carolina USA; [8]Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX; [9]Center for the Ecology of Infectious Diseases, Athens, Georgia USA. ***Trypanosoma cruzi* infection in a black bear cub and serologic survey for exposure in wild black bears from several states.**

4:30 25† **Criswell, Madison R.[1]*, Kirkendall, Katherine[1], Faulkner, Vina[2], Marcum, Matthew[1], Shock, Barbara, C.[1], Gruszynski, Karen.[2]** [1]Lincoln Memorial University, Harrogate, TN, USA; [2]Lincoln Memorial University - Richard A. Gillespie College of Veterinary Medicine, Harrogate, TN, USA. **Infectious diseases of domestic cats (*Felis catus*) in Kentucky, Virginia, and Tennessee.**

4:45 26† **Pickeral, April[1]*, McLean, Bryan S.[2], Moore, Nicholas[1], Ahmed, Rokeya[1], Greiman, Stephen E.[1]** [1]Georgia Southern University, Statesboro, GA, USA; [2]University of North Carolina Greensboro, Greensboro, NC, USA. **Summer through winter: seasonal changes in the cestode communities within two *Sorex* shrew species, *Sorex cinereus* and *Sorex fumeus*, from North Carolina.**

5:00 27† **Dunkins, Allysia [1]*, Cook, Joseph A.[2], Greiman, Stephen E.[1]** [1]Georgia Southern University, Statesboro, GA, USA; [2]University of New Mexico, Albuquerque, NM, USA. **New species of *Vampirolepis* Yamaguti, 1959 (Cyclophyllidea: Hymenolepididae) from the black myotis bat (*Myotis nigricans)* from Panama.**

5:15 **Break**

PAPER SESSION V

Friday, April 21 **5:30-6:30PM**
Location: CVM, 100
Moderator: Steve Ksepka
* Presenting Author
† Ciordia-Stewart-Porter Undergraduate Paper Competitor
‡ Byrd-Dunn Graduate Student Paper Competitor

5:30 28† **Heyward, Natalie A.[1,2]*, Needle, David B.[4], Hazelrig, Corinna M.[1], Webb, Shevenell[3], Vashon, Jennifer[3], Garrett, Kayla B.[1,2], Cleveland, Christopher A.[1], Yabsley, Michael J.[1]** [1]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [2]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA; [3]Maine Department of Inland Fisheries & Wildlife, Augusta, ME, USA; [4]New Hampshire Diagnostic Laboratory, University of New Hampshire, Durham, NH, USA. **Protozoan parasites of Canada lynx (*Lynx canadensis*) and Fisher (*Pekania pennanti*) in Maine, USA.**

5:45 29† **Skelton, Devin[1]*, Cook, Joseph A.[2], Tkach, Vasyl V.[3], Greiman, Stephen E.**[1] [1]Georgia Southern University, Statesboro, GA, USA; [2]University of New Mexico, Albuquerque, NM, USA; [3]University of North Dakota, Grand Forks, ND, USA. **New species of tapeworm *Monocercus* Villot 1982 from *Sorex monticola* collected from the Sangre de Cristo Mountains of New Mexico.**

6:00 30 **Purple, Kathryn*, Brandt, LaRoy, Chazo, Lucas, Brehm, Autumn, Faulkner, Charles.** Lincoln Memorial University, Harrogate, TN, USA. **The prevalence of *Dirofilaria immitis* in wild Canidae from the Cumberland Gap Region of Kentucky, Virginia, and Tennessee.**

6:15 31 **Blanar, Christopher A.[1]*, Barba, Daniel[2], Santis, Jacqueline[2], Gupta, Neha[1], Kerstetter, David W.[1]** [1]Nova Southeastern University, Fort Lauderdale, FL, USA; [2]Miami Dade College, Miami, FL, USA. **Microbiomes of parasitic nematode (*Ozolaimus megatyphlon*) cuticles differ from those of their iguana hosts.**

PAPER SESSION VI

Saturday, April 22 **8:00 – 10:00 AM**
Location: CVM, Rm 100
Moderators: Micah Warren & Juan Torres
* Presenting Author
† Ciordia-Stewart-Porter Undergraduate Paper Competitor
‡ Byrd-Dunn Graduate Student Paper Competitor

<u>Information for speakers:</u> *Please upload your presentation files <u>before</u> your session. There is time in the morning before the first presentation and during breaks to do this.*

7:30 – 8:00 Load presentations

7:30 – 10:30 Continental Breakfast

8:00 32‡ **Warren, Micah, B.*, Dutton, Haley, R., Bullard, Stephen, A.** Auburn University, Auburn, AL, USA. ***Nomasanguinicola dentata*** **(Paperna, 1964) Warren and Bullard, 2023 (Digenea: Sanguinicolidae Poche, 1926) infecting African sharptooth catfish, *Clarias gariepinus* (Burchell, 1822) Teugles, 1982 (Siluriformes: Clariidae) from the Okavango River, Namibia: supplemental description and phylogenetic analysis.**

8:15 33‡ **Truong, Triet N. [1]*, Whelan, Nathan V.[1,2], Johnson, Paul D.[3], Buntin, Michael L.[3], Bullard, Stephen A.[1,4]** [1]Auburn University, Auburn, AL, USA; [2]US Fish and Wildlife Service, Auburn, AL, USA; [3]Alabama Department of Conservation and Natural Resources, Marion, AL, USA; [4]North-West University, Private Bag X6001, Potchefstroom, South Africa. **Description, life cycle of a new species of *Proterometra* (Digenea: Azygiidae) from the Cahaba River, Alabama, U.S.A. and phylogenetic analyses.**

8:30 34‡ **Moore, Nicholas[1]*, McLean, Bryan S.[2], Cook, Joseph A.[3], Galbreath, Kurt E.[4], Greiman, Stephen E.[1]** [1]Georgia Southern University, Statesboro, GA, USA; [2]University of North Carolina, Greensboro, NC, USA; [3]University of New Mexico, Albuquerque, NM, USA; [4]Northern Michigan University, Marquette, MI, USA. **Diversity of tapeworms (Cestoda: Cyclophyllidea) parasitizing two shrew species, *Sorex caecutiens* and *Sorex isodon*, from Northern Mongolia.**

8:45 35‡ **Lattner, Seth P.[1], Stange, Emma[2], Brown, Patricia[3], Olfenbuttel, Colleen[4], Douglass, Kelly[5], Yabsley, Michael J.[1,6], Cleveland, Christopher A,[1].** [1]Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [2]College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [3]Franklin College of Arts and Sciences, University of Georgia, Athens, GA, USA; [4]North Carolina Wildlife Resources Commission, Raleigh, NC, USA; [5]USDA APHIS Wildlife Services, Raleigh, NC, USA; [6]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA. **Investigation of canine distemper virus and protozoan parasites in raccoons (*Procyon lotor*) of North Carolina.**

9:00 36‡ **Garrett. Kayla[1,2]*, Dukes. Casey[1], Brown, Justin[3], Van Why, Kyle[4], Casey, Christine[5], Tabora, Joshua[6], Gerhold, Richard[7], Baker, Eliza[8], Olfenbuttel, Colleen[9], Douglass, Kelly[10], Barton, Ethan[1,11], LaCour, Jim[12], Berry, Rusty[13], Dennison, Catherine[14], Purple, Kathryn[15], Miller, Erica[16], Yabsley, Michael J.[1,2], Cleveland, Christopher A.[1]** [1]Southeastern Cooperative Wildlife Disease Study, University of Georgia, Athens, GA, USA; [2]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA; [3]Department of Veterinary and Biomedical Sciences, Pennsylvania State University, University Park, PA USA; [4]USDA Wildlife Services, Harrisburg, PA USA; [5]Kentucky Department of Fish and Wildlife Resources, Frankfort, KY USA; [6]Department of Natural Resources, Flintstone, MD USA; [7]Department of Biomedical and Diagnostic Sciences, College of Veterinary Medicine, University of Tennessee, Knoxville, TN USA; [8]Comparative and Experimental Medicine Graduate Program, University of Tennessee, Knoxville, TN USA; [9]NC Wildlife Resources Commission, Wildlife Management Division, Raleigh, NC USA; [10]USDA Wildlife Services, Raleigh, NC USA; [11]West Virginia Division of Natural Resources, Elkins, WV USA; [12]LA Department of Wildlife and Fisheries, Baton Rouge, LA USA; [13]Louisiana Department of Wildlife and Fisheries, Pineville, LA USA; [14]Ohio Division of Wildlife, Columbus OH USA; [15]Lincoln Memorial University, Harrogate, TN USA; [16]Department of Pathobiology, Wildlife Futures Program, University of Pennsylvania School of Veterinary Medicine, New Bolton Center, Kennett Square, Pennsylvania USA. **Regional surveillance for *Echinococcus* species in wild canids in the Eastern United States.**

9:15 37 **Curran, Stephen S.*, Brule, John H., Ksepka, Steven P., Truong, Triet N., Warren, Micah B, Bullard, Stephen A.** Auburn University, Auburn AL, USA. **Investigating digenean diversity in an estuarine pond on the Fort Morgan peninsula, Alabama.**

9:30 38 **Wisnieski, Lauren*, Faulkner, Charles, Faulkner, Vina.** Richard A. Gillespie College of Veterinary Medicine, Lincoln Memorial University, Harrogate, TN, USA. **Factors associated with heartworm preventative use.**

9:45 39 **Georgieva, Simona[1,2]*, Khosravi, Maral[3].** [1]Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, Sofia, Bulgaria; [2]Department of Parasitology, School of Medicine, Chungbuk National University, Cheongju, South Korea; [3]Department of Marine Ecology, GEOMAR Helmholtz Centre for Ocean Research, Kiel, Germany. **Trematode communities in the potamidid gastropod *Pirenella cingulata* (Gmelin, 1791) (Cerithioidea: Potamididae) from the Persian Gulf.**

10:00 Break

PAPER SESSION VII

Saturday, April 22 **10:15AM – 12:30 PM**

Location: CVM, Rm 100
Moderator: John Brule
* Presenting Author
† Ciordia-Stewart-Porter Undergraduate Paper Competitor
‡ Byrd-Dunn Graduate Student Paper Competitor

10:15 40 **Kmentova, Nikol[1]*, Moons, Tanisha[1,2], Appy, Ralph[3], Artois, Tom[1], Justine, Jean-Lou[4], Vanhove, Maarten[1].** [1]Hasselt University, Research Group Zoology: Biodiversity and Toxicology, Centre for Environmental Sciences, Diepenbeek, Belgium; [2]Department of Parasitology, Faculty of Science, University of South Bohemia, České Budějovice, Czech Republic; [3]Cabrillo Marine Aquarium, San Pedro, CA, USA; [4]ISYEB, Institut de Systématique Évolution Biodiversité, UMR7205 CNRS, EPHE, MNHN, UPMC, Université des Antilles, Muséum National d'Histoire Naturelle, Paris, France. **Symbiosis in rhabdocoelas: from invertebrate to vertebrate hosts.**

10:30 41‡ **Ksepka, Steven P.*, Bullard, Stephen A.** Aquatic Parasitology Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, AL, USA. **A new species of *Henneguya* Thélohan, 1892 (Cnidaria: Bivalvulida: Myxobolidae) infecting the submucosa of the intestine and pyloric caeca of red drum, *Sciaenops ocellatus* (Linnaeus) (Perciformes: Sciaenidae) from coastal Alabama.**

10:45 42 **Le'Roy, Crystal J.*, Lynch, Savannah, Faulkner, Charles T.** Lincoln Memorial University Richard A. Gillespie College of Veterinary Medicine. **Canine heartworm in the Cumberland Gap Region.**

11:00 43 **Hamilton, Benjamin.*** Lincoln Memorial University, Harrogate, TN, USA. **Fecal contamination with gastrointestinal parasites of dog parks in rural and urban environments.**

11:15 44 **Zelmer, Derek A.*** University of South Carolina – Aiken, Aiken, SC USA. **Patterns of asynchrony in helminth parasites of centrarchids in J. Strom Thurmond Lake, South Carolina.**

11:30 45 **Osip, Setphanie[1], Garrett, Kayla B.[1,2]*, Ruder, Mark G.[2], Haynes, Ellen[2], Cleveland, Christopher A.[2], Nemeth, Nicole M.[2,3], Kunkel, Melanie R.[2], Goodwin, Chloe C.[2], Chamberlain, Michael[1], Mooreman, Christopher E.[4], Moscicki, David J.[4], Plumpton, Hannah[5], Kreh, Christopher[5], Van de Berg, Sarah[5], Buchholz, Richard[6], Martin, Thomas[6], Casey, Christine[7], Danks, Zak[7], Casalena, Mary Jo[8], Collier, Bret[9], Cedotal, Cody[10], Stilwell, Natalie[11], Yabsley, Michael J.[1,2]** [1]Warnell School of Forestry and Natural Resources, UGA, Athens, GA, USA; [2]Southeastern Cooperative Wildlife Disease Study, UGA, Athens, GA, USA; [3]Department of Pathology, College of Veterinary Medicine, UGA, Athens, GA, USA; [4]Department of Forestry and Environmental Resources, North Carolina State University, Raleigh, NC, USA; [5]NC Wildlife Resource

Commission, Raleigh, NC, USA; [6]University of Mississippi, University, MS, USA; [7]Kentucky Department of Fish and Wildlife Resources, Frankfort, KY, USA; [8]Pennsylvania Game Commission, Harrisburg, PA, USA; [9]LSU School of Renewable Natural Resources, Baton Rouge, LA, USA; [10]Louisiana Department of Wildlife and Fisheries, Baton Rouge, LA, USA; [11]MS State University, Starkville, MS, USA. **Prevalence and genetic characterization of blood parasites in wild turkeys (*Meleagris gallopavo*).**

11:45 46 **Russell, A. Cassiopeia[1], Schiff, Erica[1], Rice, Christopher[2], Kyle, Dennis E.[1]*** [1]University of Georgia, Athens, GA, USA; [2]Purdue University, West Lafayette, IN, USA. **Pathogenicity of *Naegleria fowleri* isolates varies significantly in the mouse model of primary amoebic meningoencephalitis.**

12:00 47 **Richards, Jessie E.[1,2]*, Kania, Stephen A.[1,2], Muller, Lisa I.[3,4], Miller, Bradley F.[5], Gerhold, Richard W.[1,2,4]** [1]University of Tennessee College of Veterinary Medicine, Knoxville, TN, USA; [2]University of Tennessee Comparative & Experimental Medicine Program, Knoxville, TN, USA; [3]University of Tennessee School of Natural Resources, Knoxville, TN; [4]University of Tennessee Center for Wildlife Health, Knoxville, TN, USA; [5]Tennessee Wildlife Resources Agency, Region IV, Morristown, TN, USA. **Development and application of an enzyme linked immunosorbent assay (ELISA) for the serological testing of *Parelaphostrongylus tenuis* in Tennessee elk (*Cervus canadensis*).**

12:15 48 **Yabsley, Michael J.[1,2,3]*, Kellow, Laura[4], Heather Barron[4,5], Kayla B. Garrett[1,2], Nicole M. Nemeth[1,6]** [1]Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [2]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA; [3]Center for Emerging Infectious Diseases, Athens, GA, USA; [4]Center for the Rehabilitation of Wildlife (CROW), Sanibel Island, FL, USA; [5]Loggerhead Marinelife Center, Juno Beach, FL, USA; [6]Department of Pathology, College of Veterinary Medicine, University of Georgia, Athens, GA, USA. **Brain worms of the snake bird (*Anhinga anhinga*) - Prevalence, pathology, and molecular characterization of *Paronchocerca helicina*.**

SSP BUSINESS MEETING & LUNCH

Saturday, April 22 **12:30 – 1:30**
Location: CVM, Rm 100
Presiding: **Elizabeth R. Gleim** (substituting for Christopher A. Cleveland)

12:30 **Business Meeting**

Thank you for supporting the Southeastern Society of Parasitologists!

