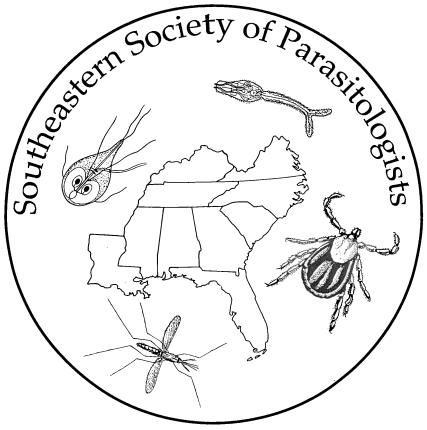
SOUTHEASTERN SOCIETY OF PARASITOLOGISTS

(Affiliate of The American Society of Parasitologists)

PROGRAM & ABSTRACTS



April 6-8, 2016

Hosted by:

Department of Natural Sciences and Mathematics
Johnson C. Smith University
Charlotte, North Carolina

SOUTHEASTERN SOCIETY OF PARASITOLOGISTS

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2004-2006	Isaure de Buron
2007	Michael Yabsley
2008-2010	Sharon Patton
2010-present	Bruce Conn

2016 Meeting of the
Southeastern Society of Parasitologists
April 6-8, 2016

PROGRAM SUMMARY

Wednesday, April 6

Check In/Late Registration	4:30 p.m. – 6:30 p.m.
SSP Executive Committee *York Meeting Room*	4:00 p.m. – 6:30 p.m.
SSP Welcome Reception *York Meeting Room*	6:30 p.m. – 9:00 p.m.

Thursday, April 7

Paper Session I *York Meeting Room*	8:15 a.m. – 10:00 a.m.
Paper Session II *York Meeting Room*	10:15 a.m. – 12:00 p.m.
Lunch *York Meeting Room*	12:00 p.m. – 1:30 p.m.
Paper Session III *York Meeting Room*	1:30 p.m. – 3:00 p.m.
Presidential Symposium *York Meeting Room*	3:30 p.m. – 5:30 p.m.
	Dinner on your own

Friday, April 8

Paper Session IV *York Meeting Room*	8:30 a.m. – 10:00 a.m.
Paper Session V *York Meeting Room*	10:15 a.m. – 11:00 a.m.
SSP Business Meeting & Lunch *York Meeting Room*	11:30 p.m. – 1:30 p.m.

SSP WELCOME RECEPTION

Wednesday, April 6 **6:30 p.m. – 9:00 p.m.**
Location: *York Meeting Room*

6:30 Alexa Rosypal, Department of Natural Sciences and Mathematics, Johnson C. Smith University, Charlotte, North Carolina. *"Welcome to Fort Mill, SC"*

6:40 Andrea Varela-Stokes, Department of Basic Sciences, Mississippi State University College of Veterinary Medicine, Mississippi State, MS. Meeting announcements.

Loading PPT files on laptop (Information for Speakers: All speakers should upload their presentations at least at the break in advance of their session. There is time reserved this evening and in the morning Thursday and Friday as well. There are no concurrent sessions.

PAPER SESSION I

Thursday, April 7 **8:15 a.m. – 10:00 a.m.**
Location: *York Meeting Room*
Moderators: Michael Yabsley and Raphael Orélis-Ribeiro
* Presenting Author
† Ciordia-Stewart Porter Undergraduate Research Competitor
‡ Byrd-Dunn Graduate Student Paper Competitor

7:30 Loading for any remaining presentation files

8:15 1† **FARROW, ABIGAIL*, PORTIA BREWER, AND GABRIEL J. LANGFORD**. Department of Biology, Florida Southern College, Lakeland, FL. **Aspects of the life cycle of *Apharyngostrigea pipientis* in central Florida wetlands.**

8:30 2† **HARPER, AMANDA B.[1#]*, JUNG KEUN LEE[2#], AMANDA LAWRENCE[3], AND ANDREAS. VARELA-STOKES[2].** [#]These authors contributed equally to this work. [1]Department of Biochemistry, Molecular Biology, Entomology, and Plant Pathology, Mississippi State University, Mississippi State, MS; [2]Department of Basic Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, MS; [3]Institute for Imaging & Analytical Technologies, Mississippi State University. **Microscopic analysis of Rickettsial co-infection in the Gulf Coast tick, *Amblyomma maculatum.***

8:45 3† **SOAFER, KELLIE*, ABIGAIL WILLEMSE, AND CHRISTOPHER A. HALL.** Center for One Health, Department of Biology, Berry College, Mount Berry, GA. **Vaccination of female ICR mice with TSA-1/Tc-24 encoding plasmids fail to significantly reduce congenital transmission of *Trypanosoma cruzi*.**

9:00 4† **SWANEPOEL, LIANDRIE[1]*, CHRISTOPHER A. CLEVELAND[1,2], TONY DENICOLA[3], AND MICHAEL J. YABSLEY[1,2].** [1]Southeastern Cooperative Wildlife Disease Study, University of Georgia, Athens, GA 30602; [2]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA 30602; [3]White Buffalo Inc., Moodus, CT 06469. **Prevalence of *Rickettsia* in ticks collected from Philippine deer (*Rusa marianna*) and feral swine (*Sus scrofa*) from Guam.**

9:15 5† **WARD, BRIDGETTE E.*, AND GABRIEL J. LANGFORD.** Department of Biology, Florida Southern College, Lakeland FL. **A parasite survey of lizards on Andros Island, Bahamas with the discovery of a new species of trematode.**

9:30 6† **WICKSON, ALEXANDRA G.[1,2]*, JAMES C. BEASLEY[2,3], AMANDA E. HOLLAND[2,3], ELLEN MARTINSEN[4], CHRIS WEST[5], A. LARRY BRYAN[3], CHRISTOPHER A. CLEVELAND[1,2], EMILY JOLLY[2], SONIA M. HERNANDEZ[1,2], AND MICHAEL J. YABSLEY[1,2].** [1]Southeastern Cooperative Wildlife Disease Study, University of Georgia, Athens, GA; [2]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA; [3]University of Georgia, Savannah River Ecology Laboratory, Aiken, SC; [4]Center for Conservation and Evolutionary Genetics, Smithsonian Conservation Biology Institute, National Zoological Park, Washington, DC; [5]The Yurok Tribe Wildlife Program, Klamath, CA. **Widespread occurrence of a novel lineage of an avian haemosporidian in a New World Vulture.**

9:45 7† **WILLEMSE. ABIGAIL*, ALFRED HARDING, AND CHRISTOPHER HALL.** Center for One Health, Department of Biology, Berry College, Mount Berry, GA. **An *in vitro* examination on the efficacy of naphthalene-based compounds on inhibiting the REL1 protein of *Trypanosoma cruzi.***

10:00 - 10:15 **Coffee Break**

PAPER SESSION II

Thursday, April 7 **10:15 a.m. – 12:00 p.m.**

Location: *York Meeting Room*

Moderators: Steve Kayes and Ash Bullard

*Presenting Author

†Ciordia-Stewart Porter Undergraduate Research Competitor

‡Byrd-Dunn Student Graduate Student Paper Competitor

10:15 8‡ **KAYLA BUCK GARRETT[1,2]*, MICHAEL J. YABLSEY[1,2], KAREN L. BAILEY[1,2,3], JUSTIN D. BROWN[4], MOLLY E. CHURCH[5], HOSSAIN FARID[6], RENÉE SCHOTT[7], AND SONIA M. HERNANDEZ[1,2].** [1] Warnell School of Forestry and Natural Resources, The University of Georgia, Athens GA, USA, [2] Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, Athens GA, USA, [3] Kentucky Wildlife Center, Georgetown, KY, USA, [4] Pennsylvania Game Commission, University Park, PA, USA, [5] School of Veterinary Medicine, Department of Pathology, Microbiology, and Immunology, University of California-Davis, Davis, CA, USA, [6] Department of Plant and Animal Sciences, Faculty of Agriculture, Dalhousie University, Truro, Nova Scotia, Canada, [7] Wildlife Rehabilitation Center of Minnesota, Roseville, MN, USA. **Distribution and prevalence of *Babesia* spp. in raccoons (*Procyon* lotor) in the United States and Canada.**

10:30 9‡ **GRAHAM, KAITLIN J.[1]*, CARLA HUSTON[2], AND ANDREA VARELA-STOKES[1].** [1]Department of Basic Sciences Department, Mississippi State University College of Veterinary Medicine, Starkville MS, [2]Department of Pathobiology and Population Medicine, Mississippi State University College of Veterinary Medicine, Starkville MS. **Evidence of tick-borne rickettsiae in Mississippi beef cattle and their associated ticks.**

10:45 10‡ **ROBERTS, JACKSON R.[1]*, RAPHAEL ORÉLIS-RIBEIRO[1], KENNETH M. HALANYCH[2], BINH D. THUY[3], AND STEPHEN A. BULLARD[1].** [1]Aquatic Parasitology Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, Auburn University, Auburn, AL. [2]Department of Biological Sciences, College of Science and Mathematics, Auburn University, Auburn, AL. [3]Department of Biology, Institute for Biotechnology and Environment, Nha Trang University, Nha Trang City, Vietnam. **Blood flukes (Digenea: Schistosomatoidea) of softshell turtles (Testudines: Trionychidae) in Asia, a previously ignored but distinctive lineage.**

11:00 11‡ **NIEDRINGHAUS, KEVIN D.[1]*, HEATHER FENTON[1], CHRISTOPHER CLEVELAND[1], A. NIKKI ANDERSON[2], AND MICHAEL J. YABSLEY[1,3].** [1]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, The University of Georgia, Athens GA. [2]Louisiana Department of Wildlife and Fisheries, Baton Rouge LA. [3]Warnell School of Forestry and Natural Resources, University of Georgia, Athens GA. Case Report: **Systemic haemosporidian infection in a fledgling great horned owl (*Bubo virginianus*) from Louisiana.**

