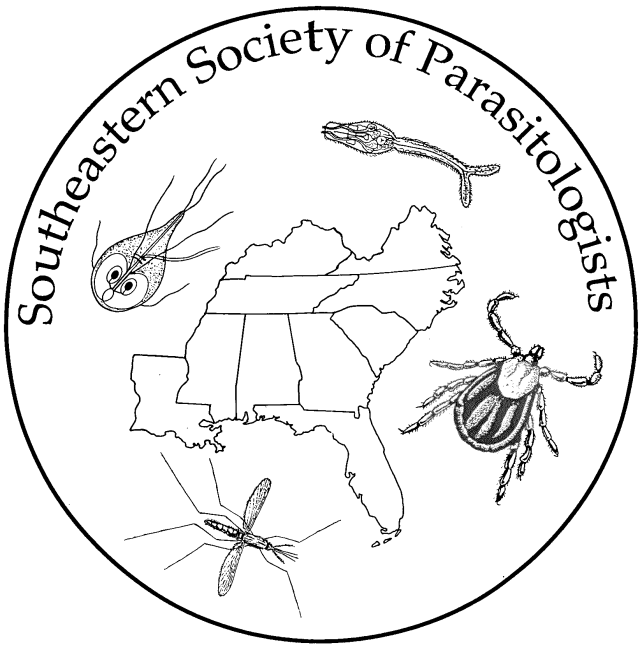
SOUTHEASTERN SOCIETY OF PARASITOLOGISTS

(Affiliate of The American Society of Parasitologists)

PROGRAM AND ABSTRACTS



April 10-12, 2013

Hosted by:

Ogden College of Science and Engineering
Western Kentucky University
Bowling Green, KY

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Southeastern Society of Parasitologists
2013 Program Summary

Meeting Registration/Check In
Wednesday, April 10, 2012 **3:00 p.m. - 7:00 p.m.**
Staybridge Suites Hotel - Main Lobby

SSP Executive Committee
Wednesday, April 10, 2013 **3:00 p.m. - 5:00 p.m.**
Staybridge Suites Hotel – Meeting Room

Social Hour
Wednesday, April 10, 2013 **5:30 p.m. - 6:45 p.m.**
Staybridge Suites Hotel – Main Lobby

Dinner and SSP Presidential Symposium
Wednesday, April 10, 2013 **7:00 p.m. - 9:30 p.m.**
Knicely Conference Center –Room 163 B

Presiding: Dr. Derek Zelmer, University of South Carolina Aiken

7:00 **Dr. Cheryl Stevens**, Dean, Ogden College of Science and Engineering, Western Kentucky University, KY. *"Dean's Welcome!"*

7:20 **Dr. Derek Zelmer,** Department of Biology and Geology, University of South Carolina Aiken, Aiken, SC. "*By way of explanation...*"

7:30 **Dr. Garriet Smith,** Department of Biology and Geology, University of South Carolina Aiken, Aiken, SC. "*Aspergilliosis: History, etiology and response to a pathogen affecting gorgonians.*"

8:10 **Dr. Julián F. Hillyer,** Department of Biological Sciences, Vanderbilt University, Nashville, TN. *"Hemocyte-mediated immune responses and hemolymph flow dynamics in the body cavity of the malaria mosquito,* Anopheles gambiae*"*

8:40 **Dr. Eric S. Loker,** Center for Evolutionary and Theoretical Immunology, Museum of Southwestern Biology, University of New Mexico, Albuquerque, NM. *"Celebrating 100 years of snails and schistosomes with a look at* Biomphalaria-Schistosoma mansoni *interactions."*

SSP Welcome Reception
Wednesday, April 10, 2013 **9:30 p.m. – 12:30 a.m.**
Staybridge Suites Hotel – Meeting Room and Patio

Session I: Ciordia-Stewart Porter and Byrd-Dunn Student Paper Competition
Thursday Morning, April 11, 2013 8:15 a.m. – 10:15 a.m.

Session I Moderators: Alice Houk and Andrea Varela-Stokes

* Presenting Author
† Ciordia-Stewart Porter Research Competitor
‡ Byrd-Dunn Student Paper Competitor

8:15 1† **SIMMONS, ALYSHA*, NANCY TENPENNY, AND DAVID S. LINDSAY.** Virginia Tech, Blacksburg, VA. Activity of decoquinate against 3 species of cat transmitted *Besnoitia* (Apicomplexa: Sarcocystidae).

8:30 2† **BOLDEN, LEAH M.** Berry College, Rome GA. Ticks on the Berry College campus: a risk assessment and survey of community awareness.

8:45 3† **REAGIN, KATIE*, GABRIEL LUGO, AND CHRIS A. HALL.** Department of Biology, Berry College, Mount Berry, GA, Distribution and prevalence of *T. cruzi* infection in *Triatoma sanguisuga spp.* from the southeastern United States.

9:00 4† **REAGIN, KATIE*[1], CAROL RUCKDESCHEL[2], AND CHRIS A. HALL[1].** [1]Department of Biology, Berry College, Mount Berry, GA. [2]Cumberland Island Museum of Natural History, Cumberland Island, GA. *Triatoma sanguisuga spp.* population and lifecycle dynamics on a barrier island.

9:15 5† **FULGHUM, CHRISTINA M.*, AND DEREK A. ZELMER.** University of South Carolina Aiken, Aiken SC. The Role of Spatial and Temporal Heterogeneity in Structuring Trematode Communities in the Freshwater Snail, *Physa pomilia*, from West Pond located in Brick Pond Park, North Augusta, SC.

9:30 6† **SOVEG, FRANK W.*, ELLIOTT ZIEMAN, F. AGUSTÍN JIMÉNEZ.** Department of Zoology, Southern Illinois University, Carbondale, Illinois 62901-6501. Taxonomic placement of *Rhopalias w*ithin the Echinostomatoidea using three genetic markers.

9:45 7‡ **ANDRES, MICHAEL J.*, AND ROBIN M. OVERSTREET**. Gulf Coast Research Laboratory, The University of Southern Mississippi, Ocean Springs, MS. Molecular phylogeny of the trematode family Opecoelidae.

10:00 8‡ **ROSSER, THOMAS G. [*1], MATT J. GRIFFIN[1,2], SYLVIE QUINIOU[3], LESTER H. KHOO[1,2], AND LINDA M. POTE[1].** [1]College of Veterinary Medicine, Mississippi State University, Mississippi State, MS. [2]Aquatic Research and Diagnostic Laboratory, Thad Cochran National Warmwater Aquaculture Center, Mississippi State University, Stoneville, MS. [3]USDA/ARS Catfish Genetics Research Unit, Thad Cochran National Warmwater Aquaculture Center, Stoneville, MS. Morphological and molecular characterization of a novel species of *Henneguya* found in the gills of farm-raised channel catfish, *Ictalurus punctatus*.

Coffee Break
Thursday Morning, April 11, 2013 10:15 a.m. – 10:30 a.m.

Session II: Byrd-Dunn Student Paper Competition (cont'd)
Thursday Morning, April 11, 2013 10:30 a.m. – 12:00 p.m.
Knicely Conference Center –Room 163 B

Session II Moderators: Katie Reagin and Richard Gerhold
*Presenting Author
‡Byrd-Dunn Student Paper Competitor

10:30 9‡ **ZIEMAN, ELLIOTT A. [*], JOHN REEVE, AND F. AGUSTÍN JIMÉNEZ.** Department of Zoology Southern Illinois University, Carbondale, Illinois 62901. The life cycle, pathogenicity and genetic structure of *Deladenus proximus*, neotylenchid parasite of the woodwasp *Sirex nigricornis* (Hymenoptera).