Safe Travels!

PRESIDENTIAL KEYNOTE TALK

Fish parasitology in the African Great Lakes: from discovering species to proposing markers for fisheries and ecosystem health

Maarten P.M. Vanhove, Ph.D.

Research Group Zoology: Biodiversity & Toxicology, Centre for Environmental Sciences,
Hasselt University, Belgium
and
Department of Morphology and Pathology, Faculty of Veterinary Medicine, University of Liège,
Belgium

Dr. Vanhove is an assistant professor in Aquatic Biodiversity at Hasselt University in Flanders, Belgium (Research Group Zoology, within the Centre for Environmental Sciences) and an invited lecturer for "Zoonoses, context and emergence dynamics" at the University of Liège (Wallonia, Belgium). He holds master's degrees in biology (2006), social-cultural anthropology (2007) and a PhD in Sciences (2012) from KU Leuven (Belgium). He was a researcher at the Royal Museum for Central Africa (Belgium), the Hellenic Centre for Marine Research (Greece), and Masaryk University (Czech Republic). He was also a policy scientist focusing on capacity development about biodiversity in the Global South at the Royal Belgian Institute of Natural Sciences (Belgium) and curator of worms at the Finnish Museum of Natural History (University of Helsinki) (Finland). He is active in the Belgian One Health Network, the IUCN Species Survival Commission Parasite Specialist Group, and the board of the Royal Belgian Zoological Society. Dr. Vanhove received the 2002 Jacques Kets Prize for Biology (Royal Zoological Society of Antwerp), Best Young Researcher Presentation Award (2013 International Symposium on Monogenea), and 2013 Henri Schouteden Prize (Royal Flemish Academy of Belgium for Science and the Arts). Dr. VAnhove studies parasite diversity and genetics in evolutionary and conservation-relevant contexts, and biodiversity policy, especially in Africa and the Mediterranean.

ORAL PRESENTATION ABSTRACTS

1. **Blanchard, Vanessa R.*, Kerstetter, David W., Blanar, Christopher A.** Nova Southeastern University, Fort Lauderdale, FL, USA. **Parasites of raptorial birds of Southeast Florida.**

   Raptors are a polyphyletic group of birds characterized by similarities in their behavior and physiology. They regulate small animal populations, playing key roles in local ecosystems as apex predators; as such, they are themselves largely regulated by their parasites. However, little is known regarding the species composition and structure of their endoparasite communities. We surveyed endoparasites of southeast Florida raptors: American Kestrels (*Falco sparverius*), Peregrine Falcons (*F. peregrinus*), Merlins (*F. columbarius*), Cooper's Hawks (*Accipiter cooperii*), Sharp-shinned Hawks (*A. striatus*), Red-shouldered Hawks (*Buteo lineatus*), Broadwing Hawks (*B. platypterus*), Eastern Screech Owl (*Megascops asio*), Barn Owl (*Tyto alba*), Barred Owl (*Strix varia*), Great Horned Owl (*Bubo virginianus*), Burrowing Owls (Athene cunicularia), and Black (*Coragyps atratus*) and Turkey Vultures (*Cathartes aura*). As of February 2022, 148 birds had been examined, and almost all were infected with at least one parasite taxon, including Digenea (primarily strigeids such as *Strigea falconis*), Cestoda, Nematoda (primarily anisakids and spirurids), and Acanthocephala. Parasite species diversity varied among hosts: Red-shouldered Hawks had both the most diverse and heaviest parasite burdens, while Turkey Vultures hosted the lowest diversity and generally the lightest parasite load. We noted new host records and range extensions, including: first report of nematodes in Black and Turkey vultures; first report of nematodes and strigeid digeneans in Merlins; first records and a range extension for Acanthocephala in Sharp-shinned Hawks and Cooper's Hawks. Multivariate analyses indicated that parasite community composition was not driven by host phylogeny but primarily driven by other factors, most likely host feeding ecology. Many raptors are protected species, and information on the parasite communities that regulate them will inform conservation and management efforts.

2. **Hilber, Alexia*, Kerstetter, David, Blanar, Christopher.** Nova Southeastern University, Fort Lauderdale, FL, USA. **An Overview of the helminth endoparasite community of wading birds in southeastern Florida.**

   In South Florida, wading birds are common along waterways. These birds live in wetland environments where their diet consists of snails, fish, crustaceans, and opportunistic prey. An understudied aspect of their biology is the diversity of endoparasites within their gastrointestinal system. These parasites play a role in forming connections between trophic levels. There are studies identifying species-level endoparasite communities, but comparisons between communities – as well as the inclusion of rare event species – have yet to be examined. This ongoing study aims to fill these gaps. As of 2/28/23, 66 birds from nine Order Gruiformes species and 144 individuals from thirteen Order Ciconiiformes and Pelecaniformes species were dissected. The esophagus, proventriculus, intestines, and cloaca are being examined. Across all birds, Acanthocephala, Nematoda, Cestoda, and Trematoda are found. In most species, acanthocephalans are the least populous, only having been found in eleven birds, and trematodes are the most. Proventriculus endoparasites are seldom found within gruiformes, Gallinules and Limpkins being the only species hosting them. In Pelecaniformes, proventriculus parasites are more prevalent, nematodes being found in 57.64% of carcasses. In all groups, esophageal parasites are seldom present, 16.67% of pelecaniform specimens contain endoparasites. Between gruiform species, Clapper Rails show the highest percentage of infected individuals and American Coots have the heaviest parasite load. Green Herons and Wood Storks have the greatest parasite load overall with an average of 1923 and 1940 parasites/ bird respectively. Snowy Egrets have the lowest infection rate among Pelecaniformes. Soras have the lightest parasite load at 1 parasite/ carcass.

3. **Williams, Stacie D.*, Wisnieski, Lauren, Gruszynski, Karen, Faulkner, Vina1, Faulkner, Charles.** Lincoln Memorial University, Harrogate, TN, USA. **A cross-sectional analysis of the knowledge, beliefs, and perceptions of canine heartworm prophylaxis use for prevention of canine heartworm disease.**

   Canine heartworm disease (CHWD) is caused by infection with the nematode parasite *Dirofilaria immitis* transmitted through the bite of a mosquito carrying the infective stage larva. The disease is insidious in its onset and 100% preventable with the use of highly effective pharmaceutical compounds that target the migrating larval stage acquired from the mosquito. However, use of canine heartworm prophylaxis among pet dog caretakers is not universally accepted and sometimes viewed with skepticism. Previous research conducted in the Cumberland Gap Region (CGR) indicated approximately 40% of dog owning individuals do not use of prophylactic products. In this study, we surveyed pet dog caretakers across the United States from October 2021-February 2022 to determine reasons for the use or non-use of canine heartworm prophylaxis to prevent CHWD. Results of 305 responses were analyzed from 31 states in the domestic United States and Puerto Rico (PR). Among survey participants, 22% of dog caretakers chose not to give their pets heartworm prophylaxis. Pet dog caretakers in the US chose not to give their pets canine heartworm prophylaxis for economic reasons (46%, 21/46), environmental factors (24%, 11/46), subscribe to beliefs associated with a holistic approach to prevention (9%, 4/46), low perceived risk of CHWD (6.5%, 3/46), or other reasons (28%, 13/46). These results can aid veterinary professionals to address the educational challenges associated with heartworm prophylaxis and disease to increase their use and gain better rapport with clients.

4. **Horton, Laura*, Ammar, Sawsan, Bruce, Megan, Gerhold, Richard.** University of Tennessee College of Veterinary Medicine, Knoxville, TN, USA. ***Histomonas meleagridis outbreak* & transmission pathway investigation on a private farm in Tennessee, United States.**

   The University of Tennessee Center for Veterinary Medicine's Molecular Parasitology lab was contacted by a veterinary student because of a possible *Histomonas meleagridis* (Blackhead) case on a family's small private farm in Oak Ridge, Tennessee (USA). On the farm, chickens and turkeys were housed in adjacent pens and allowed to graze in the same area. A turkey with clinical presentation of lethargy and sulfur-colored feces was observed and died seven days after initial clinical signs. Necropsy performed on the turkey revealed severe liver target lesions consistent with blackhead. Histological analysis confirmed the diagnosis of blackhead. Liver and cecal cultures inoculate into Dwyer's media and Hollander's fluid revealed various flagellated protozoa. Following the initial mortality, four of five remaining poults on the farm died with the same clinical signs and gross findings upon necropsy. Culture of the liver and cecum of these carcasses revealed similar organisms as seen in the initial bird. To confirm the transmission cycle from chicken to turkeys, soil from the farm was sampled and processed to collect any *Heterakis gallinarum* eggs to determine if the eggs contained *H. meleagridis* DNA. The *H. meleagridis* sequences from soil samples, if detected, will be compared to the sequences from the liver and cecum of poults with blackhead. In addition to confirming the presence of *H. meleagridis* in culture, *Tetrarrichomonas gallinarum* and *Simpliconomas* spp. were also present in culture.

5. **Grunert, Ryan K. A.[1], Howard, Amanda[2], Beaudry, Megan[2], Frederick, Julia[2], Howard, Marrisa[2], Kieran, Troy[5], Glenn, Travis C.[2,3], Brown, Justin[6], Hammond, Adam[4], Francisco, Raquel[1,4]*, Yabsley, Michael J.[1,4]** [1]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [2]Department of Environmental Health Science, University of Georgia, Athens, GA, USA; [3]Institute of Bioinformatics, University of Georgia, Athens, GA, USA; [4]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA; [5]Centers for Disease Control and Prevention, Influenza Division, Atlanta, GA, USA; [6]Department of Veterinary and Biomedical Sciences, The Pennsylvania State University, University Park, PA, USA. **Cracking the genetic code of *Sarcoptes scabiei* in American bears (*Ursus americanus*): Full mitochondrial genome reveals two distinct lineages.**

   Sarcoptic mange is a skin disease caused by the parasitic mite *Sarcoptes scabiei* that affects humans and over 140 species of domestic animals and wildlife worldwide. In the American black bear (*Ursus americanus*) population specifically, sarcoptic mange is considered a significant emerging disease and case numbers have increased dramatically in the past thirty years. Molecular techniques including DNA sequencing of phylogenetic markers are commonly used for the diagnosis of clinical cases and investigations of cross-species transmission. To genetically characterize *S. scabiei* from bears, we used custom bait sets to capture the complete mitochondrial genomes of *S. scabiei* mites in skin scrapes taken from affected black bears in the Eastern United States. Sequence analysis revealed that there are currently two distinct clades of *S. scabiei* circulating in the Eastern American black bear population suggesting the possibility of two introduction events. Comparisons with existing *S. scabiei* genomes from the US, Japan, and Australia revealed that three clades exist globally and *Sarcoptes* mites from other hosts and locations were present in two of these clades. Further analyses of additional samples from different hosts and locations are needed to determine if the US clade that currently only includes sequences from bears also infests other hosts (e.g., domestic dogs, fox, coyotes, wolves, humans). Additionally, the origins of *S. scabiei* variants are unknown so additional sampling globally would further our understanding of the lineage diversity and population genetics of this One Health pathogen.

6. **Bullard, Stephen A.*, Warren, Micah B., Brule, John J.** Southeastern Cooperative Fish Parasite and Disease Project, College of Agriculture, Auburn University, Auburn, AL USA. **The surprising (or not so surprising) discovery of a new lineage of Cathariotrematinae Bullard, 2021 (Monogenoidea: Monocotylidae) infecting the olfactory lamellae of deepwater gulper sharks, *Centrophorus granulosus* (Squaliformes: Centrophoridae) in the Gulf of Mexico.**

   Species of Monocotylidae comprise ectoparasites that collectively infect the gill, olfactory bulb, urogenital system, and body surface of sharks, rays, and chimaeras (Chondrichthyes). The recently proposed monocotylid subfamily Cathariotrematinae includes 5 genera comprised wholly of species infecting the olfactory bulb of sharks and a chimaera only. During a recent parasitological survey of epipelagic and deepwater fishes in the Gulf of Mexico, we longlined several specimens of the deepwater gulper shark, *Centrophorus granulosus* (Squaliformes: Centrophoridae) and examined them for monocotylid infections. Despite being commonly caught on deepwater longlines, relatively little is known about the parasites that infect this shark and no record of a monocotylid from this host was previously known. Upon examining these sharks, we collected several monocotylid specimens infecting the olfactory bulb. These monocotylids were fixed in 10% formalin for morphology and preserved in 95% EtOH for DNA extraction and subsequent phylogenetic analysis. The specimens comprise a new cathariotrematine genus by having a haptor comprising a central loculus (without paired depressions), 5 peripheral loculi, a tripartite attachment organ comprising the posterior-most 3 loculi, and small hamuli. This is only the second species of the subfamily documented from the Gulf of Mexico. A phylogenetic analysis based on the large subunit ribosomal DNA (28S) recovered a monophyletic Cathariotrematinae and the new species sister to monotypic *Triloculotrema*.

7. **Shurba, Jacob A.[1]*, Horton, Matthew L.[2], Johnson, Paul D.[3], Warren, Micah B.[1], Brule, John H.[1], Truong, Triet N.[1], Curran, Stephen S.[1], Dutton, Haley R.[1], Ksepka, Steven P.[1],Krol, Justin D.[1], Bullard, Stephen A.[1]** [1]Aquatic Parasitology Laboratory and Southeastern Cooperative Fish Parasite and Disease Laboratory, Auburn University, Auburn, AL, USA; [2]Arkansas Game and Fish Commission, Little Rock, AR, USA; [3]Alabama Department of Conservation and Natural Resources, Marion, AL, USA. **Parasitological survey of two newly discovered populations of exotic invasive mystery snails (*Cipangopaludina*: Viviparidae: Bellamyinae) in Alabama and Arkansas.**

   Mysterysnails were introduced into North America in the early 20th century as food products from Asia and are common in the aquarium trade. Two populations of mysterysnails (*Cipangopaludina cf. japonica*) were recently discovered in Arkansas and Alabama, alarming fisheries managers concerned with potential snail-vectored pathogens and zoonotics. Because these snail populations were un-surveyed for parasites, we collected and necropsied 464 and 213 snails from Arkansas and Alabama, respectively. Each snail was excised from its shell before each tissue was examined separately for parasitic infection using a stereo-dissecting microscope with bright and dark field stage illumination. These snails were infected with encysted, unencapsulated metacercariae of *Alloglossidium cf. corti*; which were removed from the visceral mass, excysted, observed with a compound microscope with DIC optics, heat-killed, preserved in formalin, stained, cleared, and whole-mounted. Additional specimens were preserved alive in 95% EtOH for DNA extraction and phylogenetics. These specimens were morphologically (having characteristic cercarial stylet) and genetically (nucleotide sequences for ITS2, 28S) similar to *Alloglossidium corti*, which matures in ictalurid catfishes. The snails from Arkansas were infected also by the 3rd or 4th stage (L3, L4) larva of a parasitic nematode, *Spiroxys* sp., which likely matures in snail-eating freshwater turtles. These specimens were 98–98.7% similar in the 18S to several *Spiroxys* spp. In summary, no non-native parasite nor zoonotic agent was collected. Two native parasites with complex life cycles have acquired these invasive snails as an intermediate host. We aim to surveil for additional infections in these and other mysterysnail populations.