11:15 12‡ **PURPLE, KATHRYN[1]*, BRAND, MABRE[1], BROWN, JUSTIN[2], BOYD, ROBERT[2], AND GERHOLD, RICHARD[1].** [1]Department of Biomedical and Diagnostic Sciences, College of Veterinary Medicine, The University of Tennessee. [2]Pennsylvania Game Commission. **Investigating the prevalence of *Histomonas meleagridis* shedding by captive raised Ring-necked pheasants (*Phasianus colchicus*) in Pennsylvania.**

11:30 13‡ **ORÉLIS-RIBEIRO, RAPHAEL[1]*, KENNETH M. HALANYCH[2], AND STEPHEN A. BULLARD[1].** [1]School of Fisheries, Aquaculture, and Aquatic Sciences, Auburn University, Auburn, AL. [2]Department of Biological Sciences, Auburn University, Auburn, AL. **Broad-scale phylogeny of craniate blood flukes (Digenea: Schistosomatidae), with emphasis on "fish blood flukes" (Aporocotylidae).**

11:45 14‡ **RUIZ, CARLOS[1]*, MATTHEW R. WOMBLE[1], RAPHAEL ORELIS-RIBIERO[1], JACKSON R. ROBERTS[1], JACOB M. RASH[2], DOUG A. BESLER[2], COVA R. ARIAS[1], AND STEPHEN A. BULLARD[1].** [1]Southeastern Cooperative Fish Parasite & Disease Project, School of Fisheries, Aquaculture, & Aquatic Sciences, Auburn University, 203 Swingle Hall, Auburn, Alabama 36849; [2]North Carolina Wildlife Resources Commission, 645 Fish Hatchery Road, Marion, North Carolina 28752. **"Gill lice" (Copepoda: Lernaeopodidae: *Salmincola*) infecting epithelia of rainbow trout (*Oncorhynchus mykiss*) and brook trout (*Salvelinus fontinalis*) in North Carolina rivers and aquaculture facilities.**

12:00-1:30 **Lunch in the York Meeting Room**

PAPER SESSION III

Thursday, April 7 **1:30 p.m. – 3:00 p.m.**

Location: *York Meeting Room*

Moderators: John Schaefer and Carlos Ruiz

*Presenting Author

‡Byrd-Dunn Student Paper Competitor

1:30 15‡ **SAPP, SARAH G. H. [1,2]*, SARA B. WEINSTEIN [3], CHRISTOPHER S. MCMAHAN [4], SUKWAN HANDALI [5], AND MICHAEL J. YABSLEY [1,6].** [1]Southeastern Cooperative Wildlife Disease Study and [2]Department of Infectious Diseases, College of Veterinary Medicine, University of Georgia, Athens, Georgia; [3] Department of Ecology, Evolution, and Marine Biology, University of California, Santa Barbara, California; [4] Department of Mathematical Sciences, Clemson University, Clemson, South Carolina; [5] Parasitic Diseases Branch, Centers for Disease Control and Prevention, Atlanta, Georgia;[6] Warnell School of Forestry and Natural Resources, University of Georgia, Athens, Georgia. ***Baylisascaris procyonis* infection dynamics and survival in four species of deer mice (*Peromyscus* spp.).**

1:45 16‡ **BRIANNA M. WILLIAMS[1,2]* AND MICHAEL J. YABSLEY[1,2]**. [1]Daniel B. Warnell School of Forestry and Natural Resources, Athens, GA; [2]Southeastern Cooperative Wildlife Disease Study, Athens, GA. **Identification and diversity and intensity of *Ixodes* ticks of seabirds breeding on Middleton Island, Alaska.**

2:00 17‡ **WYROSDICK, HEIDI M.[1,2]*, RICHARD GERHOLD[2], CHUNLEI SU[3], MARTINE DE WIT[4], ALYCIA CHAPMAN[2], JESSICA MARTINEZ[1,2], DEBRA MILLER[1,2], and ROBERT K. BONDE[5].** [1]University of Tennessee, Center for Wildlife Health, Department of Forestry, Wildlife, and Fisheries, Knoxville, TN. [2]University of Tennessee, Department of Biomedical and Diagnostic Sciences, College of Veterinary Medicine, Knoxville, TN. [3]University of Tennessee, Department of Microbiology, Knoxville, TN. [4]Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Research Institute, Marine Mammal Pathobiology Laboratory, St. Petersburg, FL. [5]U. S. Geological Survey, Wetland and Aquatic Research Center, Gainesville, FL. **Epidemiology of *Toxoplasma gondii* in Florida manatees (*Trichechus manatus latirostris*) and free-roaming cats in Citrus County, Florida**

2:15 18‡ **MCGAHA JR., TOMMY W.[1]*, VIVIAN PADIN-IRIZARRY[1], ANKUSH KANWAR[2], JAMES W. LEAHY[2], DENNIS E. KYLE[1].** [1]Department of Global Health, College of Public Health, University of South Florida, Tampa, FL. [2]Department of Chemistry, University of South Florida, Tampa, FL. **The use of *Plasmodium falciparum* gametocytes in the laboratory to conduct drug discovery and evaluate the spread of drug resistance of antimalarial compounds.**

2:30 19 **GALLO, SAMIRA S. M.[1]*, OLIVEIRA, FRANCISCO C. R.[1], EDERLI, NICOLE B.[1], SAWER, R. O[2], AND LINDSAY, DAVID S.[2] [1]** Laboratorio de Sanidade Animal, Universidade Estadual do Norte Fluminense, Campos dos Goytacazes, Rio de Janeiro, Brazil. [2]Department of Biomedical Sciences and Pathobiology, Virginia Tech, Blacksburg, Virginia, USA
Isolates of *Sarcocystis falcatula*-Argentina-like organisms from the South American opossums *Didelphis aurita* from Brazil

2:45 20 **WOMBLE, MATTHEW R.[1]* AND STEPHEN A. BULLARD[2].** [1]Office of the NOAA Chief Scientist, U.S. Department of Commerce, National Oceanic and Atmospheric Administration, Washington DC. [2]Aquatic Parasitology Laboratory, Southeastern Cooperative Fish Parasite and Disease Laboratory, Auburn University, Auburn AL. **What is *Leuceruthrus micropteri* (Digenea: Azygiidae)?**

3:00-3:30 Coffee Break

SSP PRESIDENTIAL SYMPOSIUM

Thursday, April 7 **3:30 p.m. – 5:30 p.m.**
Location: *York Meeting Room*

3:30 **VANESSA EZENWA, Ph.D.** Odum School of Ecology and College of Veterinary Medicine, University of Georgia, Athens, GA. **Helminth-microbe co-infection: insights from a natural system**

4:30 **STEVEN WILLIAMS, Ph.D.** Gates Professor of Biology and Biochemistry, Smith College, Northampton, MA. **Advances in Molecular Diagnostics for Neglected Tropical Diseases: Next-Gen Sequencing and Molecular Xenomonitoring**

Dinner on your own. There are numerous restaurants and pubs near the hotel in Fort Mill. Our Local Committee Chair and Program Officer recommend **Six Pence Pub (993 Market St).** Other good nearby options include Fish Market (990 Market St; more upscale), Charanda Mexican Grill and Cantina (1504 Carolina Pl Dr) and Beef O'Brady's (940 Market St; sports bar). If you need additional options or information, ask Alexa (or the hotel concierge)!

PAPER SESSION IV

Friday April, 8 **8:30 a.m. – 10:00 a.m.**
Location: *York Meeting Room*
Moderators: Reg Blaylock and Jackson Roberts
*Presenting Author

8:00 Loading for any remaining presentation files

8:30 21 **LINDSAY, DAVID S.[1]*, VERMA, S.K.[2], SCOTT, D.[3], DUBEY, J.P.[2], ROSYPAL, A.C.[4]** [1]Virginia Tech, Blacksburg, VA. [2]USDA-ARS, Animal Parasitic Diseases Laboratory, Building 1001, Beltsville, MD. [3]Carolina Raptor Center, 6000 Sample Road, Huntersville, NC. [4]Johnson C. Smith University, Charlotte, NC. **Development of a *Sarcocystis columbae*–like protozoan from a Cooper's hawk (*Accipiter cooperi*) in mammalian cells.**

8:45 22 **YABSLEY, MICHAEL J.[1,2]*, MARK L. EBERHARD[3], HUBERT ZIRIMWABAGABO[4], HENRY BISHOP[3], CHRISTOPHER A. CLEVELAND[1,2], JOHN C. MAERZ[1], ROBERT BRINGOLF[1], and ERNESTO RUIZ-TIBEN[4].** [1]Warnell School of Forestry and Natural Resources, The University of Georgia, Athens, GA. [2]Southeastern Cooperative Wildlife Disease Study, Department of

Population Health, College of Veterinary Medicine, The University of Georgia, Athens GA. [3]Division of Parasitic Diseases and Malaria, Centers for Disease Control and Prevention, Atlanta, GA. [4]The Carter Center, Atlanta, Georgia. **The role of fish and frogs as paratenic hosts of *Dracunculus medinensis*, the human guinea worm.**

9:00 23 **HEINS, DAVID C[1]*, DONA M. EIDAM[2], AND JOHN A. BAKER[3].** [1]Department of Ecology and Evolutionary Biology, Tulane University, New Orleans, LA. [2]Department of Biology, University of Alaska at Anchorage, Anchorage, AK. [3]Department of Biology, Clark University, Worcester, MA. **Timing of Infections in the threespine stickleback by *Schistocephalus solidus* in Alaska.**

9:15 24 **LEAPHART, JAMES C., AND DEREK A. ZELMER*.** Department of Biology and Geology, University of South Carolina, Aiken SC. **The life cycle of *Haematoloechus floedae* Harwood, 1932 (Digenea: Plagiorchiidae).**