10:45 10‡ **FAYTON, THOMAS J.*, RICHARD W. HEARD, and ROBIN M. OVERSTREET.** Department of Coastal Sciences, Gulf Coastal Research Laboratory, University of Southern Mississippi, Ocean Springs, Mississippi. Sympatry of 3 undescribed species of *Plagioporus* Stafford, 1904 within a Florida panhandle spring system.

11:00 11‡ **RUSHIN, TIFFANY[*1], ALYSHA SIMMONS[1], ALICE E. HOUK[1], DAVID SCOTT[2], ALEXA C. ROSYPAL[3], AND DAVID S. LINDSAY[1].** [1]Virginia Tech, Blacksburg VA, [2]Carolina Raptor Rehabilitation Center, Huntersville NC., [3]Johnson C. Smith University, Charlotte NC. Identity of *Sarcocystis* species in heart and breast muscle of raptors from the North Carolina Raptor Rehabilitation Center.

11:15 12‡ **HOUK, ALICE E. [*], AND DAVID S. LINDSAY.** Virginia Tech, Blacksburg, VA. *Cystoisospora canis*—a model for Apicomplexan tissue cyst reactivation.

11:30 13‡ **MAYS, SARAH E. [*], BRIAN M. HENDRICKS, AND REBECCA T. TROUT FRYXELL.** Entomology and Plant Pathology Department University of Tennessee, Knoxville TN. Considering *Ixodes scapularis* as a vector of concern in human tick-borne diseases in western Tennessee.

11:45 14‡ **MAESTAS, LAUREN P. [*1] REBECCA T. TROUT FRYXELL[2], AND GRAHAM J. HICKLING[1].** [1]University of Tennessee Center for Wildlife Health, Department of Forestry Wildlife and Fisheries, Knoxville TN. [2]University of Tennessee Medical Veterinary Entomology Lab, Department of Entomology and Plant Pathology, Knoxville TN. Prevalence of *Borrelia* infections in *Ixodes* species (Acari: Ixodidae) collected from the southeastern coastal United States.

12:00 p.m. – 1:15 p.m. Lunch Break

Session III: Byrd-Dunn Student Paper Competition (cont'd) & Afternoon Session I

Thursday Afternoon, April 11, 2013 **1:15 p.m. – 3:00 p.m.**

Knicely Conference Center –Room 163 B

Session III Moderators: Christina Fulghum and Reneé Carleton

*Presenting Author

‡Byrd-Dunn Student Paper Competitor

1:15 15‡ **LEE, JUNG KEUN[*1], WHITNEY CROW SMITH[2], FLAVIA GIRAO FERRARI[3], AND ANDREA VARELA-STOKES[2].** [1] Department of Pathobiology and Population Medicine, Mississippi State University, Mississippi State, MS. [2] Department of Basic Sciences, Mississippi State University, Mississippi State, MS. [3] Merck Animal Health, Desoto, Kansas. Survey of questing *Amblyomma maculatum* (Gulf Coast ticks) in Mississippi for *Borrelia* species.

1:30 16‡ **HENDRICKS, BRIAN [*1], DAVE PAULSEN[1], GRAHAM HICKLING [2], ALLAN HOUSTON[2] AND REBECCA T TROUT FRYXELL[1]** [1]Department of Entomology and Plant Pathology, University of Tennessee Institute of Agriculture, Knoxville.[2]Department of Forestry, Wildlife and Fisheries, University of Tennessee Institute of Agriculture, Knoxville. Distribution of *Ehrlichia* species within *Amblyomma americanum* at Ames Plantation in western Tennessee.

1:45 17‡ **CASEY, SARAH[*1], STEPHAN WILDEUS[2], and ANNE ZAJAC[1].** [1]Virginia Tech, Blacksburg, VA. [2]Virginia State University, Petersburg, VA. Response of alpacas and sheep to experimental *Haemonchus contortus* infection.

2:00 18 **ANDREW, GEORGE, ERIC MCELROY, AND ISAURE DE BURON[*].** Department of Biology, College of Charleston, SC. The Effects of two parasites on swimming performance in the spotted seatrout, *Cynoscion nebulosus*.

2:15 19 **KYLE, DENNIS E. [*1], SASHA V. SIEGEL[1], BEATRICE L. COLON[1], GAYLE P. NOBLET[2], AND ISAURE DE BURON[3].** [1]University of South Florida, [2]Clemson University, [3]College of Charleston. Terebellid polychaetes identified as intermediate hosts for *Cardicola laruei* (Digenea: Aporocotylidae) in spotted sea trout (*Cynoscion nebulosus*).

2:30 20 **JIMÉNEZ[*1], F. AGUSTÍN, BETH BYLES[2], R. PHILIP SCHEIBEL[1] AND SCOTT L. GARDNER[3]** . [1]Department of Zoology, Southern Illinois University Carbondale, Carbondale, IL 62901-6501, [2]College of Veterinary Medicine, University of Illinois, Urbana, IL. [3]The H. W. Manter Laboratory of Parasitology, University of Nebraska, Lincoln, NE 68588-0514. The metazoan parasites of opossums in Bolivia: an inventory of 25% of marsupial diversity

2:45 21 **FAULKNER, CHARLES T.** College of Veterinary and Comparative Medicine, Lincoln Memorial University, Harrogate TN. Why letting a few worms live isn't such a bad thing: Selective deworming as a strategy for mitigating anthelmintic resistance.

Coffee Break
Thursday, April 11, 2013 **3:00 p.m. – 3:30 p.m.**

Session IV: Afternoon Paper Session II
Thursday, April 11, 2013 **3:30 p.m. – 5:15 p.m.**
Knicely Conference Center –Room 163 B

Session IV Moderators: Alysha Simmons and Agustín Jiménez
*Presenting Author

3:30 22 **ZELMER, DEREK A.** Department of Biology and Geology, University of South Carolina Aiken, Aiken, SC. Temporal changes in the parasite community of redbreast sunfish, *Lepomis auritus*, in the Edisto River, SC.

3:45 23 **VARELA-STOKES, ANDREA[*1] AND JOB LOPEZ[2].** [1]Department of Basic Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi. [2] Department of Biological Sciences, Mississippi State University, Mississippi State, MS. *Borrelia turicatae,* an agent of tick-borne relapsing fever, in the canine animal model.

4:00 24 **GERHOLD, RICHARD[*1,2] SHARRON PATTON[1], ALY CHAPMAN[1], GRAHAM HICKLING[2], AND CHUNLEI SU[3].**[1] Department of Biomedical and Diagnostic Sciences, College of Veterinary Medicine, University of Tennessee, Knoxville, TN. [2]The Center for Wildlife Health, The University of Tennessee, Knoxville, TN. [3]Department of Microbiology, The University of Tennessee, Knoxville, TN. Transmission of *Toxoplasma gondii* in Wildlife in the Southeastern US.

4:15 25 **TYML, TOMÁŠ[*1,2], HOLZER, S. ASTRID[2] , McGURK, CHARLES[3], DYKOVÁ, IVA[4], KOSTKA, MARTIN[1,2]**. [1]Faculty of Science, University of South Bohemia, Branišovská 31, 370 05, České Budějovice, Czech Republic. [2]Laboratory of Fish Protistology, Institute of Parasitology, Biology Centre ASCR, Branišovská 31, 370 05, České Budějovice, Czech Republic. [3]Scretting Aquaculture Research Centre, Stavanger, Norway. [4]Department of Botany and Zoology, Faculty of Science, Masaryk University, Kotlářská 2, 611 37 Brno,

Czech Republic. A severe ciliate infection in the Atlantic salmon gills.