8. **Brule, John H.*, Warren, Micah B., Dutton, Haley R., Truong, Triet N., Ksepka, Steven P., Curran, Stephen S., Shurba, Jacob A., Krol, Justin D., Bullard, Stephen A.** Aquatic Parasitology Laboratory and Southeastern Cooperative Fish Parasite and

Disease Laboratory, School of Fisheries, Aquaculture, & Aquatic Sciences, College of Agriculture, Auburn University, Auburn, Alabama USA. **First taxonomically confirmed record of a gyrodactylid, *Gyrodactylus cichlidarum*, Paperna, 1968 (Monogenoidea) infecting farmed Nile tilapia, *Oreochromis niloticus* (Linnaeus, 1758) (Cichliformes: Cichlidae) in the United States.**

The parasites of Nile tilapia, *Oreochromis niloticus* (Linnaeus, 1758) (Cichliformes: Cichlidae) are poorly documented in North America. These parasites concern fisheries managers and fish culturists in North America because they comprise potential introduced (exotic, non-native) pathogens that kill cultured tilapias and could theoretically harm sympatric wild fishes. As part of a survey of the parasites of Nile tilapia cultured at high density in flow-through raceways, we observed numerous monogenoid specimens attached to the skin, fins, and gill filaments that we identified as *Gyrodactylus cichlidarum* Paperna, 1968. This parasite was originally described from the skin and gill of mango tilapia, *Sarotherodon galilaeus* (Linnaeus, 1758) (Cichlidae) from pools and streams in the Accra plains, southwestern Ghana. Live specimens of *G. cichlidarum* intended for morphology were heat-killed, formalin-fixed, routinely stained, cleared, and whole-mounted on glass slides. Additional specimens were preserved in 95% ethanol for DNA extraction and sequencing of the internal transcribed spacers 1 and 2 (ITS1, ITS2) and 5.8S ribosomal RNA gene. We identified our specimens as *G. cichlidarum* because they had a ventral bar with a distinct, dorsally-positioned postero-medial knob, and marginal hooks with a wide aperture and flat sickle base. Our two identical sequences of the ITS1-5.8S-ITS2 (783 bp and 723 bp) were nearly identical to (1 bp difference) those ascribed to *G. cichlidarum* from the United Kingdom. The present study is the first taxonomically confirmed record of a parasite infecting Nile tilapia in the United States and comprises the first genetic information for *G. cichlidarum* in the United States.

9. **Rayburn, Alexander U.*, Kerstetter, David W., Blanar, Christopher A.** Nova Southeastern University, Davie, FL, USA. **The parasites of the unwanted: endoparasite fauna of mesopredatory teleost pelagic longline bycatch.**

The ecology of the mesopelagic zone is an understudied area of the open ocean, with few diet studies even for dominant fish species. This project assesses the endoparasite community of fishes in the families Alepisauridae (lancetfishes) and Gempylidae (snake mackerels) to better understand mesopelagic food webs. These are frequent bycatch in the pelagic longline fishery which target Swordfish *Xiphias gladius* and thunnid tunas, yet the ecology of these mesopelagic species is poorly known. Whole fish specimens were collected onboard commercial vessels by observers, frozen, and examined in the laboratory. Of the 105 fishes examined to date, 95% were infected by at least one parasite. Lancetfishes commonly hosted the cestode *Pelichnibothrium speciosum* (91% prevalence, n=33), and gempylids commonly hosted the nematode *Anisakis* sp. (88% prevalence, n=72). Lancetfishes are potentially a unique case due to their high rate of cannibalism (45%), which may allow for multiple developmental stages of *P. speciosum* to coexist in the same host. These co-occurring stages of cestode may help the worm to develop before entering the definitive host, Blue Shark *Prionace glauca*. Escolar (n=22) show a low infection intensity (7 per host) relative to other studied host species. For reference, Lancetfishes *Alepisaurus* spp. (n=27) have an infection intensity of 151 per host, Oilfish *Ruvettus pretiosus* (n=19) have an intensity of 122 per host, and other gempylids combined (n=33) have an intensity of 76 per host. The high infection intensities in Lancetfishes and Oilfish may reflect their role as intermediate hosts for parasites seen in mesopelagic apex predators.

10. **Hazelrig, Corinna M.[1]*, Farrell, Terence M.[2], Palmisano, Jenna N.[3], Ortega, Jason[2], Haynes, Ellen[1], Cleveland, Christopher A.[1], Nemeth, Nicole M.[1]** [1]University of Georgia, Athens, GA, USA; [2]Stetson University, DeLand, FL, USA; [3]University of Central Florida, Orlando, FL, USA. **Snake mortalities in Florida, USA associated with *Raillietiella orientalis*.**

Raillietiella orientalis (Ro) is an invasive hematophagous lung parasite that threatens snake biodiversity in the southeastern United States. It infects native snake species and infection with Ro is often fatal in the definitive snake host. The introduction of Ro to Florida is proposed to have occurred through the establishment of invasive intermediate hosts (e.g., brown anole (*Anolis sagrei*)) and definitive hosts (e.g., Burmese python (*Python bivittatus*)). To date, detections of Ro are limited to Florida, but infections continue to spread northward given the diverse host range of Ro. During monthly surveys from November 2022 to January 2023 in Volusia County, Florida, five snakes (one common garter snake (*Thamnophis sirtalis*) and four pygmy rattlesnakes (*Sistrurus miliarius*)) were either found dead or moribund and died shortly after capture. Upon necropsy, each snake had 4-12 adult Ro pentastomes in the oral cavity, trachea, lungs, and/or free in the coelomic cavity. Four out of five snakes were in poor body condition. Two snakes were recaptured individuals that exhibited greater than 15% mass loss in the span of a month. All pygmy rattlesnakes had widely disseminated parasitic granulomas, variable lung lesions and presumed multiorgan schistosomiasis. Three snakes had crusty to ulcerative skin lesions, at least one of which had fungal hyphae microscopically consistent with *Ophidiomyces ophidiicola*. The multiple co-infections and poor health condition in snakes of multiple species at one site within a three-month period highlights the need for future work assessing pathogenicity and risk of Ro infections to native snakes.

11. **Ahmed, Rokeya [1]*, McLean, Bryan S. [2], Cook, Joseph A. [3], Galbreath, Kurt E. [4], Greiman, Stephen E.[1]** [1]Georgia Southern University, Statesboro, GA, USA; [2]University of North Carolina Greensboro, Greensboro, NC USA; [3]University of New Mexico, Albuquerque, NM, USA; [4]Northern Michigan University, Marquette, MI, USA. **Diversity of cestode species within the shrew *Sorex roboratus* (Eulipotyphla: Soricidae) collected from Mongolia.**

Despite their high prevalence within shrews and other insectivorous mammals, cestodes in the order Cylophyllidea remain a largely understudied group. Shrews, given their diet of mostly arthropods, which act as intermediate hosts to many cestode parasites, are consistently infected with a diverse array of helminths. However, very little has been done to identify global diversity a *Sorex* helminths. This is especially true for remote countries, like Mongolia. Therefore, as part of larger mammal and parasite survey project in Mongolia (summers of 2015 and 2016), 21 *Sorex roboratus* were captured and processed to obtain their helminths. Cestode species were identified through both morphological (staining and mounting) and molecular (COI and 28S gene barcode sequencing) techniques. Preliminary results based on COI barcoding show a total of 7 unique taxa present within the two shrew species. These data include the first records of cestode parasites from *S. roboratus* collected from Mongolia. Unique species, based on COI and 28S sequencing will be further processed for whole genome sequencing.

12. **Dutton, Haley R.*, Bullard, Stephen A., Kelly, Anita M.** Auburn University, Auburn, AL, USA. **Supplemental description and phylogenetics of *Dracovermis occidentalis* (Digenea: Liolopidae) infecting the intestine of an American alligator, *Alligator mississippiensis* from the Mobile–Tensaw River Delta, Alabama, USA.**

    As part of a parasitological survey of American alligators, *Alligator mississippiensis* (Crocodilia: Alligatoridae) in the southeastern United States, we examined several alligators from Louisiana, Alabama, and South Carolina. During the annual Alabama alligator hunt (August 2022), we collected several specimens of *Dracovermis occidentalis* (Platyhelminthes: Digenea: Liolopidae) from the intestine of a single alligator (alligators from Louisiana and South Carolina were not infected). These liolopid specimens were heat-killed and fixed in 10% formalin for morphology or preserved alive in 95% EtOH for DNA extraction. Liolopids comprise 5 genera of 15 species: *Liolope* spp. infecting giant salamanders, *Helicotrema* spp. infecting turtle and lizards, *Harmotrema* spp. infecting snakes, *Paraharmotrema* infecting turtles, and *Dracovermis* spp. infecting crododilians. Based on our newly-collected specimens, we emend *Dracovermis* and provide supplemental observations of *D. occidentalis*. Our specimens were assigned to *Dracovermis* because they lack tegumental spines/scales and have testes in the posterior 1/3 of the body, a pretesticular cirrus sac, a spined and eversible cirrus, a bipartite seminal vesicle, and a post-acetabular vitellarium. A phylogenetic analysis of the D1–D3 domains of the nuclear large subunit ribosomal DNA (28S), which is the largest taxon sampling for liolopids to date, recovered Liolopidae as monophyletic but did not support the previous assertion of parasite-host cophyly among liolopids and their vertebrate hosts. This is the first morphological study of new specimens of *Dracovermis* since the genus was proposed; the first record of a liolopid from Alabama; and the first phylogenetic analysis that includes *Dracovermis*.

13. **Garrett. Kayla[1,2]*, Dukes. Casey[1], Brown, Justin[3], Van Why, Kyle[4], Casey, Christine[5], Tabora, Joshua[6], Gerhold, Richard[7], Baker, Eliza[8], Olfenbuttel, Colleen[9], Douglass, Kelly[10], Barton, Ethan[1,11], LaCour, Jim[12], Berry, Rusty[13], Dennison, Catherine[14], Purple, Kathryn[15], Miller, Erica[16], Yabsley, Michael J.[1,2], Cleveland, Christopher A.[1]** [1]Southeastern Cooperative Wildlife Disease Study, University of Georgia, Athens, GA, USA; [2]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA; [3]Department of Veterinary and Biomedical Sciences, Pennsylvania State University, University Park, PA USA; [4]USDA Wildlife Services, Harrisburg, PA USA; [5]Kentucky Department of Fish and Wildlife Resources, Frankfort, KY USA; [6]Department of Natural Resources, Flintstone, MD USA; [7]Department of Biomedical and Diagnostic Sciences, College of Veterinary Medicine, University of Tennessee, Knoxville, TN USA; [8]Comparative and Experimental Medicine Graduate Program, University of Tennessee, Knoxville, TN USA; [9]NC Wildlife Resources Commission, Wildlife Management Division, Raleigh, NC USA; [10]USDA Wildlife Services, Raleigh, NC USA; [11]West Virginia Division of Natural Resources, Elkins, WV USA; [12]LA Department of Wildlife and Fisheries, Baton Rouge, LA USA; [13]Louisiana Department of Wildlife and Fisheries, Pineville, LA USA; [14]Ohio Division of Wildlife, Columbus OH USA; [15]Lincoln Memorial University, Harrogate, TN USA; [16]Department of Pathobiology, Wildlife Futures Program, University of Pennsylvania School of Veterinary Medicine, New Bolton Center, Kennett Square, Pennsylvania USA. **Regional surveillance for *Echinococcus* species in wild canids in the Eastern United States.**

    Echinococcus are zoonotic tapeworms which can cause disease in wildlife, domestic/agricultural animals, and humans (cystic or alveolar echinococcosis). Two species in North America are *Echinococcus multilocularis* and *E. granulosus* (*canadensis*). Wildlife definitive hosts are red foxes (*Vulpes vulpes*), gray foxes (*Urocyon cinereoargenteus*), coyotes (*Canis latrans*), and wolves (*Canis lupus*); intermediate hosts for *E. multilocularis* and *E. canadensis* are rodents and cervid species, respectively. Historically absent in the eastern US, *E. multilocularis* was recently reported in foxes and a domestic dog in Virginia, two domestic dogs in Missouri, and a human in Vermont; *E. canadensis* has been reported in coyotes in Maine and translocated elk in Tennessee. Our preliminary study in Pennsylvania detected two coyotes co-infected with *E. multilocularis* and *E. canadensis* (G8). During 2021-present, gastrointestinal tracts (GIT) from wild canids from Pennsylvania (n=124), Ohio (n=13), West Virginia (n=5), Virginia (n=40), Tennessee (n=13), South Carolina (n=2), North Carolina (n=49), Maryland (n=31), Kentucky (n=38), Georgia (n=15), and Louisiana (n=52) were screened for *Echinococcus*. Thus far, 382 GITs from red fox (n=133), gray fox (n=41), and coyotes (n=208) have been screened and one red fox from Pennsylvania was positive in a county in southeastern Pennsylvania (compared to our preliminary study), with an *E. canadensis* (G8) species. Positive samples are tested via real time PCR and sequenced targeting the COI gene to determine lineage. Our data supports findings that *Echinococcus* species are present in the eastern US. Continued surveillance is needed to clarify the range and better understand the possible threat to humans, wildlife, and domestic/agricultural animals in this region.

14. **Cunningham, Abigail J.[1,2]*, Garrett, Kayla B.[1,2], Nemeth, Nicole M.[2,3], Barron, Heather[4,5], Stasiak, Iga[6], Groves, Bethany[7], Gibbs, Samantha[8], Ruder, Mark G.[2], Kunkel, Melanie R.[1], Weyna, Alisia[1,3], Teo, Xuan H.[1,3], Goodwin, Chloe[1,3], Radisic, Rebecca[1], O'Reilly, Aidan[1], Yabsley, Michael J.[1,2,9]** [1]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA; [2]Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [3]Department of Pathology, College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [4]Clinic for the Rehabilitation of Wildlife (CROW), Sanibel Island, FL, USA; [5]Loggerhead Marinelife Center, Juno Beach, FL, USA; [6]Strategic Conservation Ministry of Environment, Saskatoon, SK S7N 3K3 Canada; [7]Progressive Animal Welfare Society (PAWS), Lynnwood, WA, USA; [8]United States Fish and Wildlife Service, Chiefland, FL, USA; [9]Center for Emerging Infectious Diseases, Athens, GA, USA. **Surveillance for *Trichomonas* infections in Bald Eagles (*Haliaeetus leucocephalus*) and Golden Eagles (*Aquila chrysaetos*) indicates that subclinical *T. gypaetinii* infections are common in Bald Eagles.**

    Avian trichomonosis is caused by several *Trichomonas* species, but *Trichomonas gallinae* is most commonly associated with morbidity/mortality. Although infections may be subclinical, these parasites can cause necrotizing lesions in the upper digestive tract. *Trichomonas gypaetinii* was originally described in Old World vultures in Spain. It has since been reported from red kite from Germany and several eagles including a bald eagle in Canada, Bonelli's eagles in Spain, and Stellar's sea eagle and white-tailed sea eagles in Japan. Most were subclinical infections, but oropharyngeal lesions were reported in a cinereous vulture fledgling from Spain. To better understand the prevalence and diversity of *Trichomonas* in eagles in the United States, oral swabs were collected from birds admitted to rehabilitation centers or diagnostic services. From 2018-2023, swabs from 88 bald eagles from 9 states and five golden eagles from four states were tested for *Trichomonas* spp. using PCR. All golden eagles were negative, but 68 (77.3%) bald eagles were positive, all were 100% similar to *T. gypaetinii* based on sequence analysis. No difference in prevalence was noted for sex (82.3% females vs.