9:30 25 **ADONIS MCQUEEN[1]*, NIRANJAN NAMELIKONDA[2], MICHAEL KEMP[2], TOMMY MCGAHA[3], LYNN BLAKE[2], ALA AZHARI[3], RANDY LARSEN[2], ROMAN MANETSCH[4], AND DENNIS KYLE[3].** [1]College of Medicine, USF, Tampa, FL [2]Department of Chemistry, USF, Tampa, FL. [3]College of Public Health, USF, Tampa, FL. [4]College of Pharmacy and Pharmaceutical Sciences, Northeastern University, Boston, MA. **In vitro studies and characterization of fluorescent 8-aminoquinoline molecules.**

9:45 26 **BULLARD, STEPHEN A.[1]*, CARLOS F. RUIZ[1], RAPHAEL ORELIS-RIBEIRO[1], JACKSON R. ROBERTS[1], MATTHEW R. WOMBLE[2], CANDIS RAY[1], JACOB RASH[3], DOUG BESLER[3], AND COVA ARIAS[1].** [1]Southeastern Cooperative Fish Parasite & Disease Project, Auburn, AL; [2]US Department of Commerce, Washington, DC; [3]North Carolina Wildlife Resources Commission, Marion, NC. ***Myxobolus cerebralis* (etiological agent of "whirling disease") infecting trouts and oligochaetes in North Carolina.**

10:00 - 10:15 **Coffee Break**

PAPER SESSION V

Friday April, 8 **10:15 a.m. – 11:00 a.m.**

Location: *York Meeting Room*

10:15 27 **VARELA-STOKES, ANDREA S.*, JUNG KEUN LEE, AMANDA HARPER, GAIL MORARU, JOHN STOKES, HALEY PARKER, KATIE GRAHAM, JACOB HUGHES, CATHERINE SMITH.** Department of Basic Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, MS. **Movement of *Amblyomma maculatum*-associated rickettsiae during tick feeding.**

10:30 28 **YABSLEY, MICHAEL J.[1,2]*, HEATHER FENTON[2], JESSICA MCGUIRE[3], CHRISTOPHER A. CLEVELAND[1,2], ELIZABETH W. HOWERTH[4], AND MARK G. RUDER[2].** [1]Warnell School of Forestry and Natural Resources, The University of Georgia, Athens, GA. [2]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, The

		University of Georgia, Athens GA. [3]Georgia Department of Natural Resources, Social Circle, GA. [4]Department of Pathology, College of Veterinary medicine, University of Georgia, Athens GA. **A walk on the wild side: a quiz of selected wildlife parasitology cases**
10:45	29	**WOMBLE, MATTHEW R.*** Office of the NOAA Chief Scientist, U.S. Department of Commerce, National Oceanic and Atmospheric Administration, Washington DC. **From Parasites to Policy: An overview of the Sea Grant Knauss Fellowship Program.**
11:30-1:30		**Lunch and Business Meeting**

Thank you for your participation and support of the Southeastern Society of Parasitologists!

INVITED SPEAKERS AND THEIR ABSTRACTS

Dr. Vanessa Ezenwa is an Associate Professor at the University of Georgia, USA, where she holds joint appointments in the Odum School of Ecology and College of Veterinary Medicine. She received a BA in Biology from Rice University, and PhD in Ecology and Evolutionary Biology from Princeton University. Her research focuses on the ecology of infectious diseases in animal populations, with a particular focus on helminth infections in wild ruminants.

"Helminth-microbe co-infection: insights from a natural system"
Co-infection with worms can have profound effects on a host's response to microbes, and an increasing number of studies are investigating the consequences of worm-microbe co-infection in laboratory settings. To better understand the dynamics of co-infection in natural systems, we used a free-ranging population of African buffalo to explore the consequences of worm infection for bovine tuberculosis (BTB). We followed 200 animals for four years to test the effects of anthelmintic treatment and host resistance on individual and population-level outcomes of BTB infection. We found that de-worming had no effect on individual risk of infection, but enhanced survival of BTB-infected individuals, translating into a higher basic reproductive number for BTB with treatment. Host resistance to worm infection also had no effect on individual risk, but buffalo that were naturally worm-free were more likely to die of BTB infection. The distinct effects of de-worming versus natural resistance on BTB severity arise from differences in BTB dissemination in the body. Our work shows that different ways of being worm-free (i.e. artificial treatment *vs.* natural resistance) have distinct outcomes for microbial co-infection.

More information about Dr. Ezenwa's lab and research can be found on her lab website:
http://ezenwalab.uga.edu/

Dr. Steven Williams is the Gates Professor of Biology and Biochemistry at Smith College in Massachusetts. He earned his Ph.D. from the University of California, Davis. His research is focused on the molecular biology of nematode parasites and neglected tropical diseases. This includes the parasites responsible for elephantiasis and African river blindness.

Dr. Williams will be speaking on "Advances in Molecular Diagnostics for Neglected Tropical Diseases: Next-Gen Sequencing and Molecular Xenomonitoring." In addition his projects using genomics, proteomics, bioinformatics and immunoinformatics to understand the biology and diagnosis of neglected parasitic diseases, Dr. Williams leads the annual Molecular Biology Summer Workshop, sponsored by New England Biolabs in conjunction with Smith College. He is also a member of Filariasis Research Reagent Resource Center, funded by the NIH NIAID.

More information about Dr. Williams' lab and research can be found on his lab website:
http://sophia.smith.edu/blog/sawlab/

ABSTRACTS

1. **FARROW, ABIGAIL*, PORTIA BREWER, AND GABRIEL J. LANGFORD**. Department of Biology, Florida Southern College, Lakeland, FL. **Aspects of the life cycle of *Apharyngostrigea pipientis* in central Florida wetlands.**

Apharyngostrigea pipientis (Trematoda: Strigeidae) is known to form metacercariae around the pericardium of anuran tadpoles in Michigan and other northern locations. Definitive hosts are thought to be wading birds, while the intermediate host is a freshwater snail. *Apharyngostrigea pipientis* is not commonly reported from Florida, yet we have found several populations of snails (*Biopholaria havaensis*) and tadpoles, primarily the Cuban treefrog (*Osteopilus septentrionalis*) to host this trematode. We used experimental infections to elucidate the transmission dynamics and development of *A. pipientis* inside the tadpole host. Surprisingly, we found two types (species?) of cercariae being shed from *B. havaensis* that enter Cuban treefrog tadpoles to form seemingly identical metacercariae. Further, both of these develop into metaceracariae inside the tadpoles over 5-7 days after wondering inside the host's body cavity as mesocercariae, and metacercariae are commonly concentrated around the pericardium cavity. However, they differ in entry mode, with one being ingested, whereas the other penetrates the skin. This project is ongoing, thus we will present the most current results at the meeting.

2. **HARPER, AMANDA B.[1#]*, JUNG KEUN LEE[2#], AMANDA LAWRENCE[3], AND ANDREAS. VARELA-STOKES[2].** [#]These authors contributed equally to this work. [1]Department of Biochemistry, Molecular Biology, Entomology, and Plant Pathology, Mississippi State University, Mississippi State, MS; [2]Department of Basic Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, MS; [3]Institute for Imaging & Analytical Technologies, Mississippi State University. **Microscopic analysis of Rickettsial co-infection in the Gulf Coast tick, *Amblyomma maculatum.***

The objective of this project was to understand the localization of two species of tick-associated intracellular bacteria (*Rickettsia parkeri* and "*Candidatus* Rickettsia andeanae") in the tick, *Amblyomma maculatum*. *Rickettsia parkeri* is a spotted fever group rickettsia (SFGR) and classified as a human pathogen, while "*Ca*. R. andeanae," also a member of the SFGR, has so not been proven to be so. It was hypothesized that *R. parkeri* may be "dominant" in tick tissues related to transmission over "*Ca*. R. andeanae". We examined tick midgut, salivary gland, and ovary tissues, which all play an important role in vertical and horizontal rickettsial transmission. Tissue samples with the highest levels of rickettsiae as quantified by qPCR from among 15 pools of artificially-infected adult ticks, in four experimental groups, were prepared for both TEM (transmission electron microscopy) and fluorescence microscopy. For fluorescence detection, FISH (fluorescence in situ hybridization) was used for "*Ca*. R. andeanae" and IHC (immunohistochemistry) for the GFPuv-expressing *R. parkeri*. Thus far, preliminary TEM images revealed suspect rickettsiae in the midgut of positive ticks. The analysis of samples using FISH/IHC has so far shown that the protocol is effective via control samples, although few experimental samples have been identified as positive. At the conclusion of this study, we expect to have a better understanding of tissue tropism for each bacterium when present alone or co-infecting a tick, leading to a better understanding of transmission potential and rickettsial prevalence in tick populations, as well as potential risk to public health.

3. **SOAFER, KELLIE*, ABIGAIL WILLEMSE, AND CHRISTOPHER A. HALL.** Center for One Health, Department of Biology, Berry College, Mount Berry, GA. **Vaccination of female ICR mice with TSA-1/Tc-24 encoding plasmids fail to significantly reduce congenital transmission of *Trypanosoma cruzi*.**

Previous work has demonstrated that mice injected with plasmids encoding trypomastigote surface antigen (TSA-1) and an excretory/secretory antigen (Tc-24) developed significant levels of protection against *T. cruzi*. To address whether these vaccines could block congenital transmission, a

combination of these plasmids were injected into female ICR mice either prior to (prophylactic), or after (therapeutic), infection with the SCI strain of *T. cruzi*. Infected female mice were breed with uninfected males over a 9-month period. Pups were sacrificed at 2-weeks post parturition and skeletal, heart, and spleen tissues collected for DNA extraction and PCR analysis. Among the 63 pups tested from prophylactically vaccinated and infected females, 43 (68%) were PCR positive for *T. cruzi* compared to 60 out of 71 (84%) positive in the control group (p=0.214). In the therapeutically vaccinated group, 56 out of 92 (60%) pups tested were PCR positive compared to 33 out of 46 (71%) positive for the therapeutic plasmid control group (p=0.1423). Despite a lack of statistical significance, an association seems to exist between vaccination and a decrease in the number of PCR positive pups. Interestingly, of the males mated with infected females, 24 of 35 (70%) were PCR positive by the end of the study. This supports the hypothesis that sexual transmission may represent a significant pathway for *T. cruzi* transmission.