4:30 26 **GRIFFIN, MATT J.[*1], SYLVIE QUINIOU[2], LEWIS BOGDANOVIC[3], CYNTHIA WARE[1] AND ESTEBAN SOTO[3,4].** [1]Thad Cochran National Warmwater Aquaculture Center, Aquatic Research and Diagnostic Laboratory, College of Veterinary Medicine, Mississippi State University, Stoneville, MS. [2]Thad Cochran National Warmwater Aquaculture Center, Catfish Genetics Research Unit, United States Department of Agriculture, Agricultural Research Service, Stoneville, MS. [3]Department of Pathobiology, School of Veterinary Medicine, Ross University, Basseterre, St. Kitts, West Indies. [4]Marine Research Laboratory, School of Veterinary Medicine, Ross University, Basseterre, St. Kitts, West Indies. Intraspecific rDNA variability of *Kudoa* sp. isolates from blackfin tuna *(Thunnus atlanticus*) suggests *K. crumena* and *K. thunni* are synonymous.

4:45 27 **CURRAN, STEPHEN S. [*1], VASYL V. TKACH[2], MICHAEL J. ANDRES[1], ERIC E. PULIS[1], AND THOMAS J. FAYTON[1].** The University of Southern Mississippi, Departmentof Coastal Sciences, 703 East Beach Drive, Ocean Springs, MS. [2]University of North Dakota, Department of Biology, Starcher Hall, 10 Cornell Street, Grand Forks, ND. Molecular phylogeny of some intestinal fish flukes belonging in the Apocreadiidae (Digenea: Lepocreadioidea).

5:00 28 **CARLETON, RENEÉ E.** Berry College, Mount Berry, GA. Parasitology goes viral - a review of parasitology on the world wide web.

Social Hour
Thursday, April 11, 2013 **5:30 p.m. – 7:00 p.m.**
Staybridge Suites Hotel – Main Lobby

Dinner (on your own)
Thursday, April 11, 2013 **7:00 p.m. – 8:30 p.m.**

Evening Reception
Thursday, April 11, 2013 **8:30 p.m. – 12:30 a.m.**
Staybridge Suites Hotel – Meeting Room and Patio

Friday Morning, April 12, 2013

Breakfast Buffet (for hotel guests) **6:30 a.m. – 10:00 a.m.**
Staybridge Suites Hotel – Lobby

SSP Business Meeting **10:00 a.m.-11:30 a.m.**
Staybridge Suites Hotel – Main Lobby

Check out and departure.

Sponsored by the College of Arts and Sciences, USC Upstate

and

Office of the Dean
Ogden College of Science and Technology, Western Kentucky University

PRESIDENTIAL SYMPOSIUM ABSTRACTS

I. SMITH, GARRIET. University of South Carolina Aiken, Aiken, SC. Aspergilliosis: History, etiology and response to a pathogen affecting gorgonians.

Coral reefs boast the highest diversity of all marine ecosystems, aid in the development and protection of other important, productive coastal marine communities, and have provided millions of people with food, building materials, protection, recreation, pharmaceutical products, income and social stability. However, they have been rapidly deteriorating in recent times mostly due to a continuous emergence of coral reef diseases and increase in bleaching events correlated with higher than normal water temperatures among other factors. One of these diseases is the fungal infection called aspergillosis (ASP) which has produced widespread mortalities of sea fans (*Gorgonia ventalina*) and other octocorals in the Caribbean since 1983-84. Typical signs include purple pigmentation (an increase in carotenoids in sclerites) around the area of infected, necrotic tissue with fungal hyphae. The putative pathogen was identified as the common terrestrial fungus *Aspergillus sydowii*. However, recent studies showed that other fungi colonizing sea fans can produce the same signs, and that the microbiota seem to be highly dynamic. At least 8 other abundant octocoral species throughout the wider Caribbean have been reported to be affected by ASP. Disease prevalence, incidence, virulence and impact on *G. ventalina* seem to be highly variable at spatial and temporal scales, with some colonies completely recovering after losing more than 95% of live tissues. Several innate immune responses such as melanization, increased concentration of calcium carbonate around the fungal hyphae, as well as, increased carotene in sclerites, have been identified. Recent research showed that ASP can reduce reproductive output of diseased colonies. Long term studies have showed that the prevalence of ASP has been declining in many areas indicating a potential development of resistance to the disease by natural populations.

II. HILLYER, JULIÁN. Vanderbilt University, Nashville, TN. Hemocyte-mediated immune responses and hemolymph flow dynamics in the body cavity of the malaria mosquito, *Anopheles gambiae.*

Mosquitoes are obligate vectors of *Plasmodium* sp. as well as other deadly and debilitating pathogens. A mosquito acquires *Plasmodium* when she ingests an infectious blood meal, and after a period of development and replication in/on the gut, this protozoan parasite enters the main body cavity, called the hemocoel, and migrates to the salivary glands, at which point the mosquito can transmit the infection to an unsuspecting vertebrate host. *Plasmodium*'s obligate migration across the mosquito hemocoel is inefficient, and although the reason for this inefficiency is not completely understood, multiple studies have shown that parasite migration elicits potent immune responses that cause significant pathogen destruction. In this presentation I will first describe the physical journey of malaria sporozoites from the midgut to salivary glands. Then, I will discuss how the structural mechanics of hemolymph circulation affects sporozoite migratory patterns and how the mosquito immune and circulatory systems work in concert to destroy pathogens that are flowing with the hemolymph.

III. LOKER, ERIC S. Center for Evolutionary and Theoretical Immunology, Museum of Southwestern Biology, University of New Mexico, Albuquerque, NM. Celebrating 100 years of snails and schistosomes with a look at *Biomphalaria-Schistosoma mansoni* interactions.

One hundred years ago, Miyairi and Suzuki provided the first evidence for the involvement of snails in the transmission of schistosomes. We have since learned a great deal about the basic biology of schistosomes and their interactions with snails. For example, molecular phylogenetic studies have shown the extent to which host-switching among snails of various families has played a role in diversification of schistosomes. This macroevolutionary pattern is perplexing though, given the high degree of fidelity to their snail hosts demonstrated by lab studies of extant schistosomes. Understanding the mechanisms involved in governing compatibility between snails and schistosomes provides one way to develop a more comprehensive picture of how schistosomes have evolved, and how they persist in the modern world. We have studied interactions between the trematodes Echinostoma paraensei and *Schistosoma mansoni* and their common snail host *Biomphalaria glabrata*, to reveal the general nature of gastropod immunity and the specific nature of anti-schistosome defenses. Successful infection by either trematode species results in down-regulation of many snail immune features. If, however, the parasites are successfully resisted by the snail, then a pattern of up-regulation of immune features is seen. Among the prominent features involved are fibrinogen-related proteins (or FREPs), molecules with IgSF and fibrinogen domains. Snails are capable of producing diversified FREP molecules that have opsonic and adhesive properties consistent with a role in defense. When expression of one particular FREP, FREP3, is knocked down using RNAi, susceptibility to infection can be enhanced. These studies help envision how schistosomes exhibit specificity in their interactions with snails yet may have been compromised in the past, enabling relationships with new snails to develop. Professor Miyairi would be pleased that his seminal work continues to attract considerable interest from parasitologists around the world interested in host-parasite interactions. Supported by NIH grant AI101438 and 1P20RR18754.

PROGRAM ABSTRACTS

1. SIMMONS, ALYSHA, NANCY TENPENNY, AND DAVID S. LINDSAY. Virginia Tech, Blacksburg, VA. Activity of decoquinate against 3 species of cat transmitted *Besnoitia* (Apicomplexa: Sarcocystidae).