89.3% males) or age (91.3% adults vs 75% juveniles). Only one *Trichomonas*-positive bald eagle had a small oral lesion. This study shows that *T. gypaetinii* infections are common and widespread in bald eagles, but they are rarely associated with lesions. Samples sizes were low for golden eagles so additional testing is warranted, especially since *T. gallinae* has been reported to cause disease in golden eagle chicks in the western United States.

15. **Hammond, Kimberly A.*, Gallagher, Kaitlin A.** Christian Brother's University, Memphis, TN, USA. **Parasite diversity among Sunfish species in relation to pollution.**

    Water quality is a pressing concern for the state of Tennessee since approximately 30% of its waterways cannot support stable, healthy ecosystems. One way to assess the impact of poor water quality on biological communities is to look for changes diversity and abundance of bioindicator species, such as parasites. The goal of our study was to examine how two types of pollution, municipal and runoff, might affect the diversity of fish parasite communities. We examined two river systems that branch off the Mississippi River, the Wolf River, which exhibits municipal and runoff pollution, and the Hatchie River, which only exhibits municipal pollution. We hypothesized that; the Wolf River will show lower parasite diversity than the Hatchie River. Forty-two and 58 fish, representing four species of sunfish, were collected from the Wolf and Hatchie Rivers respectively. All specimens underwent full body necropsies and parasites were preserved for identification. Approximately 42% of bluegills, 33% of longear, and 22% of green sunfish from the Hatchie River were parasitized; none of the spotted sunfish were parasitized. Meanwhile, 79% of bluegills, 50% of longear, 50% of green, and 100% of spotted sunfish from the Wolf River were parasitized. There was no significant difference in diversity between the two rivers for any of the sunfish species. There was, however, a slight significance difference in the abundance of *Lernea* in bluegills and *Posthodiplostomum* in spotted sunfish. This research is ongoing and will be expanded to increase our sample size of each of the four host species.

16. **Holt, Anna [1]*, Hamilton, Benjamin, Holt[1], Purple, Kathryn[2], Faulkner, Charles[3], Kolp, Matthew[3].** [1]University of Lincoln Memorial, Department of Veterinary Biomedical Science, Harrogate, TN USA; [2]University of Lincoln Memorial, Department of Biology and Microbiology, Harrogate, TN USA; [3]University of Lincoln Memorial - Richard A. Gillespie College of Veterinary Medicine, Harrogate, TN, USA. **Pilot study investigating the prevalence of parasites in abandoned piles of feces collected at dog parks in East Tennessee.**

    Dog parks have become popular and are great for socialization and exercise, however, previous research has revealed harmful parasites found in them. We observed that some dog parks in East Tennessee vary in visitation, park management, and awareness by dog owners of these risks. Also, the Appalachian region as a whole varies in the level of medical professionals to inform owners of potential risks. We suspect that differences within areas of Appalachia depend on location, such as urban counties and rural counties. The purpose of this study was to identify the prevalence of parasites in abandoned piles of feces collected at dog parks in East Tennessee. We hypothesized there might be more parasites found in rural dog parks on average than in suburban dog parks. Two dog parks were visited in Claiborne County (rural) and three in Knox County (urban) throughout winter and spring of 2023. We performed fecal flotation and observed samples using microscopy. To date, 79 abandoned piles of feces were collected. 19

samples (24%) were positive for at least one intestinal parasite (*Ancylostoma caninum,* n=8; *Trichuris vulpis*, n=7; *Toxocara canis*, n=7; *Capillaria* sp., n=3). There was no difference in parasite prevalence between rural and urban parks (Chi-square = 4.55; p = 0.34). Rural dog parks had 10 positive samples out of 31 (32%), while the suburban dog parks had 9 out of 48 (19%). We will continue sampling to investigate substantiate our findings and explore other factors that may correlate with increased parasitic prevalence in dog parks.

17. Simpson, Morgan D.[1]*, Ammar, Sawsan[3], Gerhold, Richard[2], Purple, Kathryn E.[1]. [1]Lincoln Memorial University, Harrogate, TN, USA; [2]University of Tennessee College of Veterinary Medicine, Knoxville, TN, USA; [3]University of Calgary Faculty of Veterinary Medicine, Calgary, Alberta, Canada. **Investigation of the prevalence of the "Trichy" protozoan parasite, *Trichomonas gallinae*, in hunter-harvested mourning doves (*Zenaida macroura*) from East Tennessee.**

The protozoan parasites, *Trichomonas* spp., have been responsible for significant mortality events in birds throughout recorded history. Mourning doves (*Zenaida macroura),* the most hunted game bird in North America, are negatively impacted by trichomonosis epizootics. Our aim is to determine the prevalence of *Trichomonas* spp. in hunter-killed mourning doves harvested over four seasons from the Forks of the River Wildlife Management Area in east Tennessee. The oral cavities of the doves were inspected for lesions and swabbed. Swabs were introduced into Hollander Fluid media, incubated at 37°C, and read by light microscopy every other day for 5 days. The prevalence of *Trichomonas* by culture was 2.1% (4/189) in 2016, 0% (0/50) in 2017, 2% (1/50) in 2021, and 2.1% (1/48) 2022, which is a similar range of that in other U.S. dove populations. Culture samples were frozen at -20°C prior to DNA extraction. PCR targeting the internal transcribed spacer region (ITS) was performed on all culture positive samples and a subset of culture negative samples from 2016. By PCR, all positive cultures were positive and 10.5% (2/19) of the negative samples were positive. We will perform sequencing on PCR positive samples and continue PCR on samples from other years.

18. **Rivera, Odette L.*, Gallagher, Kaitlin A.** Christian Brothers University, Memphis, TN, USA. **Detection of canine gastrointestinal nematodes between stray and non-stray populations.**

Dogs can host a number of gastrointestinal parasites that not only negatively impact canine health, but can also be transmitted to and harm humans. Therefore, it is important to be aware of the parasites that are present in the canine community. This study characterizes the canine parasite community in the city of Memphis by examining fecal samples from stray and pet dogs. We hypothesized that stray populations would have a higher prevalence of infection than the pet population and that hookworms would be the most abundant parasite. Canine fecal samples were collected from four dog parks and three animal shelters. Samples were tested for the presence of metazoan parasites via fecal flotation and *Giardia* via PCR. Approximately 26% of the sampled dogs were host to one or more parasites. The dog parks had a prevalence of 7.5–20%, and an average Shannon diversity of 0.00277097775, meanwhile the shelters had a prevalence of 21.7–62.5% and an average Shannon diversity of 0.002013989. As predicted, *Ancylostoma caninum* and *Trichuris vulpis* had the highest prevalence and intensity of infection across all sites. In addition, there were significant differences in the relative abundance of *T. vulpis* and *A. caninum* and overall parasite diversity of two of the animal shelters when compared to all other sites. The molecular testing for *Giardia* is currently ongoing, but so far, our results have demonstrated that zoonotic parasites are present within the Memphis canine community.

19. **Zaffiro, Briana K.[1]*, Kerstetter, David W.[2], Blanar, Christopher.[3]** [1]Halmos College of Arts and Sciences, Nova Southeastern University, Dania Beach, FL, USA; [2]Halmos College of Arts and Sciences, Nova Southeastern University, Dania Beach, FL, USA; [3]Halmos College of Arts and Sciences, Nova Southeastern University, Dania Beach, FL, USA. **Endoparasites in family Caprimulgidae birds in southeastern Florida (USA).**

    The Caprimulgidae are nocturnal birds that mainly prey on insects, which serve as intermediate hosts to several terrestrial parasite life cycles. Information on parasitism in this family remains scarce, and endoparasite community composition and structure have never fully been surveyed. To address this knowledge gap, 70 caprimulgid birds from southeastern Florida (USA) were examined for endoparasites, including Chuck Will's Widow (*Antrostomus carolinensis*, n = 47), Eastern Whip-Poor-Will (*A. vociferus*, n = 6), Common Nighthawk (*Chordeiles minor*, n = 16), and Lesser Nighthawk (*C. acutipennis*, n = 1). Frozen post-mortem at collaborating wildlife rescue centers, individuals were thawed and examined for parasites in the gastrointestinal tract. The esophagus, proventriculus, intestines, and cloaca were dissected, with the proventriculus and intestine contents further examined in washes. Parasites were stained and mounted prior to identification using standard taxonomic keys. Caprimugids hosted a diverse community of endoparasites including members of Digenea, Cestoda and Nematoda. Community composition varied among host species; Common Nighthawk were infected with mainly cestodes and nematodes, Chuck-Will's-Widow communities were largely dominated by cestodes, whereas Eastern Whip-Poor-Wills hosted more digeneans. Infection rates varied among hosts as well with Common Nighthawks having the highest infection rate at 63%. Eastern Whip-Poor-Wills have a 33% infection rate. These results may provide insight on the differing feeding ecologies and trophic dynamics of caprimulgids in South Florida.

20. **Von Holten, Zoe S.[1]*, Achatz, Tyler J.[1], Fecchio, Alan[2], Greiman, Stephen E.[3], Tkach, Vasyl V.[4]** [1]Middle Georgia State University, Macon, Georgia, USA; [2]Universidad Nacional de la Patagonia San Juan Bosco, Esquel, Chubut, Argentina; [3]Georgia Southern University, Statesboro, Georgia, USA; [4]University of North Dakota, Grand Forks, North Dakota, USA. **Revealing diversity of the Diplostomidae (Digenea) parasites in kingfishers.**

    Kingfisher birds are definitive hosts to a diversity of digeneans that use fish as second intermediate hosts. Many of these digeneans belong to the family Diplostomidae. Their larvae are well-known causes of fish health problems throughout the world, including "black spot disease". Until recently, only a limited number of diplostomid species were known from kingfishers throughout the New World. In the present study, we studied the morphology and sequenced the large ribosomal subunit (28S) rDNA and cytochrome c oxidase 1 (cox1) mtDNA genes of 7 diplostomid taxa from kingfishers in Brazil, the USA, and the Philippines. Newly generated and previously published DNA sequences were used for phylogenetic analyses to explore the interrelationships of these digeneans and their close relatives. Two new species of the previously monotypic *Crassiphiala* were described. The expansion of the genus required amendment to the generic diagnosis. A new genus was erected for a former undescribed species-level lineage of *Crassiphiala*. Our study further demonstrated the hidden diversity of digeneans infecting kingfishers throughout the New World. This study was funded in part by the National Science Foundation (grant 1852459), the National Institutes of Health (IDeA grant number P20GM103442), and the University System of Georgia STEM Initiative IV.

21. **Blevins, Hannah F.*, Shock, Barbara C., Faulkner, Vina.** Lincoln Memorial University, Harrogate, TN, USA. **Prevalence and diversity of *Ehrlichia* spp. from Ixodid ticks in the Cumberland Gap Region of Tennessee, Kentucky, and Virginia.**
Ehrlichia spp. are transmitted to animals and humans through the bite of an infected Ixodid tick, particularly bites from *Amblyomma americanum* and *Ixodes scapularis*. The main three species of *Ehrlichia* that affect humans in the United States are *E. ewingii, E. chaffeensis*, and *E. muris eauclairensis*; however, novel species continue to be discovered. Ehrlichiosis can result in fever, aches, nausea, as well as mortality. Humans, domestic animals, and wildlife are vulnerable to infection. In this study, we screened tick DNA samples from the Cumberland Gap Area of Tennessee, Virginia, and Kentucky via polymerase chain reaction. These tick samples were collected from 2016-2020 and contain the genera *Ixodes, Amblyomma, Dermacentor*, and *Rhipicephalus*. Positive amplicons were then sequenced to determine the species of *Ehrlichia*. These data will contribute to our growing knowledge of tick-transmitted diseases in Appalachia as well as the diversity of *Ehrlichia* spp. in the United States.

22. **Torres, J.[1]*, Tolliver, E. Morgan[2], Salinas, Nubia[2], Triana, Nicolas[2], Bondo, Kristin J.[3], Grisham, Blake A.[3], Sullins, D.S.[4], Kistler, Whitney M.[1]** [1]School of Mathematics and Sciences, Lincoln Memorial University, Harrogate, TN; [2]College of Veterinary Medicine, Lincoln Memorial University, Harrogate, TN; [3]Llano River Field Station and Department of Natural Resources Management, Texas Tech University, Lubbock, TX; [4]Department of Horticulture and Natural Resources, Kansas State University, Manhattan, KS. **Survey of haemosporidian parasites from Lesser Prairie Chickens (*Tympanuchus pallidicinctus*) from Texas and Kansas.**

The lesser prairie-chicken (*Tympanuchus pallidicinctus*) is a grassland grouse species with a declining population. The main driver of the population decline is loss of sand sagebrush and shinnery oak rangeland habitat across their historic range. This has led to protection for this species under the Endangered Species Act (ESA) in 2022. Their declining population makes this species especially vulnerable to infectious diseases. Therefore, we screened blood samples collected from 2008-2010 in Texas (n=173) and in 2019 from Kansas (n=17) using a nested polymerase chain reaction to detect infection of haemosporidian parasites. We detected *Plasmodium* infections in 10.5% (20/190) and sequenced a 995 base pair region of the cytochrome b gene from six (5.4%) of the samples from Texas and two (11.8%) of the samples from Kansas. We detected infected lesser prairie-chickens every year. These sequences matched 100% with *Plasmodium homopolare* from a California Condor (*Gymnogyps californianus*). This is the first report of *P. homopolare* in lesser prairie-chickens. A previous study identified *P. pedioecetii* infections in lesser prairie-chickens from New Mexico; however, that study only used morphology for species identification. *Plasmodium homopolare* is a recently described species that has broad host and geographic ranges in the western hemisphere. Although no reports of pathogenicity have been documented with *P. homopolare* infections, haemosproidian parasites are known to have negative effects on wild bird populations.

Additionally, this parasite has been documented in two species protected under the ESA, highlighting the need for further research into the effects this parasite can have on these populations.

23. **Gomez Perez, Diego A.*, Gallagher, Kaitlin A.** Christian Brothers University, Memphis, TN USA. **Canada Geese as vectors of waterfowl and zoonotic pathogens.**

The Canada goose population has more than doubled in the last few decades within the state of Tennessee. This is potentially a cause of concern since it has been documented that these geese can vector pathogens that are harmful to humans, waterfowl, and chickens. The objective of this study was to determine whether the Canada geese in Memphis are carrying any such pathogens. We collected over 160 pooled fecal samples from three sites in Memphis. We tested for the presence of metazoan parasites using fecal flotations, *Giardia* using PCR, and *E. coli* and *Salmonella* using HE and EMB bacterial plates. We also examined whether any of the parasites exhibited seasonality by sampling from one site in both the summer and winter. Possible coliforms were detected at two sites and *Salmonella* at one site through bacterial cultures. Molecular confirmation of the bacterial species is ongoing. Approximately 56% of samples were positive for one or more parasites, which include cestode eggs (prevalence of 2.4–11.36%), strongylid nematode eggs (45–56.6%), capillarid nematode eggs (prevalence of 4.54–5%), trematode eggs (prevalence of 4.8–50%), and *Giardia* (cysts identified histologically in one sample). Strongylid and trematode eggs had the highest prevalence and relative abundance, however, only the relative abundance of trematode was significantly different between sites. The molecular tests for *Giardia* and evaluation of seasonality are ongoing. Overall, this study provides evidence that the Canada geese in Memphis are carrying zoonotic pathogens and requires further studies on a larger scale in Tennessee.