4. **SWANEPOEL, LIANDRIE[1]*, CHRISTOPHER A. CLEVELAND[1,2], TONY DENICOLA[3], AND MICHAEL J. YABSLEY[1,2].** [1]Southeastern Cooperative Wildlife Disease Study, University of Georgia, Athens, GA 30602; [2]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA 30602; [3]White Buffalo Inc., Moodus, CT 06469. **Prevalence of *Rickettsia* in ticks collected from Philippine deer (*Rusa marianna*) and feral swine (*Sus scrofa*) from Guam.**

Rickettsia are obligate intracellular pathogens that use a variety of ectoparasites as vectors. Many tick-borne *Rickettsia* species can cause severe disease in humans, domestic animals, and wildlife species. Little research has been done on the prevalence and diversity of ticks on wildlife species in Guam and no work has been conducted on the infection of these ticks with *Rickettsia*. In this study, ticks were collected from Philippine deer (*Rusa marianna*) and feral swine (*Sus scrofa*) from two sites on Guam from March-April 2015. Infestation rates were noted for each animal with low=<500ticks, medium=500-1,000 ticks, and high=>1,000 ticks. Nested PCR assays were used to test ticks for *Rickettsia* spp. and specific identity will be determined by sequence analysis. *Rhipicephalus* (=*Boophilus*) *microplus* was the only species found on deer and ticks were found on 96/101 (95%) deer. Over half of the deer (n=56) had low tick burdens, although 19 deer had very high tick burdens. No differences in prevalence or tick burdens were noted between the two collection sites. Ticks (*Amblyomma breviscutatum*) were found on only 6 of 42 (14%) pigs and all had low burdens. *Rickettsia* testing is ongoing but two suspected positives have been detected in 25 *R. microplus*. These data indicate that tick infestations are common on deer and future testing for tick-borne pathogens is warranted.

5. **WARD, BRIDGETTE E.*, AND GABRIEL J. LANGFORD.** Department of Biology, Florida Southern College, Lakeland FL. **A parasite survey of lizards on Andros Island, Bahamas with the discovery of a new species of trematode.**

Lizards are one of the most abundant terrestrial vertebrates on the Bahamian islands, yet few studies have surveyed these hosts for parasites. In March 2015, we conducted a parasite biodiversity survey to ascertain the prevalence, abundance, and distribution of parasites within 6 species of lizards commonly found on Andros Island, Bahamas: *Ameiva auberi*, *Anolis carolinensis*, *Anolis distichus*, *Anolis sagrei*, *Hemidactylus frenatus*, and *Leiocephalis carinatus*. Lizards were collected from three primary regions of the large island (North, Central, South), then dissected and examined for parasites at ForFar Field Station. Parasite identification is currently being conducted at Florida Southern College, and mean abundance and prevalence of helminth, blood protozoan, and mite species will be calculated for the island and each location. Preliminary results suggest that the nematodes *Cyrtosomum* sp. and *Spinicauda spinicauda* were the most commonly encountered parasites, whereas no blood protozoans have been located to date. Differences between parasite prevalence and abundance among locations and host species will be discussed. Finally, we will discuss trematode specimens collected from *Anolis smaragdinus* that belong to the genus *Allopharynx* (Digenea: Plagiorchiidae) which appear to represent a new species. Overall, this study shows the different parasite communities within lizards on Andros Island as well as the description of an apparent new species.

6. **WICKSON, ALEXANDRA G.[1,2]*, JAMES C. BEASLEY[2,3], AMANDA E. HOLLAND[2,3], ELLEN MARTINSEN[4], CHRIS WEST[5], A. LARRY BRYAN[3], CHRISTOPHER A. CLEVELAND[1,2], EMILY JOLLY[2], SONIA M. HERNANDEZ[1,2], AND MICHAEL J. YABSLEY[1,2].** [1]Southeastern Cooperative Wildlife Disease Study, University of Georgia, Athens, GA; [2]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA; [3]University of Georgia, Savannah River Ecology Laboratory, Aiken, SC; [4]Center for Conservation and Evolutionary Genetics, Smithsonian Conservation Biology Institute, National Zoological Park, Washington, DC; [5]The Yurok Tribe Wildlife Program, Klamath, CA. **Widespread occurrence of a novel lineage of an avian haemosporidian in a New World Vulture.**

Haemosporidian parasites are common and widespread across many avian families and cause malaria in some species. In previous studies of New World vultures, prevalence and diversity of blood parasites varies considerably by species. In Turkey Vultures (TUVU, *Cathartes aura*), *Haemoproteus catharti* has been described from a single population in South Carolina and unidentified *Haemoproteus* parasites have been reported from numerous US states and Panama. In contrast, haemosporidian infections in Black Vulture (*Coragyps atratus*) are rare or absent. Our aim was to characterize haemosporidians from vultures using morphologic and molecular data and to investigate ecological or intrinsic factors associated with infection. Blood samples were collected from vultures in South Carolina, Georgia, and California and screened using PCR and/or blood smear analysis. In South Carolina, 26/96 (27%) of TUVU were positive while only 1/40 (3%) of TUVU from California were positive. No parasites were detected in 91 black vultures from South Carolina and Georgia. At the South Carolina site, no differences in prevalence or parasitemia levels were noted between capture sites, sexes, or age class but annual variation in prevalence was noted. Mitochondrial (cytochrome b) and nuclear (adenylosuccinate lyase) sequences of the TUVU parasites were most similar (97% genetic identity) to a parasite from Wood Storks (*Mycteria americana*) and clearly distinct from other *Haemoproteus* parasites (91-93%) and *Plasmodium* parasites (93-95%). Nuclear data suggest the TUVU parasites to be most similar to *Nycteria* parasites (84%) of bats. This study is the first to genetically characterize the haemosporidians of New World vultures and suggests the need for the description of a new avian malaria parasite genus.

7. **WILLEMSE, ABIGAIL*, ALFRED HARDING, AND CHRISTOPHER HALL.** Center for One Health, Department of Biology, Berry College, Mount Berry, GA. **An *in vitro* examination on the efficacy of naphthalene-based compounds on inhibiting the REL1 protein of *Trypanosoma cruzi.***

Eukaryotic parasites cause a wide variety of diseases in humans and animals alike, and are often very difficult to effectively treat due to similarities in the metabolic pathways they share with their hosts. As such, novel drug targets are needed in order to develop more efficient treatments. The editosome, an RNA editing protein complex unique to trypanosomes, is one such potential target. A series of naphthalene-based compounds (NBCs) have demonstrated the ability to bind the REL-1 subunit of the *T. brucei* editosome. Previous *in silico* work suggested that these NBCs have the potential to bind the REL-1 complex of *Trypanosoma cruzi*, the etiologic agent of Chagas disease. We have expanded this work to *in vitro* studies by exposing *T. cruzi* cultures to NBCs and assessing inhibition of proliferation. Of the four NBCs, V1 - V4, only V4 significantly reduced parasite growth *in vitro*. At 100uM V4 reduced BSFs in cultures of infected DH-82 cells by approximately 62.5% by 24 hours' post-inoculation. By 48 hours V4 had reduced BSFs in culture by 88% compared to untreated control cultures. This study supports the hypothesis that naphthalene-based compounds can effectively inhibit *T. cruzi* growth *in vitro*.

8. **KAYLA BUCK GARRETT[1,2]*, MICHAEL J. YABLSEY[1,2], KAREN L. BAILEY[1,2,3], JUSTIN D. BROWN[4], MOLLY E. CHURCH[5], HOSSAIN FARID[6], RENÉE SCHOTT[7], AND SONIA M. HERNANDEZ[1,2].** [1] Warnell School of Forestry and Natural Resources, The University of Georgia, Athens GA, USA, [2] Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, Athens GA, USA, [3] Kentucky Wildlife Center, Georgetown, KY, USA, [4] Pennsylvania Game Commission, University Park, PA, USA, [5] School of Veterinary Medicine, Department of Pathology, Microbiology, and Immunology, University of California-Davis, Davis, CA, USA, [6] Department of Plant and Animal Sciences, Faculty of Agriculture, Dalhousie University, Truro, Nova Scotia, Canada, [7] Wildlife Rehabilitation Center of Minnesota, Roseville, MN, USA. **Distribution and prevalence of *Babesia* spp. in raccoons (*Procyon* lotor) in the United States and Canada.**

Babesia spp. are tick-borne intraerythrocytic protozoans, many of which have veterinary or medical importance. Two morphologically similar species, *Babesia lotori* and *Babesia microti*-like, occur in raccoons (*Procyon lotor*). One study found both species were common in raccoons in North Carolina (~90%). However, little is known of the distribution and prevalence of these parasites in raccoons. Historically, raccoons were the only known host for these two *Babesia* spp.; however, recently maned wolves (*Chrysocyon brachyurus*) in several zoos in the Midwestern USA have been diagnosed with severe or fatal babesiosis caused by B. lotori. To obtain knowledge on the distribution and prevalence of these Babesia spp. across a wide geographic range, blood and spleen samples were opportunistically obtained from raccoons from the USA (Georgia, Florida, Kentucky, West Virginia, Pennsylvania, Kansas, Minnesota, California) and Canada (Nova Scotia). Samples were tested using species-specific PCR assays. For B. lotori, prevalence was highest in the southeastern states (67-89% [113/155]). The prevalence in Nova Scotia (0% [0/80]) was significantly lower than other sites other than Pennsylvania (5% [1/22]) and California (27% [9/33]). The *B. microti*-like sp. was detected at all sites; in general, prevalence was highest in the Southeast (67-100% [129/155]) and lowest (6% [5/80]) in Nova Scotia. Coinfections were common. These data indicate there is spatial variability in the prevalence of these two *Babesia* spp. Currently there is no known vector for either *Babesia* spp., thus these data may assist in determining potential vector(s). Susceptible species, such as maned wolves, are at a greater risk of infection with *B. lotori* in southeastern states.