Besnoitiosis is an important production problem in ruminants in Africa, Asia and parts of the Middle East. It is an emerging disease of cattle in Europe. Mortality can reach 10% and up to 80% of animals may have signs of disease. Recently besnoitiosis has been increasingly recognized in donkeys *Equus asinus* from the Northeastern United States. In the present study we developed a 24-welled cell culture assay to determine the efficacy of potential treatments. Tachyzoites of *Besnoitia darlingi*, *B. neotomofelis*, and *B. oryctofelisi* were grown in human pigmented retinal epithelial cells (HRE) or human foreskin fibroblast cells (Hs68). Dose titration studies were conducted and we determined that discreet plaques were formed in HRE cells at 3 to 4 days post-inoculation. Plaques that developed in Hs68 cells at 3 to 4 days, were larger and more destructive than those in HRE cells. Drug efficacy was determined by counting the numbers of plaques in control and drug treated wells and determining the percent reduction in number of plaques. Decoquinate is an anticoccidial approved for the treatment of intestinal coccidiosis in cattle in the US. It is believed to target the parasites electron transport chain. Decoquinate was examined at 240, 24, 2.4, 0.2 and 0.02 nM. Decoquinate when used at 2.4 nM completely protected HRE cells from infection with all 3 *Besnoitia* species examined. Decoquinate was cidal for tachyzoites at dosages of 2.4 nM or greater. We are currently conducting additional studies on the mode of action of decoquinate against *Besnoitia*.

2. BOLDEN, LEAH M. Berry College, Rome GA. Ticks on the Berry College campus: a risk assessment and survey of community awareness.

Ticks are common outdoor inhabitants and present concern because they potentially transmit disease-causing organisms. This study was conducted to estimate the risk of tick exposure on the Berry College campus, to determine which tick species are present and to evaluate the Berry community's alertness about these organisms. Tick collections were conducted on various campus locations, including: paved and wooded trails, lawns adjacent to academic buildings, large and small fields which were regularly mowed, along roadsides, and in livestock areas. Berry community members frequenting these areas were asked to complete a questionnaire about their tick encounters and knowledge of tick-borne diseases. Ticks were collected only from a wooded trail, Victory Lake, and only during the months of May through July. Out of a total of 46 ticks, 44 were identified as *Dermacentor variabilis* (96.65%) and the remaining two were *Ixodes scapularis* (2.17%) and *Rhipicephalus sanguineus* (2.17%). Out of 38 questionnaire respondents, 21% had found at least one tick on their person, 89% could name at least one tick transmitted disease and no individuals reported using any tick repellent. Results suggest the risk of encountering ticks is limited to certain on-campus locations and that members of the Berry community have some knowledge of tick-related matters. Funding for this project was provided by the Laura Maddox Smith Summer Institute for Environmental Studies Grant.

3. REAGIN, KATIE, GABRIEL LUGO, AND CHRIS A. HALL. Department of Biology, Berry College, Mount Berry, GA, Distribution and prevalence of *T. cruzi* infection in *Triatoma sanguisuga spp.* from the southeastern United States.

Trypanosoma cruzi is a highly zoonotic, vector-borne protozoan pathogen and the causative agent of Chagas disease in humans. We have conducted an on-going assessment of the endemic sylvatic and peri-domestic cycles of *Trypanosoma cruzi* in the southeastern United States. The principal arthropod vector in the region is *Triatoma sanguisuga*, a haemophagic member of the reduviid family of insects. Our efforts have resulted in the collection of approximately 350 specimens of *T. sanguisuga spp.* from widely dispersed regional sites. Although the majority of the specimens collected were *T. s. sanguisuga*, specimens of *T. s. ambigua* and *T. leticularia* were also found. Of the specimens tested (n = 301), 14.95% were positive for *T. cruzi* infection. All three of the species and subspecies contributed to the pool of positive specimens. Infected individual *triatoma* were found in all but one of the ten sites from which specimens were obtained. Utilizing the D-71/72 primer set to identify *T. cruzi* strain differences showed that 88% of those tested carried the Type I strain. This study confirms that *Trypanosoma cruzi* is widely distributed in the triatomine vector population throughout the southeastern United States. Continued monitoring of vector populations is essential to understanding the endemic cycle and epidemiology of *T. cruzi* in this region.

4. [1]REAGIN, KATIE, [2]CAROL RUCKDESCHEL, AND [1]CHRIS A. HALL. [1]Department of Biology, Berry College, Mount Berry, GA. [2]Cumberland Island Museum of Natural History, Cumberland Island, GA. *Triatoma sanguisuga spp.* population and lifecycle dynamics on a barrier island.

In order to develop a better understanding of the lifecycle and biology of the triatomine vectors of *Trypanosoma cruzi* in the southeastern United States, we undertook a long-term study of a site known to host an active endemic *T. cruzi* cycle. Cumberland Island is the southern most island in the barrier complex of coastal Georgia. Much of this island is maintained as a National Seashore, although significant tracts remain in private hands. Previously we had demonstrated a widespread distribution of *T. cruzi* in numerous mammalian species on the island. To better understand the lifecycle of the dominant vector species on the island a site known to house an active breeding population of *T. sanguisuga sanguisuga* was routinely examined over an 8-year period for population density and seasonal lifecycle stage distributions. Over the period of the study annual oscillations in the vector population density were noted. Results of lifecycle stage assessment revealed that *T. sanguisuga* likely over winter as 3rd or 4th stage nymphs, emerging in early spring to quickly feed and molt to the adult stage. Approximately mid-summer, the adult stages leave the colony to establish new colonies elsewhere. Interestingly, a second site identified on the island was exclusively inhabited by *T. sanguisuga ambigua.* In both subspecies there were seasonal periods in which males clearly dominated the population. We failed to identify similar spikes in the female population. *T. cruzi* positive specimens were found in both sites and subspecies. Efforts are currently underway to further delineate the seasonal cycles associated with reproduction and migration of T. sanguisuga in these sites.

5. FULGHUM, CHRISTINA M. AND DEREK A. ZELMER. University of South Carolina Aiken, Aiken SC. The Role of Spatial and Temporal Heterogeneity in Structuring Trematode Communities in the Freshwater Snail, *Physa pomilia*, from West Pond located in Brick Pond Park, North Augusta, SC.

Community structure in free-living organisms often is influenced by competition, but past literature suggests that competition does not play a structuring role in communities of trematodes

of freshwater snails due to the influence of spatial and temporal heterogeneity. The purpose of this investigation was to determine if spatial and temporal heterogeneity play a role in structuring component communities of trematodes in the freshwater snail, *Physa pomilia*. Four sites in Brick Pond Park, North Augusta, SC, were chosen based on varying habitat characteristics so that potential definitive hosts would differ among the sites. A total of 5556 *Physa pomilia* were collected from these sites over an eleven month period. Snails were isolated in 50 ml polystyrene containers and examined for shed cercariae. Cercariae were isolated and observed in live mounts with neutral red stain or fixed in permanent mounts to facilitate identification. Most trematode species were found to show distinct temporal patterns of prevalence, with waterfowl parasites peaking in the fall and spring and non-migratory vertebrates peaking in the summer. Component community similarity at the sites diverged as the component communities increased in richness and total prevalence suggesting that spatial and temporal heterogeneity interact in their effect.

6. FRANK W. SOVEG, ELLIOTT ZIEMAN, F. AGUSTÍN JIMÉNEZ. Department of Zoology, Southern Illinois University, Carbondale, Illinois 62901-6501. Taxonomic placement of *Rhopalias w*ithin the Echinostomatoidea using three genetic markers.