24. **Hughes, Reece[1,2]*, Francisco, Raquel[1,2], Garrett, Kayla B.[1,2], Willitts, Kevin[3], Munk, Brandon[4], Brown, Justin D.[5], Rodriguez, Carlos[6], Dohlen, Alexa Von[7], Hamer, Sarah[8], Yabsley, Michael J.[1,2,9]** [1]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, Georgia USA; [2]Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, University of Georgia, Athens, Georgia USA; [3]Lake Tahoe Wildlife Care, South Lake Tahoe, California USA; [4]California Department of Fish and Wildlife, Rancho Cordovo, California USA; [5]Department of Veterinary and Biomedical Sciences, The Pennsylvania State University, University Park, PA USA; [6]Texas A&M Veterinary Medical Diagnostic Laboratory, College Station, TX USA; [7]Department of Natural and Behavioral Sciences, College of STEM, Johnson C. Smith University, Charlotte, North Carolina USA; [8]Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX; [9]Center for the Ecology of Infectious Diseases, Athens, Georgia USA. ***Trypanosoma cruzi*** **infection in a black bear cub and serologic survey for exposure in wild black bears from several states.**

Trypanosoma cruzi is an important cause of disease in humans and dogs, and although wildlife infections are common, disease is rare. In April 2022, an orphaned black bear (*Ursus americanus*) cub was admitted to a rehabilitation center. Over the next two weeks, it became progressively weak and lethargic. A CBC/chemistry panel showed the cub was anemic, had increased γ-glutamyltransferase (GGT), and trypanosomes were detected on a Giemsa-stained blood smear. Additional blood samples were collected and submitted for *T. cruzi* culture and molecular testing. A high parasitemia was observed on the smear and the culture was positive. Sequence analysis of the 24S alpha rRNA gene confirmed the parasites were *T. cruzi* DTU1. Parasitemia had decreased for a second sample collected ~1 mo later; however, the cub's activity had increased and it had gained weight. After another two months, parasitemia was nondetectable but the blood sample was PCR positive. Activity and eating at this point was considered normal. Because this is believed to be the first report of *T. cruzi* in a wild bear, we evaluated the prevalence of *T. cruzi* exposure in wild black bears. Serum samples from NC, PA, and CA were obtained and tested using three different serologic assays (IFA, ELISA, and immunochromatography assay(ICT)). To date, 87 bears from NC and PA have been tested and 18 (21%) were positive by at least one test (13 had IFA titers >=1:20, 4 positive by ELISA, and 2 positive by ICT). Only 2 bears were positive with 2 assays. This case suggests that morbidity could occur in black bears and our serologic data suggest that exposure occurs, but in the Eastern United States it may be low. Serologic testing from California is pending, but we expect that *T. cruzi* exposure should be more common in that region.

25. **Criswell, Madison R.[1]*, Kirkendall, Katherine[1], Faulkner, Vina[2], Marcum, Matthew[1], Shock, Barbara, C.[1], Gruszynski, Karen.[2]** [1]Lincoln Memorial University, Harrogate, TN, USA; [2]Lincoln Memorial University - Richard A. Gillespie College of Veterinary Medicine, Harrogate, TN, USA. **Infectious diseases of domestic cats (*Felis catus*) in Kentucky, Virginia, and Tennessee.**

The objective of this study was to determine the prevalence of infectious diseases and parasites among shelter and community cats from neighboring portions of Virginia, Tennessee, and Kentucky. Blood and fecal samples from both groups were tested using IDEXX real-time PCR assay anemia panel and centrifugal flotation, respectively, with 62 blood samples and 75 fecal samples being tested. FIV (1/62, 1.6%), FeLV (1/62, 1.6%), and *Bartonella* spp. (2/62, 3.2%) were identified only in community cats. *Mycoplasma* spp. were detected in both shelter and community cats (11/62, 17.7%). *Toxocara cati* (14/75, 18.7%) and *Ancyclostoma tubaeforme* (4/75, 5.3%) were only identified in community cats. More shelter cat fecal samples were positive for *Cystoisospora* spp. (4/25, 16%) compared to community cats (2/50, 4%), while *Dipylidium caninum* was detected in 8% (2/25) of shelter cats compared to 5.9% (3/51) community cats. Overall, Community cats were found to harbor a wider variety of infectious diseases and parasites than shelter cats, including several pathogens of zoonotic significance. These results are especially important due to the roaming nature of community cats and the interactions that may occur with humans and household pets, but it should also be noted that several pathogens were also identified in shelter cats.

26. **Pickeral, April[1]*, McLean, Bryan S.[2], Moore, Nicholas[1], Ahmed, Rokeya[1], Greiman, Stephen E.[1]** [1]Georgia Southern University, Statesboro, GA, USA; [2]University of North Carolina Greensboro. **Summer through winter: seasonal changes in the cestode communities within two *Sorex* shrew species, *Sorex cinereus* and *Sorex fumeus*, from North Carolina.**

Cestodes of shrews are largely understudied in North America, north of Mexico, with more than half of states (USA) and provinces (Canada) having no published reports, and only 11 having greater than 2 reports. With this in mind, we collected small mammals in the Pisgah National Forest in the Appalachian Mountains of North Carolina in the summer of 2021 and the winter of 2023. In total we collected 64 *Sorex* shrews, *Sorex* cinereus (N=44) and *Sorex fumeus* (N=20). Upon examination of their gut contents 14 cyclophyllid cestode taxa from 8 genera (7 from the family Hymenolepididae and 1 from the Dilepididae) were observed. All parasites were new geographic records. *Ditestolepis, Lineolepis, Mathevolepis, Monocercus, Soricinia, Staphylocystis, Staphylocystoides, and Urocystis* were all observed within this survey. Alpha and beta diversity were significantly lower in the winter compared to the summer with genus level prevalence ranging from 3% to 97%. These taxa have been differentiated by partial 28s rDNA and morphological evaluation. Morphological differentiation was completed with traditional methods of permanent slide mounting and measurements taken via light microscopy as well as Scanning Electron Microscopy.

27. **Dunkins, Allysia [1]*, Cook, Joseph A.[2], Greiman, Stephen E.[1]** [1]Georgia Southern University, Statesboro, GA, USA; [2]University of New Mexico, Albuquerque, NM, USA. **New species of *Vampirolepis* Yamaguti, 1959 (Cyclophyllidea: Hymenolepididae) from the black myotis bat (*Myotis nigricans)* from Panama.**

    Vampirolepis is a cosmopolitan genus within the Hymenolepididae infecting bats (Chiroptera). A new species of *Vampirolepis* is described from the black myotis bat, *Myotis nigricans*: The new species was collected from El Llano, Llano Carti in Guana Yala province, Chepo District Panama in October of 2016. Morphological characteristics and mitochondrial (mt) genome sequences were used to differentiate the new species from its congeners. We sequenced, assembled, and annotated the mt genomes of the new species. Protein coding amino acid sequences were used to generate a more comprehensive phylogeny of the family Hymenolepididae infecting small mammals. Mitochondrial genomes were assembled from Illumina HiSeq whole genome sequence data. Bioinformatic programs NOVOPlasty and Geneious were used to isolate and assemble the mt genomes, which were annotated using both Geneious (protein coding genes (12) and rRNAs (2)) and ARWEN (tRNAs (22)). Bayesian inference methods for phylogenetic analyses were performed using MrBayes and RAxML respectively on the CIPRES Science Gateway.

28. **Heyward, Natalie A.[1,2]*, Needle, David B.[4], Hazelrig, Corinna M.[1], Webb, Shevenell[3], Vashon, Jennifer[3], Garrett, Kayla B.[1,2], Cleveland, Christopher A.[1], Yabsley, Michael J.[1]** [1]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [2]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA; [3]Maine Department of Inland Fisheries & Wildlife, Augusta, ME, USA; [4]New Hampshire Diagnostic Laboratory, University of New Hampshire, Durham, NH, USA. **Protozoan parasites of Canada lynx (*Lynx canadensis*) and Fisher (*Pekania pennanti*) in Maine, USA.**

    Diseases of Canada lynx (*Lynx canadensis*) and fishers (*Pekania pennanti*) from the northeastern US are understudied. In recent years, Canine Distemper Virus (CDV) has become a concern in the Northeast. CDV can cause mortality directly or secondarily through immunosuppression and disease caused by various protozoan parasites. The objective of this study was to survey lynx and fishers for CDV and selected apicomplexan parasites. Tissues from 62 lynx and 104 fishers from Maine, USA collected from 2006 to 2021 were tested for apicomplexan parasites using 18s rRNA and ITS gene targets and CDV by P gene RT-PCR. We did not detect CDV, *Cytauxzoon*, or *Babesia*, but three parasites were detected in lynx including *Hepatozoon* spp. (60%), *Sarcocystis* spp. (11%), and *Toxoplasma gondii* (3%). Two parasites were detected in fishers, including one positive for a *Hepatozoon* sp. and 16% with *Cystoisospora* spp. No demographic variables (sex, age, weight, location, cause of death, and body condition) were associated with infection. To better characterize the *Hepatozoon, Cystoisospora* spp., and *Sarcocystis* spp. detected, cox1 and longer 18S rRNA gene sequences were obtained. The *Cystoisospora* spp. in fisher was 99.6% (764/767bp) similar to a *Cystoisospora* sp. from a Eurasian badger from Spain and was next 98.9-99.0% similar to numerous *Cystoisospora* spp. including *C. canis, C. felis, C. belli,* and *C. timoni*. This indicates a probable novel species of *Cystoisospora* in fisher. The *Hepatozoon* sp. from lynx was 98% (999/1,019) similar to *H. felis* from a wildcat in Hungary and the *Hepatozoon* sp. from the fisher was 99.7% (610/612) similar to a *Hepatozoon* sp. from an opossum from Brazil. Analysis of the *Sarcocystis* sp. is ongoing. This study provides new data on the diversity of apicomplexan parasite infections of lynx and fisher and some of the potential risk alongside CDV coinfections.

29. **Skelton, Devin[1]*, Cook, Joseph A.[2], Tkach, Vasyl V.[3], Greiman, Stephen E.**[1] [1]Georgia Southern University, Statesboro, GA, USA; [2]University of New Mexico, Albuquerque, NM, USA; [3]University of North Dakota, Grand Forks, ND, USA. **New species of tapeworm *Monocercus* Villot 1982 from *Sorex monticola* collected from the Sangre de Cristo Mountains of New Mexico.**

    Shrews, small insectivorous mammals, host a diversity of tapeworms mostly in the family Hymenolepididae, but one genus is in the Dilepididae (i.e. *Monocercus*). This genus, with only one described species, *Monocercus soricis*, is greatly understudied in North America. In the fall of 2015, we collected 15 montane shrews (*Sorex monticola*) from Cowles, New Mexico in the Sangre de Cristo Mountains. From two individuals, we identified a new species of *Monocercus*. Morphological characteristics, 28S rDNA sequences, and complete mitochondrial (mt) genome sequences were used to differentiate this new species from *M. soricis* and Eurasian species. We sequenced, assembled, and annotated the mt genome of the new species. Mitochondrial genomes were assembled from Illumina HiSeq whole genome sequence data. Bioinformatic programs NOVOPlasty and Geneious were used to isolate and assemble the mt genomes, which were annotated using both Geneious (protein coding genes (12) and rRNAs (2)) and ARWEN (tRNAs (22)). A phylogenetic analysis of the Cyclophylidea was ran and is the first to include any species in the family Dilepididae.

30. **Purple, Kathryn*, Brandt, LaRoy, Chazo, Lucas, Brehm, Autumn, Faulkner, Charles.** Lincoln Memorial University, Harrogate, TN, USA. **The Prevalence of *Dirofilaria immitis* in wild Canidae from the Cumberland Gap Region of Kentucky, Virginia, and Tennessee.**

The increasing occurrence of canine heartworm disease (CHW) in pet dogs is a significant cause of mortality and economic burden to pet caretakers. Infections with the nematode parasite, *Dirofilaria immitis* responsible are well documented in wild canids throughout the Southeast U.S. Coyotes (*Canis latrans*) and red foxes (*Vulpes vulpes*) with circulating microfilariae are hypothesized as important reservoirs for infection of mosquito vectors and subsequent transmission of infection to unprotected pet dogs. Coyote (n=49) and red fox (n=2) cadavers obtained from varmint hunts, exterminators, or as road-killed animals were examined by necropsy for CHW infection between 2018 and 2022. Adult CHW were found in the hearts of 6.1% (3/49) of coyotes and 0% (0/2) of red foxes. Two coyotes had single worm infections and one coyote had a multi-worm infection. The occurrence of heartworm positive wild Canidae in this rural region confirms their role as a reservoir of CHW and appears to lend support to research suggesting that CHW prevalence in rural areas may be comparatively lower than urban communities. Our ongoing research is expected to add clarity to the role wild Canidae play as a reservoir for facilitating transmission of CHW between mosquito vectors and pet dogs in the Cumberland Gap region.

31. **Blanar, Christopher A.[1]*, Barba, Daniel[2], Santis, Jacqueline[2], Gupta, Neha[1], Kerstetter, David W.[1]** [1]Nova Southeastern University, Fort Lauderdale, FL, USA; [2]Miami Dade College, Miami, FL, USA. **Microbiomes of parasitic nematode (*Ozolaimus megatyphlon*) cuticles differ from those of their iguana hosts.**

Florida iguanas (*Iguana iguana, Ctenosaura similis*) are heavily infected with the nematode parasite *Ozolaimus megatyphlon*. We noted an apparent microbial community associated with the cuticle of these nematodes. As studies of parasite ectomicrobiomes are rare, we characterized the cuticular microbiome of *O. megatyphlon* and contrasted it with the gut microbiome of its host, using a combination of morphological observations and molecular analysis. Scanning Electron Microscopy (SEM) revealed a diverse community of coccoid and coliform bacteria associated with dense mats of segmented filamentous bacteria embedded in the worm cuticle; this community was absent from the host gut or digested food. Metabarcoding of this microbiome (sequencing variable regions of 16S rRNA using PCR [primer 319F/806R] and Illumina cBot to generate clusters for sequencing on MiSeq) allowed for molecular level characterization of both parasite and host bacterial communities; these differed in both species composition and community structure: nematode microbiomes were dominated by Lachnospiraceae, *Clostridium*, and Bacteroidetes, whereas the host gut featured a more diverse community of taxa typical of plant-eating vertebrates. The presence of cellulose-fermenting bacteria on nematode cuticles may indirectly benefit the host, raising the possibility that the *O. megatyplhon* – iguana relationship may be at least partially mutualistic, rather than strictly parasitic.