9. **GRAHAM, KAITLIN J.[1], CARLA HUSTON[2], AND ANDREA VARELA-STOKES[1]**. [1]Department of Basic Sciences, Mississippi State University College of Veterinary Medicine, Starkville MS, [2]Department of Pathobiology and Population Medicine, Mississippi State University College of Veterinary Medicine, Starkville MS. **Evidence of tick-borne rickettsiae in Mississippi beef cattle and their associated ticks.**

An increase in growth in the Mississippi cattle industry has sparked an interest in natural tick resistance within *Bos indicus*-influenced breeds. While cross-breeding with *B. indicus* has recently increased, it is tempered by the more aggressive nature of this species, which is less desirable for management. The aim of this study was to evaluate tick infestation and associated rickettsial exposure in beef cattle breeds from four genetic groups differing by percentage of *Bos taurus* and *Bos indicus* influence. Polymerase Chain Reaction was used to detect DNA of spotted fever group rickettsiae in whole blood from cattle as well as ticks collected from sampled cattle. Positive samples were submitted for sequencing. We collected a total of 194 samples from cattle in the four groups. Ticks were collected from 19 cattle; all ticks were identified as *Amblyomma maculatum*. Using an indirect fluorescent antibody assay (IFA) we tested sera for antibodies to rickettsiae. Of 59 ticks collected, five were positive by PCR for *Rickettsia parkeri*, while 41 were positive for "*Candidatus* Rickettsia andeanae." All blood samples tested negative by PCR for rickettsiae. By IFA, we detected 73 seropositive cattle out of 125 analyzed thus far. Interestingly, of these seropositive animals, eight also had *Rickettsia*-positive ticks attached and were in the 50-100% *Bos indicus*-influenced group. The results of the study will add to the knowledge of tick resistance in beef cattle, particularly whether resistance, if present, impacts transmission of rickettsiae that may be present in attached ticks.

10. **ROBERTS, JACKSON R.[1]*, RAPHAEL ORÉLIS-RIBEIRO[1], KENNETH M. HALANYCH[2], BINH D. THUY[3], AND STEPHEN A. BULLARD[1]**. [1]Aquatic Parasitology Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, Auburn University, Auburn, AL. [2]Department of Biological Sciences, College of Science and Mathematics, Auburn University, Auburn, AL. [3]Department of Biology, Institute for Biotechnology and Environment, Nha Trang University, Nha Trang City, Vietnam. **Blood flukes (Digenea: Schistosomatoidea) of softshell turtles (Testudines: Trionychidae) in Asia, a previously ignored but distinctive lineage.**

Turtle blood flukes comprise 21 genera and 85 accepted species. Several of these genera (*Cardiotrema, Coeuritrema, Enterohaematotrema, Hapalorhynchus, Vasotrema*) include species that infect softshell turtles (Testudines: Trionychidae), but *Coeuritrema* and *Vasotrema* are wholly comprised of blood flukes infecting trionychids of Asia (species of *Lissemys* and *Amyda*) and North America (*Apalone* spp.), respectively. In June 2015, we collected specimens of a turtle blood fluke from the vascular system of several aquacultured Chinese softshell turtles (*Pelodiscus sinensis*) from the Da Rang River Basin, Phu Yen Province, Vietnam. These flukes had ventrolateral muscular papillae like those of the 2 other Asiatic trionychid blood flukes: *Hapalorhynchus lyssimus* from the Indian flapshell turtle (*Lissemys punctata*) and *Hapalorhynchus rugatus* from the Asiatic softshell turtle (*Amyda cartilaginea*). The Vietnam specimens differed from those of *H. lyssimus* by having ventrolateral papillae in the hindbody only, a hindbody width not exceeding 1.4× forebody width, and a short cirrus sac and metraterm. They differed from *H. rugatus* by having a pharynx wider than the anterior esophageal swelling and a postovarian Laurer's canal pore. The results of the present study indicated that the specimens collected from Vietnam comprise a new species and that *Coeuritrema* represents a distinct, natural group that accommodates papillate blood flukes of Asiatic softshell turtles. Including the present report, 12 blood fluke species of 4 genera are now documented to infect Asiatic softshell turtles.

11. **NIEDRINGHAUS, KEVIN D.[1]*, HEATHER FENTON[1], CHRISTOPHER CLEVELAND[1], A. NIKKI ANDERSON[2], AND MICHAEL J. YABSLEY[1,3].** [1]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, The University of Georgia, Athens GA. [2]Louisiana Department of Wildlife and Fisheries, Baton Rouge LA. [3]Warnell School of Forestry and Natural Resources, University of Georgia, Athens GA. Case Report: **Systemic haemosporidian infection in a fledgling great horned owl (*Bubo virginianus*) from Louisiana.**

Avian haemosporidians are generally considered to cause chronic subclinical infections in most free-ranging raptors. We present a case report of avian haematozoan mortality in a free-ranging, fledgling, female great-horned owl (*Bubo virginianus*) from Livingston Parish, Louisiana. The owl was found moribund in May 2015 and was covered in mosquitoes. It did not attempt to fly when approached, and it died overnight while in captivity. Aside from general pallor of all tissues, particularly the subcutis and lungs, no other significant gross lesions were observed. Histopathological analysis revealed necrosis and abundant schizonts containing numerous merozoites in the liver, kidney, spleen, and heart. Although difficult to distinguish histologically, many erythrocytes appeared to be parasitized with pigmented, intracytoplasmic *Haemoproteus* gametocytes and numerous leukocytes had intracytoplasmic *Leucocytozoon* merozoites. PCR testing of spleen samples and analysis of partial cytochrome b (cytb) gene sequence confirmed a coinfection with *Haemoproteus* sp. lineage hSTVAR01 and *Leucocytozoon* sp. lineage lSTOCC16, both of which are common in several owl species. The dual infection is believed to be significant enough to have contributed to mortality in this individual. To the authors' knowledge, this is the first report of a fatal Haemoproteus and *Leucocytozoon* coinfection in an owl other than a single *Haemoproteus noctuae/Leucocytozoon ziemanni* coninfection of a snowy owl (*Nycetea scandiaca*). Further investigation of host-parasite dynamics may be warranted to better understand the potential impacts of haemosporidian infections, especially dual infections, on fledgling success of free-ranging raptors.

12. PURPLE, KATHRYN[1]*, BRAND, MABRE[1], BROWN, JUSTIN[2], BOYD, ROBERT[2], AND GERHOLD, RICHARD[1]. [1]Department of Biomedical and Diagnostic Sciences, College of Veterinary Medicine, The University of Tennessee. [2]Pennsylvania Game Commission. **Investigating the prevalence of *Histomonas meleagridis* shedding by captive raised Ring-necked pheasants (*Phasianus colchicus*) in Pennsylvania.**

Ring-necked pheasants (*Phasianus colchicus*) were introduced into multiple regions of Pennsylvania, USA, producing substantial hunting opportunities. Pheasants can harbor multiple pathogens in the absence of overt disease including *Histomonas meleagridis*, which is considered to be one of the most important pathogens for native game birds including wild turkey (*Meleagris gallopavo*), ruffed grouse (*Bonasa umbellus*), and northern bobwhite (*Colinus virginianus*). In addition, *H. meleagridis* has caused significant impacts in the commercial turkey industry. The Pennsylvania Game Commission annually raises and releases about 200,000 pheasants from 4 game farms, and as a responsible wildlife management agency, was interested the infection status of *H. meleagridis* in pheasants. Fifty-one pheasants from a single game farm were examined for *H. meleagridis* by inoculating cloacal swabs into flasks containing Dwyer's media. Flasks were shipped to the University of Tennessee using a published protocol for survival of *H. meleagridis* in transit. Flasks were examined daily for seven days for histomonad growth. In addition, an aliquot from twenty randomly chosen flasks was used for DNA extraction and PCR targeting the internal transcribed spacer (ITS) regions of the ribosomal RNA. All flasks were culture-negative via light microscopy and DNA extract from the twenty samples was PCR-negative. These data suggest that propagated ring-necked pheasants may not always be carriers of *H. meleagridis*, as historically was believed. However, more research is needed to examine the frequency of *H. meleagridis* shedding in captive and wild pheasants, under varying conditions, and other species to further understand the eco-epidemiology of blackhead disease.

13. ORÉLIS-RIBEIRO, RAPHAEL[1]*, KENNETH M. HALANYCH[2], AND STEPHEN A. BULLARD[1]. [1]School of Fisheries, Aquaculture, and Aquatic Sciences, Auburn University, Auburn, AL. [2]Department of Biological Sciences, Auburn University, Auburn, AL. **Broad-scale phylogeny of craniate blood flukes (Digenea: Schistosomatidae), with emphasis on "fish blood flukes" (Aporocotylidae).**

Ambiguity regarding fish blood fluke interrelationships obstructs a deeper understanding of the evolutionary origins of flatworm parasitism in craniates, including the origin of schistosomes. We herein analyzed new and all available sequence data for the partial D1–D3 domains of 28S rDNA from 119 blood flukes to test monophyly of fish blood flukes (Aporocotylidae) and their interrelationships with tetrapod blood flukes (i.e., Schistosomatidae and "Spirorchiidae"). We also tested monophyly of the blood flukes infecting gastropods compared with those of bivalves plus polychaetes. Monophyly of Aporocotylidae was not wholly supported; however, those aporocotylids infecting principally marine bony fishes clearly were monophyletic. Also based on this analysis, the blood flukes infecting chondrichthyans are monophyletic, as well as the blood flukes infecting primary division freshwater fishes. Putative aporocotylid cercariae from freshwater gastropods need further taxonomic attention and may represent a phylogenetically unique lineage. Blood flukes that utilize gastropod intermediate hosts were monophyletic and those utilizing bivalves and polychaetes were monophyletic. Noteworthy is that this result represents the first phylogenic reconstruction that includes 28S rDNA sequences derived from a dense taxon sampling that includes blood flukes of early-branching fish lineages and primary division freshwater fish. The present phylogenetic analysis reiterated support for monophyly of Schistosomatidae and paraphyly of Spirorchiidae, with the blood flukes of freshwater turtles sister to those of marine turtles plus schistosomes. Moreover, resolution within deep nodes suggests that a phylogenomic approach should prove valuable in future studies to improving our comprehension of the evolutionary expansion of these blood parasites in craniates.