The genus *Rhopalias* includes six species of trematodes that infect didelphimorph marsupials. Traditionally, these organisms have been characterized and distinguished from related trematodes by the presence of two anterior proboscides armed with spines, which can be invaginated into a muscular pouch. Their relationships with other families in the superfamily Echinostomatoidea remain unclear. Herein, we present a molecular analysis of *Rhopalias* aimed at clarifying their taxonomic standing among the Echinostomatoidae and understanding the evolution of the tentacle and tentacle pouches. Worms were collected in Illinois and Mexico from the Virginia and the four eyed gray opossum. A fragment of the hindbody of the worms was excised and used to isolate DNA and amplify the the mitochondrial cytochrome oxidase C subunit 1 (COX1), nicotinamide adenine dinucleotide dehydrogenase (ND1), and the nuclear internal transcribed spacer region (ITS). The rest of the worms was stained and mounted on permanent slides. The three sets were used in the construction of a datamatrix including homologous sequences available in Genbank. Sequences were aligned and analyzed using maximum likelihood as optimality criterion and Bayesian inference was used to calculate the probability of the branches. In addition, a coalescent model was inferred to reconstruct the species tree for *Rhopalias*. The analysis suggests that *Rhopalias* is closely related to organisms in the families Echinostomatidae (*Isthmiophora* and *Petasiger*) and Cathemasidae (*Cathemasia*). Our findings also suggest a single origin for the tentacles and muscular pouch within members of Echinostomatoidea.

7. ANDRES, MICHAEL J. AND ROBIN M. OVERSTREET. Gulf Coast Research Laboratory, The University of Southern Mississippi, Ocean Springs, MS. Molecular phylogeny of the trematode family Opecoelidae.

The Opecoelidae is one of the largest trematode families restricted primarily to fishes. It occurs in freshwater, brackish, and marine fishes, including some from the deep sea. Understanding the systematics of the group is difficult because of the relatively unspecialized features of its members, the acceptance of several poorly defined genera, and the great species diversity within the family. The Opecoelidae is presently comprised of 4 recognized subfamilies: Opecoelinae, Opecoelininae, Stenakrinae, and Plagioporinae. Though a few previous authors suggest the latter may be paraphyletic. To date, molecular phylogenetic studies of the family have been based on a few representatives, aimed at elucidating life-cycles, focused on determining the placement of

the family within the Digenea, or used to establish the affinity of a particular species. This study investigates the molecular interrelationships of members of the 2 principle subfamilies of opecoelids to examine for paraphyly of the Plagioporinae based on partial sequences of the nuclear 28S rRNA gene. Our phylogeny is built from 5 species of Opecoelinae, 19 species of Plagioporinae, and 2 species of *Paragonimus*, as outgroups. Our estimated phylogeny strengthens the paraphyly of the Plagioporinae, shows a surprisingly close affinity of deep-water and freshwater plagioporines, and reveals a grouping of shallow-water marine plagioporines. This study was supported by NSF No. 0529684; NOAA, OHHI award NA08NOS4730322; and USWFP CIAP, award M10AF20151 MS.R.798.

8. ROSSER, THOMAS G.[1], MATT J. GRIFFIN[1,2], SYLVIE QUINIOU[3], LESTER H. KHOO[1,2], AND LINDA M. POTE[1]. [1]College of Veterinary Medicine, Mississippi State University, Mississippi State, MS. [2]Aquatic Research and Diagnostic Laboratory, Thad Cochran National Warmwater Aquaculture Center, Mississippi State University, Stoneville, MS. [3]USDA/ARS Catfish Genetics Research Unit, Thad Cochran National Warmwater Aquaculture Center, Stoneville, MS. Morphological and molecular characterization of a novel species of *Henneguya* found in the gills of farm-raised channel catfish, *Ictalurus punctatus*.

Channel catfish *Ictalurus punctatus* is host to at least eight different species of myxozoan parasites in the genus *Henneguya*. Four of these species have been molecularly characterized; however, the life cycles of only two have been experimentally and molecularly confirmed. Some of these species can illicit severe pathology upon infection, such as *H. ictaluri*, the causative agent of proliferative gill disease in cultured channel and hybrid catfish. Recently, during a routine health screening of farm-raised channel catfish, several fish presented with deformed primary lamellae harboring nodular white cysts approximately 1.25 mm in diameter. These cysts contained numerous *Henneguya* myxospores, with a lanceolate shaped spore body 17.1 ± 1.0 μm (mean ± SD; range = 15.0-19.3 μm) in length and 4.8 ± 0.4 μm (3.7-5.6 μm) in width. Pyriform shaped polar capsules were 5.8 ± 0.3 μm in length (5.1-6.4 μm) and 1.7 ± 0.1 μm (1.4-1.9 μm) in width. The two caudal processes were 40.0 ± 5.1 μm in length (29.5-50.0 μm) with a total spore length of 57.2 ± 4.7 (46.8-66.8 μm). The contiguous 18S rRNA sequence generated from five excised cysts did not match any *Henneguya* spp. currently in GenBank. The greatest sequence homology (91% over 1900 bp) was to *Henneguya pellis*, a parasite associated with blister-like lesions on the skin of blue catfish, *Ictalurus furcatus*. Based on the unique morphology and 18S rRNA sequence of this isolate, we believe this isolate to be a previously undocumented species of the genus *Henneguya*.

9. ZIEMAN, ELLIOTT A., JOHN REEVE, AND F. AGUSTÍN JIMÉNEZ. Department of Zoology Southern Illinois University, Carbondale, Illinois 62901. The life cycle, pathogenicity and genetic structure of *Deladenus proximus*, neotylenchid parasite of the woodwasp *Sirex nigricornis* (Hymenoptera).

Deladenus proximus (Neotylenchidae) is a nematode associated to pine trees and to the woodwasp, *Sirex nigricornis* (Hymenoptera), previously little was known on the geographic distribution and variability of *D. proximus*. We present information relative to their life cycle, pathogenicity, and variability. Our study indicates variable prevalence across localities and years. Infected wasps were sterilized as indicated by presence of nematodes in eggs. From 2009-2012 1,635 woodwasps were collected from four locations. Woodwasps were dissected and live

nematodes reared on cultures of *A. chailletii* and examined upon maturation. Reared nematodes were compared against type specimens of *D. ipini* and published descriptions of *D. proximus.* Reared specimens possess a conspicuous post uterine sac, which is the proposed diagnostic character of *D. ipini*. This and other morphometric differences suggest that *D. ipini* is a junior synonym of *D. proximus*. DNA was isolated and amplified from individual nematodes. Nuclear DNA was invariable from all 4 locations and had 99% identity to the invasive species *Deladenus siricidicola*. Analysis of mitochondrial DNA showed more variability and was used to evaluate the distinction of populations across these localities. The analysis of a portion of COX1 suggests the presence of 8 haplotypes and the absence of any geographic clusters or subpopulations. The pattern of transmission of this nematode and pathogenicity is similar to that of *Deladenus siricidicola*, which is used as a biocontrol against the invasive species *Sirex noctilio*. Experimental infections of *Deladenus proximus* in *Sirex noctilio* are recommended to test their viability as a biocontrol agent.

10. FAYTON, THOMAS J., RICHARD W. HEARD, and ROBIN M. OVERSTREET. Department of Coastal Sciences, Gulf Coastal Research Laboratory, University of Southern Mississippi, Ocean Springs, Mississippi. Sympatry of 3 undescribed species of *Plagioporus* Stafford, 1904 within a Florida panhandle spring system.