32. **Warren, Micah, B.*, Dutton, Haley, R., Bullard, Stephen, A.** Auburn University,Auburn, AL, USA. ***Nomasanguinicola dentata* (Paperna, 1964) Warren and Bullard, 2023 (Digenea: Sanguinicolidae Poche, 1926) infecting African sharptooth catfish, *Clarias gariepinus* (Burchell, 1822) Teugles, 1982 (Siluriformes: Clariidae) from the Okavango River, Namibia: supplemental description and phylogenetic analysis.**

Fish blood flukes (Digenea: Chimaerohemecidae; Acipensericolidae; Sanguinicolidae; Elopicolidae; Aporocotylidae) comprise 175 species assigned to 46 genera, are occasional pathogens of cultured fishes, and are the ancestor to the schistosomes. Sanguinicolids infecting catfishes (Siluriformes) (10 species; *Nomasanguinicola* spp., *Plehniella* spp., monotypic *Cladocaecum*, monotypic *Kritsky*; *Sanguinicola chalmersi*) are morphologically and ecologically diverse. *Nomasanguinicola* spp. (*N. canthoensis* [type] infecting bighead catfish [Clariidae], *N. dentata*, and *N. clarias* infecting African sharptooth catfish) are unique by having denticles in two columns flanking the mouth. Like many freshwater fish blood fluke lineages, *N. dentata* and *N. clarias* have not been sequenced. Herein, we provide a supplemental description of *N. dentata* and reconstruct a 28S phylogeny. On 7 Dec 2021, we examined the heart of an African sharptooth catfish from the Okavango River (northeastern Namibia) that was infected with adults of *N. dentata*. Presently, no type-material exist for *N. dentata* (type locality Israel) nor *N. clarias* (Egypt). *Nomasanguinicola dentata* differs from *N. canthoensis* by having an intestine with 4 radial ceca and a testis with laterally directed lobes extending anterior to the intestine as well as lacking regularly spaced aggregates of tegumental papillae. We suspect that *N. dentata* and *N. clarias* are conspecific. The 28S sequence for *N. dentata* differed from *N. canthoensis* by 143 base pairs, and the phylogenetic analysis recovered the 2 species sister to one another. This is the first report of a fish blood fluke from sub-Saharan Africa, and the first report of a species of *Nomasanguinicola* in Africa in nearly 40 yrs.

33. **Truong, Triet N. [1]*, Whelan, Nathan V.[1,2], Johnson, Paul D.[3], Buntin, Michael L.[3], Bullard, Stephen A.[1,4]** [1]Auburn University, Auburn, AL, USA; [2]US Fish and Wildlife Service, Auburn, AL, USA; [3]Alabama Department of Conservation and Natural Resources, Marion, AL, USA; [4]North-West University, Private Bag X6001, Potchefstroom, South Africa. **Description, life cycle of a new species of *Proterometra* (Digenea: Azygiidae) from the Cahaba River, Alabama, U.S.A. and phylogenetic analyses.**

We herein describe a new species of *Proterometra* (Digenea: Azygiidae: Azygiinae) from the Cahaba River, Alabama, USA, and document that it asexually reproduces in the compact elimia, *Elimia showalteri* (Lea, 1860) (Cerithioidea: Pleuroceridae) and matures in the esophagus of the blackbanded darter, *Percina nigrofasciata* (Agassiz, 1854) (Perciformes: Percidae). Adults of the new species differ from congeners by having a small body and eggs having a wholly fimbriated surface, appearing colloquially as a cilia-like brush border. Naturally-shed cercariae of the new species differ from those of its congeners by having a strongly claviform tail stem bearing aspinose mammillae, a single furca, excretory pores that open on the posterior margin of the single furca, and few eggs in the cercarial distome. The behavior of the cercaria further differentiates the new species. Live naturally-shed cercariae of the new species secreted a jelly-like adhesive that coated the surface of the furca and evidently facilitated attachment to the surface of glass, plastic, and snail shell. The attached cercariae vigorously wiggled and thrashed about once attached, perhaps as if mimicking the larva of a stream insect. Phylogenetic analyses recovered monophyletic Azygiidae, which comprised a monophyletic Leuceruthrinae Goldberger, 1911 and polyphyletic Azygiinae Lühe, 1909. The present study is the largest taxon sampling for Azygiidae and the first to include 28S sequences of a species of *Leuceruthrus*. Compact elimia and blackbanded darter are new host records for *Proterometra*. The new species is the 3rd congener reported from the Cahaba River.

34. **Moore, Nicholas[1]*, McLean, Bryan S.[2], Cook, Joseph A.[3], Galbreath, Kurt E.[4], Greiman, Stephen E.[1]** [1]Georgia Southern University, Statesboro, GA, USA; [2]University of North Carolina Greensboro USA; [3]University of New Mexico, Albuquerque, NM, USA; [4]Northern Michigan University, Marquette, MI, USA. **Diversity of tapeworms (Cestoda: Cyclophyllidea) parasitizing two shrew species, *Sorex caecutiens* and *Sorex isodon*, from Northern Mongolia.**

Despite their high prevalence within shrews and other insectivorous mammals, cestodes in the order Cylophyllidea remain a largely understudied group. Shrews, given their diet of mostly arthropods, which act as intermediate hosts to many cestode parasites, are consistently infected with a diverse array of helminths. However, very little has been done to identify global diversity a *Sorex* helminths. This is especially true for remote countries, like Mongolia. Therefore, as part of larger mammal and parasite survey project in Mongolia (summers of 2015 and 2016), 21 *Sorex roboratus* were captured and processed to obtain their helminths. Cestode species were identified through both morphological (staining and mounting) and molecular (COI and 28S gene barcode sequencing) techniques. Preliminary results based on COI barcoding show a total of 7 unique taxa present within the two shrew species. Only one taxon is present within *S. isodon*, showing a prevalence of 25%. 7 taxa are present within *S. caecutiens* samples, with prevalence ranging from 5% to 29%. These data include the first records of cestode parasites from *S. roboratus* collected from Mongolia. Unique species, based on COI and 28S sequencing will be further processed for whole genome sequencing.

35. **Lattner, Seth P.[1], Stange, Emma[2], Brown, Patricia[3], Olfenbuttel, Colleen[4], Douglass, Kelly[5], Yabsley, Michael J.[1,6], Cleveland, Christopher A,[1].** [1]Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [2]College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [3]Franklin College of Arts and Sciences, University of Georgia, Athens, GA, USA; [4]North Carolina Wildlife Resources Commission, Raleigh, NC, USA; [5]USDA APHIS Wildlife Services, Raleigh, NC, USA; [6]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA. **Investigation of canine distemper virus and protozoan parasites in raccoons (*Procyon lotor*) of North Carolina.**

Canine distemper virus (CDV) is a highly infectious Morbillivirus (Family Paramyxoviridae) that causes morbidity and mortality in numerous mammalian species. Coinfections with CDV and protozoan parasites (such as *Toxoplasma gondii* and *Sarcocystis* spp.) have frequently been documented in wild and domestic carnivores, occasionally associated with severe neurologic disease. This ongoing investigation aims to identify the prevalence of CDV and multiple protozoal parasites (*T. gondii*, *Sarcocystis* spp., *Neospora* spp., and *Trypanosoma cruzi*) in wild raccoons (*Procyon lotor*) in North Carolina. Lung, heart, and spleen samples were collected from raccoons obtained through nuisance trapping, hunter/trapper harvest, roadkill, or clinical cases. To date, CDV has been detected in 44.2% (19/43) of raccoon lung samples via real-time RT-PCR (Ct <37). Presence of CDV was confirmed in 5 samples with high Ct values (>21) by FA and/or conventional PCR. Apicomplexans and *T. cruzi* were detected in 50.0% (18/36) and 44.1% (15/34) of spleen and heart samples, respectively. Sequencing for apicomplexan speciation is ongoing. Of the 19 CDV-positive raccoons, prevalence of coinfection with CDV and an apicomplexan parasite or *T. cruzi* were 26.3% (5) and 21.1% (4), respectively. These findings increase the understanding of CDV and coinfections in wild raccoons in North Carolina. Because raccoons are considered to be an important reservoir host for CDV in the eastern United States, understanding the prevalence of CDV and protozoan infections, particularly in asymptomatic raccoons, provides important information regarding virus maintenance, transmission to other susceptible hosts, and the impacts of coinfections.

36. **Curran, Stephen S.*, Brule, John H., Ksepka, Steven P., Truong, Triet N., Warren, Micah B, Bullard, Stephen A.** Auburn University, Auburn AL, USA. **Investigating digenean diversity in an estuarine pond on the Fort Morgan peninsula, Alabama.**

    We investigated the digenean community from a ̴5 Acre estuarine pond adjacent to the southern portion of Mobile Bay in Alabama (30°14' 04.54" N, 87°58' 09.84" W). Opportunistic collections of invertebrates and estuarine fishes were conducted on several occasions during the Spring of 2023. Parasites were collected and preserved for morphological observation and DNA extraction. The internal transcribed spacer 2 region and a portion of the 28S ribosomal gene were sequenced from digenean parasites. Preliminary identifications from collections revealed: 7 adult digenean species infecting 5 species of fishes; metacercariae of 2 other digenean species infecting *Menidia beryllina*, and the metacercaria of *Microphallus cf. turgidus* infecting the grass shrimp *Palaemon pugio*; and cercariae representing at least 5 species (3 *Haploporidae* spp., 1 *Heterophyidae* sp., and 1 *Microphalloidea* sp.) infecting 3 snail species: *Littoridinops monroensis, Heleobops* sp., and *Pyrgophorus* sp. (all Littorinimorpha: Cochliopidae). Digenean identifications will be reported to lowest possible taxonomic level. The most significant result thus far is the discovery of an undescribed species of *Saccocoelioides* (Haploporidae) maturing in *M. beryllina*. This species is identical to specimens collected and identified as undescribed by our former president, William F. Font. Bill collected the worm from *M. beryllina* in creeks emptying into Lake Pontchartrain in Louisiana in 2011. Ribosomal DNA from adults of the new material matched one of the cercaria collected in the study pond.

37. **Wisnieski, Lauren*, Faulkner, Charles, Faulkner, Vina.** Richard A. Gillespie College of Veterinary Medicine, Lincoln Memorial University, Harrogate, TN, USA. **Factors associated with heartworm preventative use.**

    The reported prevalence of heartworm preventative use is low, some estimates falling around 50% of dogs. However, there are very few reported estimates of prevalence. We aimed to estimate prevalence and evaluate factors, including vaccination status, demographics, lifestyle, physical conditions, medications and supplements, and environment and living conditions, for their association with heartworm preventative use in a large dataset from the Golden Retriever Lifetime Study (N = 2998). In our sample, the prevalence of heartworm use was 39.5%. Due to the large number of predictors evaluated, we built a bootstrapped elastic net logistic regression model, which is robust to overfitting and multicollinearity. Variables were evaluated by calculating covariate stability and statistical significance. In our elastic net regression, receiving vaccinations (rabies, Bordetella, or any other vaccine), being located in the Southern U.S., being altered, being in the top quartile of height, having an infectious disease or ear/nose/throat system disease diagnosis, being on heartworm preventatives in the past, currently being on tick preventative, having sun exposure in an area with concrete flooring, living in a house with more rooms with carpeted floors, and spending time on hardwood flooring inside were associated with greater odds of heartworm preventative use. Supplementation use was associated with lower odds of heartworm preventative use. The explanatory factors we identified can be used to improve client communication. In addition, target populations for educational interventions and outreach can be identified. Future studies can validate the findings in a more diverse population of dogs.

38. **Georgieva, Simona[1,2]*, Khosravi, Maral[3].** [1]Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, Sofia, Bulgaria; [2]Department of Parasitology, School of Medicine, Chungbuk National University, Cheongju, South Korea; [3]Department of Marine Ecology, GEOMAR Helmholtz Centre for Ocean Research, Kiel, Germany. **Trematode communities in the potamidid gastropod *Pirenella cingulata* (Gmelin, 1791) (Cerithioidea: Potamididae) from the Persian Gulf.**

    The Persian Gulf is among the highest anthropogenically impacted regions in the world. Harsh environmental condition, such as extreme seasonal temperatures and salinity fluctuations select for species with high tolerance and adaptability to short-term changes. Marine biodiversity data from the region are still scarce mainly covering larger taxa, while a substantial portion of the invertebrates remain poorly known. In this study we applied an integrative taxonomy approach to assess the trematode diversity in one of the most abundant mollusc species, the marine mud snail *Pirenella cingulata* (Gmelin, 1791) along the coast of Iran. Examination of 1,745 *P. cingulata* sampled at eight distinct locations between December 2019 and February 2020 revealed diverse trematode fauna accounting for a total of 29 species. The genetic population structures of both the snail host and the most abundant digenean trematodes recovered were further characterised and contrasted. Component community analysis revealed distinctive trematode community composition at the different sampling locations. Higher overall prevalence of infection was detected along the northern coast which is characterised with lower temperature and salinity levels. Overall, our study: (i) revealed a species-rich and diverse trematode fauna in the mud snail populations along the hottest marine coastline, (ii) represent an important step to the knowledge on the most heat tolerant host-parasite systems in the world oceans, (iii) highlights the importance of molecular systematics in the assessment of larval trematode diversity and elucidation of their life cycles, and (iv) provides an important baseline data to build a framework to model host-parasite dynamics in the region over time.

39. **Kmentova, Nikol[1]*, Moons, Tanisha[1,2], Appy, Ralph[3], Artois, Tom[1], Justine, Jean-Lou[4], Vanhove, Maarten[1].** [1]Hasselt University, Research Group Zoology: Biodiversity and Toxicology, Centre for Environmental Sciences, Diepenbeek, Belgium; [2]Department of Parasitology, Faculty of Science, University of South Bohemia, České Budějovice, Czech Republic; [3]Cabrillo Marine Aquarium, San Pedro, CA, USA; [4]ISYEB, Institut de Systématique Évolution Biodiversité, UMR7205 CNRS, EPHE, MNHN, UPMC, Université des Antilles, Muséum National d'Histoire Naturelle, Paris, France. **Symbiosis in rhabdocoelas: from invertebrate to vertebrate hosts.**

    Platyhelminthes provide a high diversity of evolutionary shifts towards a symbiotic way of life. There are at least five known lineages of rhabdocoel flatworms with representatives displaying a certain form of symbiotic lifestyle. Although less attention is given to the mostly free living relatives of neodermatans, the endosymbiotic and parasitic rhabdocoelas can give us important insights on the evolution of parasitism in one of the most successful parasitic groups in the animal kingdom. In the current study, specimens of rhabdocoelas found on gills or skin of different gobiid and coral reef fish hosts in the US and Australia, respectively, were collected. Examination of serial sections and stained whole mounts combined with observation of life animals enabled detailed morphological characterisation. Phylogenetic placement was based on portions of ribosomal markers. Infection parameters ranged from 1 to 8 per host individual. Higher infection intensity by juveniles compared to adult flatworms was observed. Morphological characterisation suggests the presence of two species of *Paravortex*, representatives of which are typically found in the gut or gills of bivalves. We provide the first molecular data of parasitic turbellarians from vertebrate hosts and elucidate mitogenome level evolution and gene order rearrangements within these rhabdocoels. Symbiotic rhabdocoelas provide independent and repeated transition to both invertebrate and vertebrate hosts and as such genome wide comparative analyses could reveal common signatures of a symbiotic and parasitic lifestyle across Platyhelminthes. Due to its remarkable host range and distribution, *Paravortex* figures as an ideal lineage to determine adaptation mechanisms towards parasitic lifestyle.

40. **Ksepka, Steven P.*, Bullard, Stephen A.** Aquatic Parasitology Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, AL, USA. **A new species of *Henneguya* Thélohan, 1892 (Cnidaria: Bivalvulida: Myxobolidae) infecting the submucosa of the intestine and pyloric caeca of red drum, *Sciaenops ocellatus* (Linnaeus) (Perciformes: Sciaenidae) from coastal Alabama.**

A new species of *Henneguya* Thélohan, 1892 (Bivalvulida: Myxobolidae) is described from the submucosa of the intestine and pyloric caeca of red drum (*Sciaenops ocellatus* [Linnaeus, 1766] [Perciformes: Sciaenidae]) from the Gulf of Mexico off Gulf Shores, Alabama, United States. The new species differs from all congeners by the combination of myxospore dimensions, polar tubule coil count, the presence of an iodinophilic vacuole in the sporoplasm, and small subunit ribosomal DNA (SSU rDNA) sequence. A phylogenetic analysis of the SSU rDNA recovered the new species sister to *Henneguya cynosioni* Dykova, de Buron, Roumillat, and Fiala, 2011 in a clade composed of 11 species of *Henneguya* and 1 species of *Myxobolus* Bütschli, 1882 (Bivalvulida: Myxobolidae) that collectively infect fishes in marine or estuarine systems. Histological sections of infected intestine and pyloric caeca revealed plasmodia of the new species developing in the loose connective tissue of the submucosa. The new species comprises the second species of *Henneguya* reported from red drum.