14. RUIZ, CARLOS[1]*, MATTHEW R. WOMBLE[1], RAPHAEL ORELIS-RIBIERO[1], JACKSON R. ROBERTS[1], JACOB M. RASH[2], DOUG A. BESLER2, COVA R. ARIAS[1], AND STEPHEN A. BULLARD[1]. [1]Southeastern Cooperative Fish Parasite & Disease Project, School of Fisheries, Aquaculture, & Aquatic Sciences, Auburn University, 203 Swingle Hall, Auburn, Alabama 36849; [2]North Carolina Wildlife Resources Commission, 645 Fish Hatchery Road, Marion, North Carolina 28752. **"Gill lice" (Copepoda: Lernaeopodidae: Salmincola) infecting epithelia of rainbow trout (*Oncorhynchus mykiss*) and brook trout (*Salvelinus fontinalis*) in North Carolina rivers and aquaculture facilities.**

Salmincola (Copepoda: Lernaeopodidae) comprises 17 species that infect the epithelial surfaces (gill, buccal cavity, fins) of 11 genera of freshwater fishes assigned to Salmonidae, Esocidae, Cottidae, and Gadidae of North America, Europe, and Asia. Southeastern United States trout fisheries comprise rainbow trout *Oncorhynchus mykiss*, brook trout *Salvelinus fontinalis*, and brown trout *Salmo trutta*. Of which, two (rainbow trout and brook trout) are infected by species of Salmincola: S. californiensis infects gill of rainbow trout (primarily) and brook trout in 13 states; whereas, *S. edwardsi* infects gill of brook trout (primarily) and rainbow trout in 4 states. Herein, we report *Salmincola* cf. *californiensis* from gill and buccal cavity of rainbow trout from a private trout farm on the Watauga River (100% prevalence; 9.3 mean intensity), adjacent sites on that river (11% prevalence; 2.0 mean intensity), and from the West Fork Pigeon River. We report *Salmincola* cf. *edwardsi* from gill, buccal cavity, and fins of brook trout from Big Norton Prong (100% prevalence; 8.9 mean intensity) and the upper Cullasaja River. Gross observations, histopathology, and SEM revealed alterations to the normal gill filament architecture in heavily-infected rainbow and brook trout. The marked lesion could be interpreted as a 'mismatched' host-parasite relationship, speculatively resulting from a recent introduction of the parasite, or that of trout strains, into river systems. This is the first confirmed occurrence of *Salmincola* in rivers of North Carolina and the Southeastern United States, although unpublished anecdotes of previous infections among hatchery-reared fishes there exist.

15. SAPP, SARAH G. H. [1,2]*, SARA B. WEINSTEIN [3], CHRISTOPHER S. MCMAHAN [4], SUKWAN HANDALI [5], AND MICHAEL J. YABSLEY [1,6]. [1] Southeastern Cooperative Wildlife Disease Study and [2] Department of Infectious Diseases, College of Veterinary Medicine, University of Georgia, Athens, Georgia; [3]Department of Ecology, Evolution, and Marine Biology, University of California, Santa Barbara, California; [4]Department of Mathematical Sciences, Clemson University, Clemson, South Carolina; [5] Parasitic Diseases Branch, Centers for Disease Control and Prevention, Atlanta, Georgia; [6] Warnell School of Forestry and Natural Resources, University of Georgia, Athens, Georgia. ***Baylisascaris procyonis* infection dynamics and survival in four species of deer mice (*Peromyscus* spp.).**

Wild rodents such as *Peromyscus* spp. are intermediate hosts for the zoonotic ascarid *Baylisascaris procyonis* (raccoon roundworm), and *P. leucopus* likely serves an important role in parasite ecology. Natural infections have been sporadically identified in a few *Peromyscus* species, but no data are available on differences in susceptibility among the many other species. We compared survival and infection dynamics of *B. procyonis* in four species (*P. leucopus*, *P. maniculatus*, *P. californicus*, *P. polionotus*) from regions of varying habitat types and *B. procyonis* prevalence. Groups of six captive-bred mice of each species were inoculated per os with one of three doses (~10, ~50, or ~500) of embryonated *B. procyonis* eggs. Animals were monitored twice daily for clinical sings and behavioral abnormalities, and were euthanized at the onset of severe neurological symptoms or at 45 days post infection. Larvae were enumerated in the brain via microscopic examination and in skeletal muscle and visceral organs via artificial digestion. In the high-dose group, mortality was 100% for all species except *P. californicus* in which one mouse survived. In the medium-dose group, mortality ranged from 33-85% across species. Little to no disease was observed in the low-dose group. Survival analysis reveals *P. leucopus* survived longer than the other species, which did not differ significantly. Interestingly, larval recovery percentages were nearly identical across species and doses. These data indicate that *P. leucopus* may be more resilient towards severe baylisascariasis compared to the other species, and that even closely-related rodents may experience differential mortality.

16. **BRIANNA M. WILLIAMS[1,2]* AND MICHAEL J. YABSLEY[1,2]**. 1Daniel B. Warnell School of Forestry and Natural Resources, Athens, GA; 2Southeastern Cooperative Wildlife Disease Study, Athens, GA. **Identification and diversity and intensity of *Ixodes* ticks of seabirds breeding on Middleton Island, Alaska.**

Population fluctuations with an overall decline in nesting bird colonies have been noted on Middleton Island, Alaska. While population declines are likely due to several factors, high ectoparasite loads could be a contributing factor as studies on other bird species indicate fitness may be reduced with high tick intensities. During June-August 2014 and 2015, we sampled Black-legged Kittiwakes (*Rissa tridactyla*) (n=324, 287 respectively), Pelagic Cormorants (*Phalocrocorax pelagicus*) (n=97, 57), Tufted Puffins (*Fratercula cirrhata*) (n=3, 82), and Rhinoceros auklets (*Cerorhinca monocerata*) (n=43, 82) to (1) Determine the prevalence and diversity of ixodid ectoparasites associated with the nesting populations and (2) determine if ticks impacted the health of kittiwake chicks by treating some nest sites with a mild insecticide (carbaryl). We hypothesized that there would be high levels of ectoparasites associated with nesting colonies of kittiwakes and cormorants and lower numbers associated with puffins and auklets because the latter two breed in individual burrows. Preliminary data indicate that untreated Black-legged Kittiwake chicks had high burdens of *Ixodes uriae* and low burdens of *Ixodes signatus*. Cormorants also had high tick burdens (mean 5, range 0-20) whereas lower tick burdens were noted on puffins (mean 1, range 0-3) and auklets (mean 1, range 0-2). Kittiwake chicks sampled in 2015 had significantly higher tick burdens compared to 2014 (mean 3.86 and mean 7.12, respectively) which may be due to warmer dryer conditions in 2015. This preliminary data suggests the need for further studies on the effects of ectoparasitism on the health of seabirds breeding on Middleton Island, Alaska.

17. **WYROSDICK, HEIDI M.[1,2]*, RICHARD GERHOLD[2], CHUNLEI SU[3], MARTINE DE WIT[4], ALYCIA CHAPMAN[2], JESSICA MARTINEZ[1,2], DEBRA MILLER[1,2], and ROBERT K. BONDE[5].** [1]University of Tennessee, Center for Wildlife Health, Department of Forestry, Wildlife, and Fisheries, Knoxville, TN. [2]University of Tennessee, Department of Biomedical and Diagnostic Sciences, College of Veterinary Medicine, Knoxville, TN. [3]University of Tennessee, Department of Microbiology, Knoxville, TN. [4]Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Research Institute, Marine Mammal Pathobiology Laboratory, St. Petersburg, FL. [5]U. S. Geological Survey, Wetland and Aquatic Research Center, Gainesville, FL. **Epidemiology of *Toxoplasma gondii* in Florida manatees (*Trichechus manatus latirostris*) and free-roaming cats in Citrus County, Florida**

Toxoplasma gondii is a protozoan parasite of felids reported to cause mortality in Antillean manatees (*Trichechus manatus manatus*) in Puerto Rico and Florida manatees (*T. m. latirostris*). Our study is an expansion on the most recent report of the seroprevalence of *T. gondii* in Florida manatees and the first attempt to determine an association between toxoplasmosis in manatees and free-roaming cats. The objectives of the study are to determine prevalence of *T. gondii* in Florida manatees and free-roaming cats in Citrus County, Florida, and, if detected, to compare the *T. gondii* genotypes between the two populations. Potential transmission dynamics will be presented based on these results. Sera, plasma, or serosanguinous fluid from live-captured and necropsied Florida manatees (n=187) were tested using the MAT (Modified Agglutination Test) to determine seroprevalence of *T. gondii*. Eighty-four free-roaming cat fecal samples were tested by centrifugal floatation for *T. gondii* oocysts to determine parasite prevalence. Preliminary results include 185 negative manatee sera or plasma samples and no *T. gondii* oocysts detected in any of the felid fecal samples. Final results will be presented.