Although 21 valid species of plagioporines (Digenea: Opecoelidae) representing 7 genera have been described from North American freshwater hosts, undocumented diversity persists within these trematodes in Neartic freshwater habitats. We report 3 species of *Plagioporus* Stafford, 1904 that occur sympatrically in Williford Spring, an artesian spring in the panhandle of Florida. Data on the prevalence of these digenean species across time in a single spring-associated cyprinid definitive host, *Notropis harperi* Fowler, 1941, is presented. The three opecolids occur in either in the gall bladder (*Plagioporus* sp. A) and the upper half or lower third of the intestine (*Plagioporus* sp. B and *Plagiopourus* sp. C, respectively) of their definitive host. We review and expand upon the literature on sympatry previously observed among plagioporines from freshwater hosts of the Nearctic and discuss the difficulties associated with the taxonomy and life history studies associated with sympatric species of plagioporids.

11. RUSHIN, TIFFANY[1], ALYSHA SIMMONS[1], ALICE E. HOUK[1], DAVID SCOTT[2], ALEXA C. ROSYPAL[3], AND DAVID S. LINDSAY[1]. [1]Virginia Tech, Blacksburg VA, [2]Carolina Raptor Rehabilitation Center, Huntersville NC., [3]Johnson C. Smith University, Charlotte NC. Identity of *Sarcocystis* species in heart and breast muscle of raptors from the North Carolina Raptor Rehabilitation Center.

Protozoal encephalitis due to *Sarcocystis* species has been observed in bald eagles, golden eagles, and great horned owls from the United States. Sarcocysts were observed in the skeletal muscles of bald and golden eagles and possibly the great horned owl. Schizonts were observed in lung tissue of the eagles. Immunohistochemistry and PCR studies indicated that a *S. falcatula*-like species was the cause of the disease. To determine the prevalence of muscular *Sarcocystis* and determine the species identity we examined the muscles of raptors submitted to the North Carolina Raptor Rehabilitation Center, Huntersville, NC for treatment and rehabilitation. Birds that died or were humanely euthanized due to poor clinical prognosis were used in the present study. Hematoxylin and eosin (H&E) stained tissue sections of heart and breast muscle were examined microscopically for parasites. DNA was isolated from heart and breast muscle of H&E positive samples using PCR primers JNB 34/55 for *Sarcocystis neurona*/*S. falcatula*/*S. lindsayi*,

and ITS primers 859L/851H for *Sarcocystis* species. Sarcocysts were observed more often in breast muscle than in heart. Sarcocysts were microscopic. We are presently examining DNA from muscle samples using PCR for *S. calchasi* a recently described pathogen of pigeons that completes its life cycle in hawks in the genus *Accipiter*. Supported in part by a grant from the Historically Black Universities and Colleges-Undergraduate Program (HBCU-UP) and Smith Institute for Applied Research grant to ACR and an IRC grant from Virginia Tech to DSL.

12. HOUK, ALICE E., AND DAVID S. LINDSAY. Virginia Tech, Blacksburg, VA. *Cystoisospora canis*—a model for Apicomplexan tissue cyst reactivation.

Cystoisospora canis are parasites of the small intestine of dogs that can cause diarrhea in young dogs. Biologically *C. canis* is similar to *C. belli* which causes intestinal coccidiosis in humans, especially those with AIDS. Relapse often occurs in *C. belli* patients due to reactivation of monozoic tissue cysts (MZT) in lymph nodes and re-colonization of the gut. *C. canis* also produces MZT that are similar to the polyzoic tissue cyst of *Toxoplasma gondii*, a parasite of medical and veterinary importance, which can reactivate and cause Toxoplasmic encephalitis. We hypothesized that *C. canis* would be a novel model for studying tissue cyst biology. Oocysts were collected from experimentally infected beagles, purified, sporulated, and sterilized in bleach prior to excystation. Sporozoites were released from sporocysts in excystation solution for inoculations. We infected 8 cell lines and observed MZT formation and no multiplication in all cell lines studied. Excystation solution induced motility in zoites present in MZT, zoites exited the intact tissue cysts, and were then able to penetrate new cells and develop into new MZT. We were able to demonstrate that the zoites remained infective for up to 4 cycles of encystment and reactivation from MZT. In other tissue cyst systems, replicative stages occur prior to tissue cyst wall formation and induction of dormancy but in our system this is not the case making studying the tissue cyst less complex. Our system provides a simple model to produce tissue cysts and to study host factors that cause reactivation of tissue cysts.

13. MAYS, SARAH E., BRIAN M. HENDRICKS, AND REBECCA T. TROUT FRYXELL. Entomology and Plant Pathology Department University of Tennessee, Knoxville TN. Considering *Ixodes scapularis* as a vector of concern in human tick-borne diseases in western Tennessee.

The status of tick-borne diseases (TBD) in the southeastern US is uncertain due to the identification of new pathogens, the spread of existing diseases, the misdiagnosis of disease, and warming weather trends. *Ixodes scapularis* (the black-legged tick) is known to transmit the causal agents of Anaplasmosis (*Anaplasma phagocytophilum*), Babesiosis (*Babesia microti*), Lyme disease (*Borrelia burgdorferi*), and Rickettsiosis (*Rickettsia montanensis*). Recently, incidences of TBD have been reported at Ames Plantation Research and Education Center (AMES) located in western Tennessee, and personal correspondence suggests TBD incidence may be on the rise. The objective of this study was to determine if future *I. scapularis* research in western Tennessee is warranted by screening 17 adult *I. scapularis* collected from white-tailed deer for five common TBD genera. In the fall of 2012, 17 adult *I. scapularis* were collected from 6 white-tailed deer harvested at AMES, and were PCR screened for infection with *Anaplasma, Babesia, Borrelia, Ehrlichia*, and *Rickettsia* species with genera-specific primers. None of the ticks tested positive for *Borrelia*, *Babesia*, or *Ehrlichia* species. A total of 10 ticks (59%) tested positive for 3 different non-pathogenic *Rickettsia* species. One tick tested positive

for both a *Rickettsia* species (uncultured *Rickettsia*) and *Anaplasma phagocytophilum* (97% homologous to Genbank EF647585), the causal agent of Human Anaplasmosis. Finding *A. phagocytophilum* in *I. scapularis* merits additional studies surveying pathogen prevalence in *I. scapularis* at AMES, both because of the risk of human exposure to disease agents, and to aid in accurate diagnosis of TBD cases in western Tennessee.

14. MAESTAS, LAUREN P.[1] REBECCA T. TROUT FRYXELL[2], AND GRAHAM J. HICKLING[1]. [1]University of Tennessee Center for Wildlife Health, Department of Forestry Wildlife and Fisheries, Knoxville TN. [2]University of Tennessee Medical Veterinary Entomology Lab, Department of Entomology and Plant Pathology, Knoxville TN. Prevalence of *Borrelia* infections in *Ixodes* species (Acari: Ixodidae) collected from the southeastern coastal United States.