41. **Le'Roy, Crystal J.*, Lynch, Savannah, Faulkner, Charles T.** Lincoln Memorial University Richard A. Gillespie College of Veterinary Medicine. **Canine heartworm in the Cumberland Gap Region.**

Cases of canine heartworm (CHW) disease continue to increase in incidence annually despite efforts to increase awareness of its adverse impact and availability of effective and affordable prophylactic medications. Research in the Cumberland Gap region (CGR) has focused on the occurrence of CHW in the local pet dog and mosquito vector populations. Wild Canidae, primarily coyotes (*Canis latrans*), have also been surveyed opportunistically to assess their role as a source of microfilariae for transmission to suitable mosquito vectors. This study was undertaken to better estimate the contribution to CHW transmission of stray and surrendered dogs resident in CGR shelters. Local shelters are visited weekly and whole blood samples (n=133) collected and tested for

CHW antigen without immune complex disassociation by heat treatment. Additionally, canines obtained extra-locally (n =200) from regional shelters for use in the LMU-CVM surgery program were tested for CHW antigen and screened for microfilaremia. To date, a total of 333 dogs from all sources have been tested for CHW antigen with an estimated local prevalence of 8.2% and extra-local prevalence of 3.5%. Blood from CHW antigen positive dogs were examined microscopically for microfilariae. Circulating microfilaria (>30 um) of *Dirofilaria immitis* were observed in 8 (72.7%) dogs locally, and 5 (71.4%) dogs extra-locally supporting their role as transmission sources for infection of the regional mosquito vector population.

42. **Hamilton, Benjamin.*** Lincoln Memorial University, Harrogate, TN, USA. **Fecal contamination with gastrointestinal parasites of dog parks in rural and urban environments.**

Several studies have identified dog parks as areas of high risk for pathogenic contamination, and as sources of transmission between visiting dogs. Previous research has shown the prevalence of gastrointestinal parasites promotes zoonotic transmission. The phenomenon of dog fouling among public dog parks exacerbates the issue and emphasizes attention be given to dog parks as a source of communal outbreaks. Recent studies have investigated parasite prevalence at a regional level, but evidence suggests that dog park contamination can be variable between geography and demography. Environmental contamination and exposure to parasitic infections is likely regionally dependent, and conclusions about public health risks should be informed by prevalence data specific to regional areas. The goal of this study was to characterize the prevalence of intestinal parasites in dog parks in East Tennessee and determine if significant disparities in parasite abundance between rural and urban parks exists. We used centrifugal fecal flotation to identify parasites microscopically in abandoned poop piles collected from 6 dog parks in spring 2023. Samples were noted either "fresh" or "old" and relative abundance as well as taxa were documented. We report a slightly higher abundance in rural parks than urban parks, *with A. caninum* (10.1%) being the predominant taxa found. Our long-term goal is to determine if the prevalence of intestinal parasites varies between urban and rural locations, and if that is based on socioeconomics and demographics such as population density, use of anthelmintics, and proximity to wildlife.

43. Zelmer, Derek A.* University of South Carolina – Aiken, Aiken, SC USA. **Patterns of asynchrony in helminth parasites of centrarchids in J. Strom Thurmond Lake, South Carolina.**

The likelihood of metapopulation persistence is dependent upon recolonization of local extinction events (the so-called "rescue effect"), which in turn is made more likely when the component subpopulations exhibit asynchronous subpopulation dynamics. The influence of stochastic environmental effects on subpopulation dynamics, combined with the tendency for these stochastic effects to be spatially correlated, leads to the prediction that the degree of asynchrony between subpopulations should covary positively with inter-site distance. Fishes within the genus *Lepomis* were collected monthly from 4 localities along the eastern shoreline of J. Strom Thurmond Lake, from

July 2016 to July 2017. Parasite abundances were correlated among the localities in a pairwise fashion to generate metrics of subpopulation synchrony, and the degree of synchrony was examined for correlation with between-site distances, habitat characteristics, and centrarchid community structure. Of the 7 parasite species examined, 2 (*Tylodelphys scheuringi* and *Crinicleidus* sp.) demonstrated correlations between asynchrony and distance, and 2 species (*Posthodiplostomum minimum* and *Spinitectus* sp.) had patterns of asynchrony that could not be associated with any of the site variables measured. Three parasite species (*Clavunculus bifurcatus*, *Crepidostomum cornutum*, and *Neoechinorhynchus cylindratus*) had patterns of asynchrony that covaried with habitat variables, which, in concert with the steady decline in the water level of the reservoir over the course of the investigation, suggests that large-scale effects can be "refracted" by differences in habitat characteristics, resulting in asynchrony over relatively short distances.

44. **Dukes, Casey G.[1]*, Coker, Sarah M.[1], Yabsley, Michael J.[1,2] and Cleveland, Christopher A.[1]** [1]Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine, UGA, Athens, GA, USA; [2]Warnell School of Forestry and Natural Resources, UGA, Athens, GA USA. **Finding needles in the haystack: the development of a rapid, field-based RT-PCR for Guinea worm detection and confirmation.**

    Since 1986, the Global Guinea worm Eradication Program has reduced Guinea worm (GW, *Dracunculus medinensis*) infections in humans worldwide from 3.5 million to only 13 in 2022. Despite this phenomenal achievement, complete eradication has been complicated by discoveries of GW infections in domestic dogs, cats, and baboons. This highlights the need for rapid field-based diagnostics to confirm GW infections in novel hosts to further prevent transmission among humans, domestic animals, and wildlife. Currently, we are adapting our recently developed GW RT-PCR targeting the cytb gene for use with a field-deployable thermocycler and custom lyophilized reagents. This highly portable system produces results in <2 hours and can be operated in remote locations with limited specialized equipment. Our objective is to validate a custom assay with multi-functional purposes, including confirming emerging suspect GW from hosts, identifying larvae from aquatic paratenic hosts, and detecting larvae in copepods from water. Validation is being conducted using molecularly confirmed GW samples, non-target parasite samples, and host tissue from various endemic countries (Chad, Ethiopia, South Sudan, Mali, Cameroon, and Angola). To date, we have tested 144 samples (host=36, non-target parasites=37, Guinea worm= 71) and specificity is similar to our lab-based methods (100% for the GW RT-PCR assay). Also, we will test this assay's ability to detect GW larvae in water samples spiked with different numbers of copepods and larvae. Field-based rapid assays are a critical tool to reduce the spread of GW among animals and humans, and support countries nearing eradication of this debilitating parasite.

45. **Osip, Setphanie[1], Garrett, Kayla B.[1,2]*, Ruder, Mark G.[2], Haynes, Ellen[2], Cleveland, Christopher A.[2], Nemeth, Nicole M.[2,3], Kunkel, Melanie R.[2], Goodwin, Chloe C.[2], Chamberlain, Michael[1], Mooreman, Christopher E.[4], Moscicki, David J.[4], Plumpton, Hannah[5], Kreh, Christopher[5], Van de Berg, Sarah[5], Buchholz, Richard[6], Martin,**

Thomas[6], Casey, Christine[7], Danks, Zak[7], Casalena, Mary Jo[8], Collier, Bret[9], Cedotal, Cody[10], Stilwell, Natalie[11], Yabsley, Michael J.[1,2] [1]Warnell School of Forestry and Natural Resources, UGA, Athens, GA, USA; [2]Southeastern Cooperative Wildlife Disease Study, UGA, Athens, GA, USA; [3]Department of Pathology, College of Veterinary Medicine, UGA, Athens, GA, USA; [4]Department of Forestry and Environmental Resources, North Carolina State University, Raleigh, NC, USA; [5]NC Wildlife Resource Commission, Raleigh, NC, USA; [6]University of Mississippi, University, MS, USA; [7]Kentucky Department of Fish and Wildlife Resources, Frankfort, KY, USA; [8]Pennsylvania Game Commission, Harrisburg, PA, USA; [9]LSU School of Renewable Natural Resources, Baton Rouge, LA, USA; [10]Louisiana Department of Wildlife and Fisheries, Baton Rouge, LA, USA; [11]MS State University, Starkville, MS, USA.

Prevalence and genetic characterization of blood parasites in wild turkeys (*Meleagris gallopavo*).

Wild turkeys (*Meleagris gallopavo*) are of ecological, recreational, and economic importance in the US. Recently, populations have decreased in the eastern/midwestern US for unknown reasons; however, disease is always a concern. Wild turkeys are hosts for blood parasites (*Plasmodium* spp., *Haemoproteus meleagridis*, and *Leucocytozoon smithi*). We sampled 591 turkeys from 14 states and tested for blood parasites using PCRs targeting the cytb gene. *Haemoproteus* was detected in 292 (49%) birds from 13 states and *Leucocytozoon* was detected in 33 (6%) birds from 6 states. None were positive for *Plasmodium*. Of the 33 *Leucocytozoon*-positive turkeys, 31(94%) were co-infected with *Haemoproteus*. Genetic characterization of *Haemoproteus* samples indicated there are two lineages with lineage 1 (54%) being more common than lineage 2 (25%) and coinfections were common. *Haemoproteus* lineage 1 was 98% similar to *Haemoproteus* sp. lineage AFR151 whereas lineage 2 was 99% similar to *Haemoproteus* sp. lineage TETURO01. Only one lineage of *Leucocytozoon* was detected. Demographic data were analyzed for North Carolina samples. Adults were more commonly infected with *Haemoproteus* spp. than juveniles and *Leucocytozoon* was only detected in adults. *Haemoproteus* and *Leucocytozoon* prevalences were lower in the Piedmont and Appalachian Mountain regions compared to the Coastal region. No differences between sexes were noted. These findings indicate that wild turkeys are commonly infected with *Haemoproteus* and less commonly *Leucocytozoon*. Genetic characterization revealed two lineages of *Haemoproteus* and they likely represent distinct species. Because both of these vector-borne parasites have been documented to cause morbidity and mortality in turkeys in the eastern US, additional studies are needed to determine risk factors for disease.

46. **Russell, A. Cassiopeia[1], Schiff, Erica[1], Rice, Christopher[2], Kyle, Dennis E.[1]*** [1]University of Georgia, Athens, GA, USA; [2]Purdue University, West Lafayette, IN, USA.

Pathogenicity of *Naegleria fowleri* isolates varies significantly in the mouse model of primary amoebic meningoencephalitis.

Naegleria fowleri, colloquially known as “brain-eating amoeba”, causes an acute, fatal disease called primary amoebic meningoencephalitis (PAM). *N. fowleri* is commonly present in warm freshwater and soil and although PAM is a rare disease, it results in >97% mortality rate. One persisting question is why so few people succumb to disease when so many are potentially exposed? We hypothesized that clinical isolates vary in inherent virulence and these variabilities affect the minimum infectious dose required to induce PAM. Utilizing a mouse model of PAM, we intranasally inoculated clinical isolates of *N. fowleri* (Nf69, V067, V631, Villa Jose, and V596) at three concentrations per mouse: 100, 1000, and 5000 amoebae. Results showed significant variability in onset of severe disease and mortality rates among isolates and within genotypes. The highest infectious dose (5000 amoebae) induced 100% mortality by all isolates except V067 (87.5%), with a large variance in onset of endpoint symptoms from 4 days post inoculation (dpi) to > 20 dpi. Remarkably, for isolate V596, only 100 amoebae produced 100% mortality by dpi 4-5 and we observed deaths with as few as 10 V596 amoebae. Concurrently, we assessed in vitro pathogenicity by comparing feeding rates among isolates seeded onto Vero cells. We observed variability in feeding rates for 12 *N. fowleri* isolates and although not all isolates were tested in vivo, our data suggest a positive correlation between an increased feeding rate in vitro and increased virulence in vivo. Overall, these results support our hypothesis of inherent differences in pathogenicity between isolates that result in variance in minimum infectious doses. We acknowledge support from US NIH (R03AI141709 to DEK and 5T35OD010433-14 to ES) and the Georgia Research Alliance (to DEK).

47. **Richards, Jessie E.[1,2]*, Kania, Stephen A.[1,2], Muller, Lisa I.[3,4], Miller, Bradley F.[5], Gerhold, Richard W.[1,2,4]** [1]University of Tennessee College of Veterinary Medicine, Knoxville, TN, USA; [2]University of Tennessee Comparative & Experimental Medicine Program, Knoxville, TN, USA; [3]University of Tennessee School of Natural Resources, Knoxville, TN; [4]University of Tennessee Center for Wildlife Health, Knoxville, TN, USA; [5]Tennessee Wildlife Resources Agency, Region IV, Morristown, TN, USA. **Development and application of an enzyme linked immunosorbent assay (ELISA) for the serological testing of *Parelaphostrongylus tenuis* in Tennessee elk (*Cervus canadensis*).**

Parelaphostrongylus tenuis, often referred to as brainworm or meningeal worm, is a neurotropic parasite of wild cervids that can cause neurological disease through aberrant migration within the central nervous system (CNS). While white-tailed deer (*Odocoileus virginianus*) are the natural host and rarely have clinical disease, other cervid species including moose (*Alces alces*), elk (*Cervus canadensis*), and caribou (*Rangifer tarandus*) have variable to severe morbidity and mortality leading to potential population impacts. *Parelaphostrongylosis* is a common disease of restored elk within the eastern United States and elk in Tennessee are at significant risk where they cohabitate with large populations of white-tailed deer regularly. The identification of novel antigens using liquid chromatography and mass spectrometry combined with transcriptomic data has enabled the creation of an antemortem serological assay for this parasite that has yielded promising results. Within 20 captured Tennessee elk, we saw a seroprevalence of 5-15%. This serological test is still in the process of more rigorous validation using serum from known *P. tenuis*-positive animals, determined via necropsy. However, thus far the ELISA has provided promising results and insights into the exposure of aberrant hosts without the need for post-mortem diagnosis. Numerous applications of this test are planned for future research projects that can have significant management implications

48. **Yabsley, Michael J.[1,2,3]*, Kellow, Laura[4], Heather Barron[4,5], Kayla B. Garrett[1,2], Nicole M. Nemeth[1,6]** [1]Southeastern Cooperative Wildlife Disease Study, College of

Veterinary Medicine, University of Georgia, Athens, Georgia USA; [2]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, Georgia USA; [3]Center for Emerging Infectious Diseases, Athens, Georgia USA; [4]Center for the Rehabilitation of Wildlife (CROW), Sanibel Island, Florida USA; [5]Loggerhead Marinelife Center, Juno Beach, Florida USA; [6]Department of Pathology, College of Veterinary Medicine, University of Georgia, Athens, Georgia USA. **Brain worms of the snake bird (*Anhinga anhinga*) - Prevalence, pathology, and molecular characterization of *Paronchocerca helicina*.**

"Brain worms" (*Paronchocerca helicina* (Onchocercidae: Splendidofilariinae)) in anhinga (*Anhinga anhinga*) were first described in Brazil in 1858. These parasites were subsequently found in anhinga from the United States; in 1868 and in 1957. Despite the large geographic range, little is known about its prevalence, pathology, or phylogenetic position with related parasites. From 2022-2023, 15 anhingas were admitted to a rehabilitation center in Southwest Florida for various reasons; eleven had variable severity of neurologic signs. PCV/TS and complete blood counts (CBC) were performed on 13/15 individuals, with 7/15 demonstrating anemia and hypoproteinemia and 1/15 having microfilariae. A total of 9 (60%) anhinga had grossly visible nematodes bundles on the cerebellum surface. Eight of 9 (89%) adult birds were infected while 5 of the 6 negative (83%) birds were juveniles. Parasites collected from four anhinga were morphologically identified as *P. helicina*. The18S rRNA gene sequence was most similar to *Loa loa* (903/912bp, 99%) followed by other *Onchocercidae* species (98-99%). Phylogenetically*, P. helicina* grouped with *Breinlia mundayi*, a zoonotic Splendidofilariinae parasite of Australian wallabies. The brain of four anhingas was evaluated histologically. Microscopically, 4/4 anhinga had variable thickening of the dura mater with hyperplastic epithelium. Three had subdural hemorrhage associated with nematodes and one of these had mild hemorrhage in subjacent neuroparenchyma. Many microfilariae were observed in vessels. Overall*, P. helicina* was common in anhingas in south Florida and to our knowledge, this is the first study to investigate the phylogenetic position of *a Paronchocerca* species confirming its placement in the Splendidofilariinae. There was debate if this parasite was in the Onchocercinae because this subfamily has markedly dissimilar spicules similar to *Paronchocerca* spp. Because some birds presented with neurologic signs and birds had microscopic lesions associated with the parasites, additional work is needed to determine if this parasite can be pathogenic in anhingas.