18. MCGAHA JR., TOMMY W. [1]*, VIVIAN PADIN-IRIZARRY [1], ANKUSH KANWAR [2], JAMES W. LEAHY [2], DENNIS E. KYLE [1]. [1]Department of Global Health, College of Public Health, University of South Florida, Tampa, FL. [2]Department of Chemistry, University of South Florida, Tampa, FL. **The use of *Plasmodium falciparum* gametocytes in the laboratory to conduct drug discovery and evaluate the spread of drug resistance of antimalarial compounds.**

The need of blocking transmission for malaria from host to vector has driven researchers to investigate *Plasmodium* gametocytes more in depth than previously. Sexual gametocytes possess different metabolic and growth characteristics than the asexual blood stages of *Plasmodium*. These different characteristics along with difficult in vitro culturing of gametocytes provide researchers with challenges when conducting laboratory studies. Production of viable *Plasmodium falciparum* gametocytes can allow researchers to investigate processes which occur in the human host and the mosquito vector. Here, applications of the use of in vitro generated gametocytes are described along with how they can be used to investigate the discovery of transmission-blocking compounds and even the spread of drug resistance.

19. GALLO, SAMIRA S. M.[1]*, OLIVEIRA, FRANCISCO C. R.[1], EDERLI, NICOLE B.[1], SAWER, R. O[2], AND LINDSAY, DAVID S.[2] [1]Laboratorio de Sanidade Animal, Universidade Estadual do Norte Fluminense, Campos dos Goytacazes, Rio de Janeiro, Brazil. [2]Department of Biomedical Sciences and Pathobiology, Virginia Tech, Blacksburg, Virginia, USA. **Isolates of *Sarcocystis falcatula*-Argentina-like organisms from the South American opossums *Didelphis aurita* from Brazil**

The present study was done to identify the *Sarcocystis* species that infect opossums, *Didelphis aurita*. Sporocysts were obtained from 5 opossums trapped near Campos dos Goytacazes city in Rio de Janeiro state, Brazil. The small intestinal epithelium was scraped off and digested in 10% bleach to obtain sporocysts. The bleach was washed off and sporocysts were deposited in the crop of budgerigars *Melopsittacus undulatus* via feeding needle. At necropsy, portions of organs were fixed in 10% buffered formalin and processed for histology and transmission electron microscopy (TEM). Additional, tissues were stored in absolute alcohol for PCR using primers JNB (*S. falcatula*/*S. neurona* complex) and ITS (all *Sarcocystis* species). The JNB amplification products were subjected to RFLP using restriction endonucleases DraI and HinfI. Sporocysts were oval and measures 12.0 by and 8.7 µm. One bird died 13 days PI, another was euthanized 16 days PI due to illness, and the others were euthanized 60 days PI. Sarcocysts were found in the breast, thigh and tongue of the birds examined 60 days PI and they measured 40.2 by 23.5 µm with a wall ~1.5 µm thick. TEM demonstrated immature sarcocysts in the thigh that had finger-like protrusions on the parasitophorous vacuolar membrane. Tissues were positive by PCR with both primer pairs. RFLP on the JNB product cut with both restriction enzymes indicating a *S. falcatula*-Argentina like species was present. This is the first report of *D. aurita* being a definitive host for *S. falcatula*-Argentina like sporocysts.

20. WOMBLE, MATTHEW R.[1]* AND STEPHEN A. BULLARD[2]. [1]Office of the NOAA Chief Scientist, U.S. Department of Commerce, National Oceanic and Atmospheric Administration, Washington DC. [2]Aquatic Parasitology Laboratory, Southeastern Cooperative Fish Parasite and Disease Laboratory, Auburn University, Auburn AL. **What is *Leuceruthrus micropteri* (Digenea:Azygiidae)?**

Monotypic *Leuceruthrus* (Digenea: Azygiidae) (as *Leuceruthrus micropteri*) is among the most neglected azygiid genera with respect to published works, cercarial and adult descriptions, available molecular sequence data, and life cycles elucidated. In fact, adult specimens of L. micropteri were last described 104 years ago (1911) and only once before that, in 1905.This is unexpected considering that their adults and cercariae are macroscopic, their fish hosts are among the most commonly captured North American inland fishes (Centrarchidae), and their snail hosts (Pleuroceridae) are extraordinarily biodiverse, highly regionally endemic, and of high conservation concern. Herein, adults and cercariae of *Leuceruthrus* spp. were collected from centrarchids and pleurocerids in rivers and streams of Alabama and Florida. Specimens for morphology were studied with light and scanning electron microscopy and compared with published descriptions of congeners and type materials of *L. micropteri*. Sequences of

the ribosomal internal transcribed spacer 2 (ITS2) were obtained for comparative purposes. Contrary to the longstanding monotypic status of *Leuceruthrus*, our results identified 4 species of *Leuceruthrus*: one as *L. micropteri* (sensu lato) and 3 as probable innominate species. Additionally, and comprising the largest phylogenetic analysis for Azygiidae to date, molecular data confirmed conspecificity among corresponding cercariae and adults (thereby elucidating those life cycles), did not reject monophyly of *Leuceruthrus*, and recovered *Leuceruthrus* and *Proterometra* as sister taxa. This result is noteworthy in that it does not reject azygiids infecting North American pleurocerid snails as monophyletic.

21. LINDSAY, D.S.[1]*, VERMA, S.K.[2], SCOTT, D.[3], DUBEY, J.P.[2], ROSYPAL, ALEXA C.[4] [1]Virginia Tech, Blacksburg, VA. [2]USDA-ARS, Animal Parasitic Diseases Laboratory, Building 1001, Beltsville, MD. [3]Carolina Raptor Center, 6000 Sample Road, Huntersville, NC. [4]Johnson C. Smith University, Charlotte, NC. **Development of a *Sarcocystis columbae*–like protozoan from a Cooper's hawk (*Accipiter cooperi*) in mammalian cells.**

We are interested in understanding the diversity of *Sarcocystis* species that use birds of prey as intermediate and definitive hosts. We report isolation of a *Sarcocystis* species from the feces of a Cooper's hawk (*Accipiter cooperi*) and analysis of DNA isolated from merozoites. Hawks of the genus *Accipiter* are definitive hosts for *S. accipitris, S. calchasi*, *S. columbae*, and *Sarcocystis* sp. ex *A. nisus* in Europe. A Cooper's hawk was admitted to the Carolina Raptor Center for treatment. It was euthanized because of poor prognosis. Its intestinal tract was removed and examined for parasites by making several direct smears and examining them with light microscopy. Sporocysts measuring 12.9 by 7.9 µm containing 4 sporozoites and a granular sporocyst residuum were present. Sporocysts were subjected to in vitro excystation and inoculated on to African Green monkey kidney cells. Extracellular merozoites were observed 33 days PI and intracellular schizonts were seen 34 days PI. Subcultures of merozoites were done 40 days PI and the parasite has been maintained by subculture since that time. Transmission electron microscopy demonstrated that the parasites developed directly in the host cell cytoplasm, that development was by endopolyogeny, that merozoites lacked rhoptries, and that they contained all organelles typical of *Sarcocystis* merozoites. Phylogenetic analysis demonstrated that the parasite was more closely related to S. columbae than other *Sarcocystis* species using *Accipiter* hawks as definitive host. Supported by grant # 1505407 from the NSF to ACR and by an IRC grant from Virginia Tech to DSL.

22. YABSLEY, MICHAEL J.[1,2*], MARK L. EBERHARD[3], HUBERT ZIRIMWABAGABO[4], HENRY BISHOP[3], CHRISTOPHER A. CLEVELAND[1,2], JOHN C. MAERZ[1], ROBERT BRINGOLF[1], and ERNESTO RUIZ-TIBEN[4]. [1]Warnell School of Forestry and Natural Resources, The University of Georgia, Athens, GA. [2]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, The University of Georgia, Athens GA. [3]Division of Parasitic Diseases and Malaria, Centers for Disease Control and Prevention, Atlanta, GA. [4]The Carter Center, Atlanta, Georgia. **The role of fish and frogs as paratenic hosts of *Dracunculus medinensis*, the human guinea worm.**

The campaign to eradicate Guinea worm disease has assisted 17 of 21 affected countries interrupt transmission with a decrease from about 3.5 million cases annually in 1986 to only 22 in 2015. In Chad, an unusual epidemiology has developed with dogs emerging as potential reservoirs. In this study, we experimentally exposed fish and tadpoles to *D. medinensis*-infected copepods to determine their paratenic host capability. Also, these hosts were fed to domestic ferrets to determine if any L3 present would develop. In July 2015, copepods from Chad were exposed to L1s collected from infected dogs. Once infective L3 were noted in copepods, fish and tadpoles were exposed to the infected copepods. After 14 days, L3 larvae were found in exposed green frogs (*Lithobates clamitans*) but not in Fowler's toads (*Bufo fowleri*), Nile tilapia (*Oreochromis niloticus*) or fathead minnows (*Pimephalis promelas*). A domestic ferret fed infected tadpoles was necropsied 70-83 days after being fed and three immature female *D. medinensis* worms were found in subcutaneous tissues. A ferret fed fish was negative. These results confirm that *D. medinensis*, like *Dracunculus insignis*, can utilize an aquatic paratenic host, specifically tadpoles. However, the absence of larvae in the two species of fish we included in this study

does not rule out a role of fish as paratenic hosts. These data also confirm that ferrets, like domestic cats and dogs and monkeys, can serve as experimental definitive hosts for the human guinea worm, *D. medinensis*. Knowing a paratenic host exists can assist with eradication efforts.

23. HEINS, DAVID C[1]*, DONA M. EIDAM[2], AND JOHN A. BAKER[3]. [1]Department of Ecology and Evolutionary Biology, Tulane University, New Orleans, LA. [2]Department of Biology, University of Alaska at Anchorage, Anchorage, AK. [3]Department of Biology, Clark University, Worcester, MA. **Timing of Infections in the threespine stickleback by *Schistocephalus solidus* in Alaska.**

This study provides direct evidence for the timing of infections by *Schistocephalus solidus* in the threeespine stickleback of south-central Alaska. Young-of-the-year fish in Cheney Lake were infected during their first summer within a few months after hatching in May-June. Infections appear to continue under ice cover on the lake during the subsequent fall and winter. Few, if any, 1-yr-old fish seemed to be infected for the first time, although 1-yr-old hosts with established parasites apparently acquired additional infections.