The classic Lyme borreliosis (LB) cycle, involving the vector *Ixodes scapularis* and the etiological agent *Borrelia burgdorferi s.s.* (*Bbss*), has been well documented in the Northeastern US, where this disease is becoming increasingly prevalent in humans and canines. In the Southeast, however, human LB prevalence is much lower and the disease cycle is not well understood. We are investigating whether the geographic pattern of human disease corresponds with geographic variation in *Bbss* prevalence in the vector ticks. We have found much higher rates of *Borrelia* spp. infection among *I. affinis* than *I. scapularis* from Virginia through northern coastal North Carolina (NC), which confirms a similar recent finding in NC. Although active at different times of year, these two tick species are morphologically challenging to discriminate and only *I. scapularis* is known to bite humans. Winter counts of *I. scapularis* increased as we surveyed southwards into South Carolina and Florida, yet to date we have found no infected ticks of either species south of middle NC, which thus appears to represent a line of demarcation for the southwards spread of the Northeastern Lyme disease endemic region. Further spring tick counts during the peak seasonal activity period of *I.affinis* are planned, to test hypotheses about the relative importance of these two species in the LB cycle. Preliminary data with regard to southwards spread of northern-clade *I. scapularis* will also be discussed.

15. LEE, JUNG KEUN[1]*, WHITNEY CROW SMITH[2]*, FLAVIA GIRAO FERRARI[3], AND ANDREA VARELA-STOKES[2]. [1] Department of Pathobiology and Population Medicine, Mississippi State University, Mississippi State, MS. [2] Department of Basic Sciences, Mississippi State University, Mississippi State, MS. [3] Merck Animal Health, Desoto, Kansas. * These authors contributed equally to this work. Survey of questing *Amblyomma maculatum* (Gulf Coast ticks) in Mississippi for *Borrelia* species.

Borrelia species are causative agents for Lyme disease and relapsing fever. In the United States, the primary vector for Lyme disease is the hard tick, *Ixodes scapularis,* while vectors for relapsing fever are soft ticks in the genus *Ornithodoros.* Relapsing fever-type borreliae have also been found in hard ticks. For example, *B. miyamotoi* in *I. scapularis* was recently associated with human disease, while *B. lonestari* is found in *Amblyomma americanum,* although disease potential for *B. lonestari* is unclear. Both *B. burgdorferi* and *B. lonestari* were recently detected in *Amblyomma maculatum*. In this study, DNA extracts from 306 questing adult *A. maculatum* collected in Mississippi were tested for *Borrelia* spp. DNA by PCR amplification of *Borrelia* spp. *flaB* and 16S rDNA targets, and amplicons sequenced. 16S rDNA amplicons from two tick extracts were 97 to 98% identical to various *Borrelia* spp. including *B*. spp. "tAG158M", *B. turcica*, and *B. hermsii*; *flaB* amplicons from these two ticks were 89% and 95% identical to *B.*

turcica. These two ticks were collected from the same location in central Mississippi. Three other tick extracts had 100% *flaB* sequence identity to *B. hermsii* or *B. burgdorferi*. However, these were negative using the 16S rDNA target. These results demonstrate a *Borrelia* sp. in unfed *A. maculatum* ticks that appears unique from other species in the NCBI database. Further characterization of this *Borrelia* sp., though detected in only 2/306 (0.6%) of sampled ticks, is necessary to explore implications for occurrence and diagnosis of borreliosis in the South.

16. HENDRICKS, BRIAN [1], DAVE PAULSEN[1], GRAHAM HICKLING [2], ALLAN HOUSTON[2] AND REBECCA T TROUT FRYXELL[1] [1]Department of Entomology and Plant Pathology, University of Tennessee Institute of Agriculture, Knoxville.[2]Department of Forestry, Wildlife and Fisheries, University of Tennessee Institute of Agriculture, Knoxville. Distribution of *Ehrlichia* species within *Amblyomma. americanum* at Ames Plantation in western Tennessee.

The status of tick-borne diseases (TBD) in the southeastern United States is uncertain due to a number of factors but not limited to emerging pathogens, misdiagnoses, and modifications to landscapes. Ehrlichiosis is one of the most common TBDs in Tennessee; consequently, the objective of this study was to identify and locate different species of *Ehrlichia* associated with *Amblyomma americanum* in western Tennessee. Ticks were collected from April to September 2012, using vegetation drags for passive collections and CO_2 traps for active collections. Adult *A. americanum* (n = 926) were screened to determine the prevalence of *Ehrlichia*. Positive samples were sequenced to confirm pathogen identity and mapped with ArcGIS to determine the location of each pathogen. A total of 18 *A. americanum* (1.9%) were PCR positive for *Ehrlichia* spp, and were collected during the months of May, July, and August from 14 different sites. Several of the *Ehrlichia* species identified were previously implicated in human cases of TBD and may be responsible for the Ehrlichiosis cases reported at the research center. Further investigation is warranted to understand the role *A. americanum* and other ticks species serve in the transmission cycle of Ehrlichiosis in western Tennessee.

17. CASEY, SARAH[1], STEPHAN WILDEUS[2], and ANNE ZAJAC[1]. [1]Virginia Tech, Blacksburg, VA. [2]Virginia State University, Petersburg, VA. Response of alpacas and sheep to experimental *Haemonchus contortus* infection.

Haemonchus contortus is a nematode of the small ruminant abomasum. Heavy infections may cause anemia and death. Alpacas are South American camelids first introduced into the U.S. in the 1980s. Although not true ruminants, alpacas can be infected with *H. contortus* and develop disease. Previous research suggests alpacas may be more resistant to infection than cograzed sheep. We hypothesized that, given equal exposure to *H. contortus*, alpacas would be less susceptible than sheep to experimental infection. Twenty four adult male alpacas and 12 rams were administered *Haemonchus contortus* infective larvae orally in the following groups: 1) 20,000 larvae as a single dose (alpacas and rams), 2) 20,000 larvae in daily doses of 4,000 larvae for 5 days (alpacas and rams), 3) 50,000 larvae once (alpacas) and 4) 50,000 larvae in daily doses of 10,000 larvae for 5 days (alpacas). Fecal samples were collected every 2 days from 14 to 42 days post infection and then at 5 day intervals until day 62. Blood samples were collected weekly for determination of packed cell volume (PCV). Weight and body condition scores were evaluated weekly. Overall, alpacas responded differently to infection than sheep. Average fecal

egg counts were lower in alpacas than rams. Average alpaca PCV were affected less by infection than ram PCV. We conclude that the results support the hypothesis that alpacas are less susceptible to *H. contortus* infection than sheep.

18. GEORGE ANDREW, ERIC MCELROY, AND ISAURE DE BURON. Department of Biology, College of Charleston, SC. The Effects of two parasites on swimming performance in the spotted seatrout, *Cynoscion nebulosus*.

Parasites are often associated with detrimental impacts on host physiology, but very few studies have examined the impact of parasites on the swimming performance of fish. In this study, we aimed to determine the impacts of two parasite species, *Cardicola laruei* (Aporocotylidae) and *Kudoa inornata* (Myxosporea), on the swimming performance of spotted seatrout, *Cynoscion nebulosus*. We measured burst (anaerobic) and endurance (aerobic) swimming performance of 18 fish using a swimming flume. Many of the fish (72%) were infected with *C. laruei*, and a significant positive relationship was found between density of infection and endurance swimming performance. All of the fish (100%) were infected with *K. inornata* and a significant positive relationship was found between density of infection and burst swimming performance. These results suggest that these parasites are aiding, rather than impeding, swimming performance.

19. KYLE, DENNIS E.[1], SASHA V. SIEGEL[1], BEATRICE L. COLON[1], GAYLE P. NOBLET[2], AND ISAURE DE BURON[3]. [1]University of South Florida, [2]Clemson University, [3]College of Charleston. Terebellid polychaetes identified as intermediate hosts for *Cardicola laruei* (Digenea: Aporocotylidae) in spotted sea trout (*Cynoscion nebulosus*).