POSTER PRESENTATION ABSTRACTS

1. **Garrett, Kayla, B.[1,2]*, Murray, Lance[3], Wolff, Peregrine, L.[3,4], LaHue, Nate [3], Yabsley, Michael, J.[1,2]** [1]Southeastern Cooperative Wildlife Disease Study, University of Georgia, Athens, GA, USA; [2]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA; [3]Nevada Department of Wildlife, Reno, NV, USA; [4]Wildlife Disease Association, Moorepark, CA, USA. **Free-ranging ungulates in Nevada, USA are infected with a high diversity of piroplasm parasites.**

There are several *Babesia* and *Theileira* species of concern for the health of wild and domestic ruminants in North America, and wildlife may serve as reservoirs for species important to public and animal health. Most known life cycles include an ixodid tick vector and a vertebrate host. Blood samples from ungulate species in Nevada were tested for piroplasms using PCR. 447 animals were tested –California bighorn sheep (Ovis canadensis californiana; n=46), Desert bighorn sheep (*O.c. nelsoni*; n=16), Rocky bighorn sheep (*O.c canadensis*; n=12), mountain goat (*Oreamnos americanus*; n=6), Rocky mountain elk (*Cervis canadensis nelson*i; n=53), moose (*Alces alces*; n=4), mule deer (*Odocoileus hemionus*; n=255), and pronghorn (*Antilocapra americana*; n=55). 115 samples from four host species were positive (two bighorn sheep spp, mule deer, elk, pronghorn). Four piroplasm species (*B. duncani*, *B.* sp. RD63*, B. odocoilei*, and *Theileria cervi*-like sp.) and three strains of *B. duncani* were detected. *Babesia duncani* was the most common piroplasm detected (83%) and occurred in three species. The highest prevalence was in California bighorn sheep (61%), all of which were *B. duncani*. Mule deer and elk had the highest diversity, each with three piroplasm species or strains. The single *Theileria* sp. and *B. odocoilei* detections were in pronghorn. This study shows that ungulates in Nevada are infected with a high diversity of piroplasms, several of which are zoonotic or can cause disease in some cervids. Additional research is warranted to understand the prevalence, distribution and risk of these piroplasm infections on the health of ungulate species.

2. **Karl, Kaitlin M.[1]*, Catenazzi, Alessandro M.[2], Jiménez, F Agustín.[3]** [1]Southern Illinois University, Carbondale, IL, USA; [2]Florida International University, Miami, FL, USA; [3]Southern Illinois University, Carbondale, IL, USA. **Documentation of helminth diversity in Peruvian anurans.**

   There is currently a limited amount of information available on the helminths of Peruvian anurans, with emphasis on lowland species. The focus of this project is to document and identify the helminth species that infect frogs in the Eastern slopes of the Andes, with a focus on anuran species belonging to *Telmatobius, Pristimantis, Rhinella*, and Boana. Nematode, cestode, and trematode specimens were collected from the digestive tracts and internal organs of 66 individual frogs comprising 12 different species found in Manu National Park in Peru. These amphibian species exhibit a diverse range of life history strategies and ecological niches, and information concerning their helminth diversity will be helpful in further understanding the anuran species' roles in the ecosystem and as parasitic hosts. The helminth species are currently being identified using both morphological and molecular methods. These parasite specimens are undergoing the process of DNA extraction and amplification, followed by characterization through the sequencing of genetic fragments, including Cox1, Cytochrome b, and Internal Transcribed Spacer (ITS). The species identity and abundance will be used to determine if parasite load varies with host species, geographic elevation, habitat, and amphibian life history strategy. The results of this research project will help broaden our scientific understanding of this subject by providing further information on the prevalence and diversity of helminth species from the Andean region and describing the parasites' presence in multiple anuran host species that have not previously been recorded.

3. **de Buron, Isaure*, Hill-Spanik, Kristina.** College of Charleston, Charleston, SC, USA. **Using SSP meeting sites and participants' expertise to increase global and local parasite diversity via the BioBlitz approach.**

   Parasites are ubiquitous and significant players in ecological communities. However, global parasite diversity knowledge is proportionally scant, and consequences of environmental changes such as warming waters, sea level rise, and flooding on parasite diversity and distribution are largely unknown. BioBlitzes are short-term intensive surveys carried out by experts to identify and catalogue as many species as possible in any given area, and thus enhance both local and global biodiversity knowledge. Traditionally, Bioblitzes have focused on macroflora and macrofauna; adapting the BioBlitz concept to parasites would allow to expand our knowledge of parasite biodiversity quickly and create learning opportunities for students. Incorporating such parasite BioBlitzes into the framework of a regional parasitology society annual meeting such as SSP has several advantages: a small group of experts are gathering, the meetings are often at natural sites such as biological stations that offer sampling habitats, and the meetings are student focused. While logistics would vary among sites and organizers, one approach to ensure effectiveness and productivity could be to 1) designate one day before or after each annual conference for parasite and data collection, 2) request volunteer participation to sample and/or identify specimens, 3) request specimens be identified within a year, and 4) present results as a group at the next conference. Important details such as source(s) of funding and authorship would need to be discussed and agreed upon. We are looking forward to a constructive discussion with the members of the Southeastern Society of Parasitologists in hopes of making this an actuality.

4. **Francisco, Raquel[1,3]*, Hui Teo, Xuan[1,2], Hammond, Adam[3,4], Nemeth, Nicole M.[1,2], Yabsley, Michael J.[1,3]** [1]Southeastern Cooperative Wildlife Disease Study (SCWDS), Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [2]Department of Pathology, College of Veterinary Medicine, University of Georgia, Athens, GA, USA; [3]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA; [4]Georgia Department of Natural Resources (GADNR), Wildlife Resources Division, Social Circle, GA, USA. ***Ursicoptes americanus*: A case report in an American black bear (Ursus americanus).**

    Ursicoptes americanus is follicular mite that has been documented on American black bears. It can cause generalized audycoptid or ursicoptic mange in both captive and free-roaming black bears. The nymphal and female morphology, epidemiology, and current range of this mite are not well understood. Most reports of ursicoptic mange in black bears have originated from the western USA, although sporadic cases have been reported in eastern regions. In August 2022, GADNR submitted the carcass of a black bear from Pickens County to SCWDS. Upon necropsy, crusty skin at the tips of both ear pinna were observed, in addition to poor nutritional condition and pale mucus membranes. A skin scrape of the ears revealed few *U. americanus* and histopathology revealed minimal cellular reaction. The bear was determined to have died of unrelated causes (anticoagulant rodenticide toxicosis). While ursicoptes has been associated with debilitating, generalized skin disease, the mange lesions in this case were mild and limited to the ears; thus unlikely to have contributed to the bear’s poor condition. Previously, SCWDS diagnosed rare cases of ursicoptic mange in Virginia and West Virginia, while others have reported cases in Michigan and Tennessee. However, this is the first detection in Georgia. This incidental detection of *U. americanus* in a bear demonstrates that ursicoptes may be present on seemingly normal bears with little to no alopecia. Moving forward, the presence of *U. americanus* should be ruled out when minor alopecia of the head is present to better assess prevalence and range of disease manifestations.

5. **Georgieva, Simona*, Choe, Seongjun.** Chungbuk National University, Cheongju, Republic of Korea. **Helminth diversity in freshwater fishes in Korea.**

Riverine ecosystems are among the most species-rich on earth, offering ideal conditions for diverse parasite communities. Parasites exhibit essential roles in ecosystem functioning and are commonly used as indicator taxa in biomonitoring surveys. While their immense significance is generally recognized, the current knowledge on their diversity in riverine systems is highly uneven and heavily biased towards specific sampling locations and research efforts. To expand our knowledge of the parasite diversity in the largely understudied Korean riverine systems, we examined 266 fishes belonging to 40 species of 12 families. Fishes were sampled opportunistically from eleven locations in 2021 and 2022. Helminths recovered were subject to morphological and molecular characterization. Altogether, fishes examined harboured a diverse helminth fauna with 21 distinct species including important pathogens of zoonotic importance. Overall, analysis of the entire dataset revealed significant effects of hosts and sampling location on the infection parameters. To the best of our knowledge this is the first comprehensive exploration of the fish helminth diversity in the Korean riverine system providing baseline data for their contemporary diversity and distribution. Our result will help advance further ecological studies on the distribution and host ranges of important helminths in the temperate Asian riverine ecosystems.

6. **Grey, Kayla*, Amspacher, Katelyn, Nielsen, Clayton, Jiménez, F. Agustín.** Southern Illinois University – Carbondale, Carbondale, IL USA. **Of intestinal helminths and *Mephitis mephitis*: the importance of DNA barcoding**.

   Seventy-eight striped skunks (*Mephitis mephitis*) from southern Illinois were examined for gastrointestinal parasites. The helminthological record consists of 9 species, including the digenean *Alaria taxidea*, the cestodes *Mesocestoides corti* and *Oshmarenia mephitis*, the acanthocephalans *Macracanthorhynchus ingens* and *Oncicola canis,* and the nematodes *Baylisascaris columnaris, Molineus barbatus, Physaloptera maxillaris* and *Placoconus lotoris*. An unidentified species of acanthocephalan and *Dipetalonema* spp. were recovered from the body cavity. The most abundant and prevalent gastrointestinal parasite species found was P. maxillaris at 90%, followed by *P. lotoris* and *B. columnaris* both at 30%. We documented 3 additional species to the previous helminthological record, which includes O. canis, M. barbatus and *Dipetalonema* sp. Furthermore, 5 of the species found are shared with other carnivores present in the region. We propose to generate barcodes for each of these species to enable the monitoring and surveillance of these pathogens. This analysis is important because it helps us to see if there are any occurrences of coinfections with microparasites, including babesiosis and canine distemper virus.

7. Smith, Catherine A.*, Yabsley, Michael J., Kurimo-Beechuk, Elizabeth, Ruder, Mark G., Garrett, Kayla B., Barton, Ethan P. University of Georgia, Athens, GA, USA. **Abomasal parasites in white-tailed deer (*Odocoileus virginianus*) in West Virginia.**

   Abomasal nematode abundance in white-tailed deer (*Odocoileus virginianus*) has historically been used by wildlife managers as an indicator of host density relative to carrying capacity and in setting localized herd management goals. White-tailed deer in agricultural areas can be infected by parasites of importance to domestic ruminants and subsequently serve as reservoirs. *Haemonchus contortus*, for example, is commonly found to infect deer and is also an important pathogen of sheep, goats, and exotic ruminants. Additionally, little is known about anthelmintic-resistant abomasal nematode infections in deer that may spillover from domestic ruminants and subsequently cycle in the wildlife-agriculture interface. In the Southeast, white-tailed deer may be infected by various species of *Haemonchus*, *Ostertagia*, *Mazamastrongylus*, and *Trichostrongylus*. However, there are few contemporary studies on abomasal nematode abundance, distribution, and genetic characterization in West Virginia. During white-tailed deer herd health exams at four sites in West Virginia, abomasa were collected and screened for nematodes. Parasites were morphologically identified, and a random subset of those worms were genetically classified. Although data collection is ongoing, we have found a high prevalence of abomasal parasites (40% with *Haemonchus*, 100% with medium-sized worms [*Ostertagia* or *Mazamastrongylus]*, and 90% with *Trichostrongylus*). Among medium-sized nematodes, four species were detected including *O. dikmansi*, *O. mossi*, *M. pursglovei*, and *M. odocoilei* with the last species being most common. Deer exhibited a wide range of infection intensities (100-3660 worms). These new data will provide West Virginia deer biologists a more complete picture of white-tailed deer herd health

8. **Von Holten, Zoe S.[1]*, Achatz, Tyler J.[1], LaFond, Lynda R.[2], Martens, Jakson R.[2], Tkach, Vasyl V.[2]** [1]Middle Georgia State University, Macon, Georgia, USA; [2]University of North Dakota, Grand Forks, North Dakota, USA. **Improving diagnostics of *Crassiphiala bulboglossa*, the type-species of *Crassiphiala* and a common causative agent for black spot disease in fishes.**

   Crassiphiala is a genus of diplostomid digeneans parasitic in kingfishers throughout the Western hemisphere. Its members use fishes as second intermediate hosts, and are commonly associated with the black spot disease in a variety of fishes. The type-species, *Crassiphiala bulboglossa*, was originally described by Van Haitsma in 1925 based on material from belted kingfishers collected in Michigan. Many descriptions of adult diplostomids have been based on laterally oriented and contracted specimens. The description by Van Haitsma is no exception and lacked measurements of many features commonly used in diplostomid taxonomy. No prior study sequenced morphologically identified *C. bulboglossa*. In the present study, we collected new specimens of *C. bulboglossa* from a belted kingfisher in North Dakota. Initial examination of specimens revealed several morphotypes with seemingly substantial differences. A fragment of the cytochrome c oxidase I (cox1) mtDNA gene was sequenced from hologenophores and vouchers of different morphotypes. No genetic differences were detected among individuals. Based on the combination of molecular and morphological data, we provide descriptions and illustrations of each morphotype based on both ventro-dorsally and laterally oriented specimens. The combination of our new DNA sequences and detailed morphological data of *C. bulboglossa* provide substantially enhanced diagnostic tools for this pathogenic digenean. This study was funded in part by the National Science Foundation (grant 1852459), the National Institutes of Health (IDeA grant number P20GM103442), and the University System of Georgia STEM Initiative IV.


Southeastern Society of Parasitologists

We are grateful for the meeting support provided by:

Our colleagues at Lincoln Memorial University, Drs. Charles T. Faulkner, Vina Faulkner, Barbara C. Shock, and Ms. Stacie Williams (CVM Class 2026)

and the financial support from our sponsors

Lincoln Memorial University, Richard A. Gillespie College of Veterinary Medicine
and
The American Heartworm Society

LMU
Richard A. Gillespie
College *of* Veterinary Medicine
LINCOLN MEMORIAL UNIVERSITY

AMERICAN
HEARTWORM
SOCIETY™
EST.1974