24. LEAPHART, JAMES C., AND DEREK A. ZELMER*. Department of Biology and Geology, University of South Carolina, Aiken SC. **The life cycle of *Haematoloechus floedae* Harwood, 1932 (Digenea: Plagiorchiidae).**

Haematoloechus floedae was originally described from bullfrogs (*Rana catesbeiana*) captured in Texas, but subsequently was interpreted as a junior synonym of *H. varioplexus* or of *H. breviplexus*. Recent molecular and morphological descriptions have established *H. floedae* as a valid species infecting bullfrogs in the southern United States, and four other ranid species in Mexico and Central America. It is likely that prior synonymy of *H. breviplexus* and *H. floedae* account for an apparent discrepancy in the life cycle of *H. breviplexus*. The planorbid snail, *Gyraulus similaris*, serves as a first intermediate host for *H. breviplexus* collected from *R. pretiosa* in Idaho, but successful infections of *H. breviplexus* from Texas were reported in a species of *Ferrissia*, an ancylid snail, but snails in the genus *Gyraulus* failed to become infected. *Ferrissia fragilis* isolated from a pond in South Carolina were observed shedding cercariae morphologically consistent with those of *Haematoloechus*. Exposure of libellulid and odonate naiads to these cercariae resulted in the recovery of encysted metacercariae within the branchial basket of the odonates. Those metacercaria produced an infection of adult worms identified as *H. floedae* when fed to lab-raised bullfrogs. In addition, a second cercaria with similar morphology but smaller than that of *H. floedae* and exhibiting different behavior, has been observed being shed from ancylids from the same pond.

25. ADONIS MCQUEEN[1]*, NIRANJAN NAMELIKONDA[2], MICHAEL KEMP[2], TOMMY MCGAHA[3], LYNN BLAKE[2], ALA AZHARI[3], RANDY LARSEN[2], ROMAN MANETSCH[4], AND DENNIS KYLE[3]. [1]College of Medicine, USF, Tampa, FL [2]Department of Chemistry, USF, Tampa, FL. [3]College of Public Health, USF, Tampa, FL. [4]College of Pharmacy and Pharmaceutical Sciences, Northeastern University, Boston, MA. **In vitro studies and characterization of fluorescent 8-aminoquinoline molecules.**

Malaria is the world's most widespread tropical disease, with 584,000 deaths in 2014. Most of these were in children under 5 years old (WHO 2014). The two most prevalent species causing human disease are *Plasmodium falciparum* and *P. vivax*, both of which are increasingly difficult to treat and control due to the emergence of drug resistance and lack of effective preventive drugs for the populations at highest risk: children and pregnant women. Primaquine (PQ) is the only anti-malarial compound commercially available that can act to clear late stage gametocytes and the dormant liver form known as the hypnozoite, which is responsible for relapsing infections with *P. vivax* and *P. ovale*. PQ's mechanism of action is dependent upon reactive metabolites formed by P-450 enzymes; however, the mechanism in which these metabolites act on hepatic schizonts and late stage gametocytes is also unknown. In this study we demonstrate the successful synthesis and characterization of both primaquine and tafenoquine fluorescent probes. Localization of the probes

primarily occurs in the cytosol of the parasite infecting erythrocytes. The anti-malarial activities of these probes do not differ significantly from the parent drug molecules in asexual blood or liver stages. In addition these probes are not toxic to HepG2 liver carcinoma cells. These new probes offer the opportunity to further investigate the mechanism(s) of action of 8-aminoquinoline drugs against various stages of the life cycle.

26. BULLARD, STEPHEN A.[1]*, CARLOS F. RUIZ[1], RAPHAEL ORELIS-RIBEIRO[1], JACKSON R. ROBERTS[1], MATTHEW R. WOMBLE[2], CANDIS RAY[1], JACOB RASH[3], DOUG BESLER[3], AND COVA ARIAS[1]. [1]Southeastern Cooperative Fish Parasite & Disease Project, Auburn, AL; [2]US Department of Commerce, Washington, DC; [3]North Carolina Wildlife Resources Commission, Marion, NC. ***Myxobolus cerebralis*** **(etiological agent of "whirling disease") infecting trouts and oligochaetes in North Carolina.**

The myxozoan parasite *Myxobolus cerebralis* was introduced into North America in the mid-twentieth century with infected brown trout (*Salmo trutta*) imported from Europe and is now recorded in 24 states and 26 countries. This parasite is the causative agent of whirling disease; an economically and ecologically devastating disease of salmonids, especially rainbow trout (*Oncorhynchus mykiss*). Heavily-infected (diseased) fishes exhibit "whirling" behavior (tail chasing, disequilibrium, erratic swimming) plus skeletal and pigment abnormalities that are obvious to and can alarm anglers. The first occurrence of infection by *M. cerebralis* from North Carolina (rainbow trout, brown trout, and oligochaetes) was confirmed by the Southeastern Cooperative Fish Parasite and Disease Laboratory (Auburn University) in July 2015. Herein, we report on infection prevalence among rainbow trout, brown trout, and oligochaetes from streams and culture settings, discuss the geographic distribution of *M. cerebralis* in North America more broadly, and detail the clinical signs of whirling disease that indicated the presence of the disease in North Carolina. This comprises the first documented occurrence of the pathogen and corresponding disease in the southeastern United States south of Virginia. Surveillance for infections by *M. cerebralis* in North Carolina waters is ongoing.

27. VARELA-STOKES, ANDREA S.*, JUNG KEUN LEE, AMANDA HARPER, GAIL MORARU, JOHN STOKES, HALEY PARKER, KATIE GRAHAM, JACOB HUGHES, CATHERINE SMITH. Department of Basic Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi. **Movement of *Amblyomma maculatum*-associated rickettsiae during tick feeding.**

Influence of non-pathogenic rickettsiae on movement, maintenance and transmission of sympatric pathogenic rickettsiae in ticks is not well-understood. Our laboratory is using the Gulf Coast tick, *Amblyomma maculatum,* to explore movement of the pathogen, *Rickettsia parkeri,* and non-pathogen, *"Candidatus* Rickettsia andeanae," during tick feeding. Using adult ticks infected with *R. parkeri,* "*Ca.* R. andeanae", co-infected, or uninfected, and fed on rabbit hosts, we consistently found "*Ca*. R. andeanae" by qPCR in the salivary gland and midgut from *"Ca.* R. andeanae" and co-infected groups on Days 0, 6 and 12. *Rickettsia parkeri* was rarely detected, though levels were highest in salivary glands from the co-infected group at Day 12, when presence is not likely biologically important for transmission. DNA extracts from rabbit blood on Days 0 and 6, skin biopsies, lymph node and spleen were negative by PCR. Exposure to rickettsiae was evident in all treatment groups based on serological testing by immunofluorescent antibody tests. Additional co-feeding studies, using *R. parkeri*-infected adult *A. maculatum* and recipient nymphs infected or uninfected with *"Ca.* R. andeanae," demonstrated transmission of *R. parkeri* only to uninfected nymphs, suggesting populations of *"Ca.* R. andeanae"-infected ticks may not easily acquire infections with *R. parkeri.* Currently, monoclonal antibodies generated using peptides from over-expressed proteins in salivary gland and midgut, will be tested for additional tick tissue identification. Future studies will explore questions to include other microbes in the tick as we continue to discern the impact of species of known or unknown pathogenicity on pathogen maintenance and transmission.

28. YABSLEY, MICHAEL J.[1,2]*, HEATHER FENTON[2], JESSICA MCGUIRE[3], CHRISTOPHER A. CLEVELAND[1,2], ELIZABETH W. HOWERTH[4], AND MARK G. RUDER[2]. [1]Warnell School of Forestry and Natural Resources, The University of Georgia, Athens, GA. [2]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, The University of Georgia, Athens GA. [3]Georgia Department of Natural Resources, Social Circle, GA. [4]Department of Pathology, College of Veterinary medicine, University of Georgia, Athens GA. **A walk on the wild side: a quiz of selected wildlife parasitology cases**

The Southeastern Cooperative Wildlife Disease Study receives approximately 800 to 1,000 wildlife case submissions a year. The diagnoses are variable and include trauma, toxicoses, bacterial, fungal, and viral causes of significant morbidity and mortality, but in some cases, parasitism seems to have a significant negative impact on the health of the animal. In this talk we will give case histories for a selected group of cool parasite cases and challenge the audience to provide differentials. We will then proceed through the case diagnostics and final diagnosis for each case.

29. WOMBLE, MATTHEW R.*. Office of the NOAA Chief Scientist, U.S. Department of Commerce, National Oceanic and Atmospheric Administration, Washington DC. **From Parasites to Policy: An overview of the Sea Grant Knauss Fellowship Program.**

The Sea Grant Knauss Marine Policy Fellowship is an educational and professional opportunity for graduate students to spend one year in Washington, D.C., learning about marine and environmental policy. The program was established in 1979 by the National Oceanic and Atmospheric Administration's (NOAA's) National Sea Grant College Program to fulfill the legislative mandate of the Sea Grant Act, and its broad educational responsibilities. Briefly, the fellowship provides a unique educational and professional experience to students who have an interest in ocean, coastal and Great Lakes resources, and in the national policy decisions affecting those resources. The fellowship matches graduate students with "hosts" in the legislative and executive branches of the federal government in the Washington, D.C. area, for a one year paid fellowship, where fellows' work on a range of policy and management projects related to the focus area of their respective host office. An eligible applicant is any student, regardless of citizenship, who is enrolled towards a degree in a graduate or professional program and has an interest in ocean, coastal and Great Lakes resources. In the intervening years since its establishment, the Knauss Marine Policy Fellowship has blossomed into a nationally recognized program that has aided in bridging the gap between science and policy, by helping to support and advance the careers of hundreds of alumni, whom are now spread throughout government and academia.

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