Aporocotylidae comprises a diverse family of fish blood flukes, with adults found in the blood or body cavity of marine, brackish, or freshwater fish. Aporocotylids are unique among Digenea with development of larval forms in polychaetes (Annelida) or bivalves. Few cercariae of the family Aporocotylidae have been described previously and the complete life cycle has been elucidated for only two species that develop in marine polychaetes. Examination of *Enoplobranchus sanguineus* and *Amphitrite ornata*, both terebellid polychaetes collected from the South Carolina (SC) coast revealed infections with sporocysts and cercariae not previously described. The cercariae observed from *E. sanguineus* and *A. ornata* most closely resemble the cercariae of the family Aporocotylidae. The morphological characteristics of the cercariae include being apharyngeate, brevifurcate, and possessing an anterior organ instead of an oral sucker. Analysis of ITS-2 sequences from sporocysts and cercariae revealed 100% identity of sporocysts dissected from the coelom of both polychaetes. Whereas lsrDNA and ITS-2 sequences revealed close identity with the *Cardicola* clade of the Aporocotylidae, these were not identical to any sequence available from GenBank. Conversely, ITS-2 sequences were 100% identical to those of adult *Cardicola laruei* collected from local spotted seatrout *Cynoscion nebulosus*. This parasite is highly prevalent in SC and our results confirmed conspecific infections in spotted seatrout and the terebellid polychaetes. This is the first report of larval aporocotylids in *E. sanguineus* and *A. ornata* and the first life cycle of aporocotylid discovered in the western Atlantic Ocean.

20. F. AGUSTÍN JIMÉNEZ[1], BETH BYLES[2], R. PHILIP SCHEIBEL[1] AND SCOTT L. GARDNER[3] . [1]Department of Zoology, Southern Illinois University Carbondale, Carbondale, IL 62901-6501, [2]College of Veterinary Medicine, University of Illinois, Urbana, IL. [3]The H. W. Manter Laboratory of Parasitology, University of Nebraska, Lincoln, NE 68588-0514. The metazoan parasites of opossums in Bolivia: an inventory of 25% of marsupial diversity

The diversity of marsupials in Bolivia includes 27 species from the orders Didelphimorphia and Paucituberculata that have been recorded from almost all biomes of the country. This number of species roughly represents a quarter of the marsupial diversity in the New World. Herein, we present the helminthological records for 16 of these species, which include 21 species of nematodes, 3 species of tapeworms and 2 species of trematodes. Our results show that species of didelphimorph marsupials or opossums share up to 60% of their parasites and that these parasites occur over vast areas of the country. With the exception of two species, most parasites are known to infect only marsupials and correspond to taxa that appear to be specific to these mammals. However, the phylogenetic reconstructions of Viannaiidae, Oxyuridae, and Aspidoderidae reveal that the sister taxa for these groups occur in caviomorph rodents, armadillos, and even monkeys. These phylogenies indicate that the diversity of these parasites resulted from events of host switching and subsequent adaptive diversification.

21. FAULKNER, CHARLES T. College of Veterinary and Comparative Medicine, Lincoln Memorial University, Harrogate TN. Why letting a few worms live isn't such a bad thing: Selective deworming as a strategy for mitigating anthelmintic resistance.

Anthelmintic resistance is the inevitable consequence of intense selection pressure from the use of highly effective drugs on parasitic nematode populations. *Hemonchus contortus* is the most pernicious parasite affecting small ruminants in the Southeast and has been the target of suppressive deworming strategies carried out by producers for the last 25 years. The impact of this strategy has resulted in the widespread establishment of parasite strains that demonstrate genetic resistance to all major classes of deworming products. Selective deworming of "*wormy"* animals is based on the premise that parasite populations are over-dispersed in their host populations. Deworming animals with the highest parasite egg counts reduces hazardous pasture contamination and reinfection, and has the potential to maintain genetic susceptibility to anthelmintic products. Analysis of fecal samples collected from an East TN sheep flock demonstrated that approximately 30% of the sheep were responsible 85% of the total fecal egg count. Deworming the high egg count shedding animals resulted in a 72% decrease in the flock's total fecal egg count over the one year observation period.

22. ZELMER, DEREK A. Department of Biology and Geology, University of South Carolina Aiken, Aiken, SC. Temporal changes in the parasite community of redbreast sunfish, *Lepomis auritus*, in the Edisto River, SC.

Previous examination of the parasite communities of redbreast sunfish (*Lepomis auritis*) from sites along the Edisto River, SC, demonstrated that the patterns of parasite community similarity were more similar to patterns of host community similarity than to patterns indicative of extrinsic or intrinsic abiotic influences, or site continuity. Although these results suggest that parasite community structure is a reflection of host community structure, the lack of a temporal component precludes drawing any conclusions regarding changes in parasite communities in

response to host changes. To examine the extent to which parasite communtiy structure changed as host communities changed, fished and invertebrates were sampled from a single locality (Davis Bridge Landing) on the south fork of the Edisto River over an 11 month period. Redbreast sunfish were transported on ice, and frozen until necropsy. The component community structure of parasites of redbreast sunfish did not covary with any of the habitat parameters examined, and did not correspond to existing patterns of host community similarity. Introducing a time lag of one month, however, produced a close association between parasite community similarity and fish community similarity.

23. VARELA-STOKES, ANDREA[1] AND JOB LOPEZ[2]. [1]Department of Basic Sciences, College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi. [2] Department of Biological Sciences, Mississippi State University, Mississippi State, MS. *Borrelia turicatae,* an agent of tick-borne relapsing fever, in the canine animal model.

Tick-borne relapsing fever is recognized in humans, although various wildlife species, particularly rodents, may serve as reservoirs for the spirochetal agents. The vectors for relapsing fever in the United States are *Ornithodoros* spp., argasid ticks found in arid regions where they often reside in nesting/sleeping areas of hosts. Among *Borrelia* spp. that cause relapsing fever, *Borrelia turicatae* is unusual in having been recently associated with spirochetemia and clinical signs in dogs from Texas. This suggests that canids may serve as reservoirs for *B. turicatae*. Further, canids may be a more appropriate model for studying relapsing fever than the current murine model. In this pilot study, five *B. turicatae*-infected *Ornithodoros turicata* were allowed to feed to repletion on a 6-month-old hound. Two febrile episodes, coinciding with lethargy, depression, and increased numbers of spirochetes in blood, occurred 8 and 12 days after tick feeding. Blood abnormalities included low platelet numbers during febrile episodes; most abnormalities resolved a week later. No other episodes occurred. The hound was eventually treated with doxycycline and is currently healthy. It is unclear whether canids recover from infection or if spirochetes circulate at undetectable levels, potentially also residing in immune privileged sites. Although only one animal was used, the presence of detectable spirochetes as well as clinical signs suggests disease is possible in canids and they may be a relevant model for human disease. Results open new avenues of investigation that include identifying diagnostic antigens for human relapsing fever and understanding the role of canids in natural maintenance.

24. GERHOLD, RICHARD[1,2] SHARRON PATTON[1], ALY CHAPMAN[1], GRAHAM HICKLING[2], AND CHUNLEI SU[3].1 Department of Biomedical and Diagnostic Sciences, College of Veterinary Medicine, University of Tennessee, Knoxville, TN. [2]The Center for Wildlife Health, The University of Tennessee, Knoxville, TN. [3]Department of Microbiology, The University of Tennessee, Knoxville, TN. Transmission of *Toxoplasma gondii* in Wildlife in the Southeastern US.

Toxoplasmosis, caused by *Toxoplasma gondii*, is one of the most common infections of humans and animals worldwide. Toxoplasmosis is considered one of the Neglected Parasitic Infections, which is a group of parasitic diseases that has been targeted by the Centers of Disease Control and Prevention for public health action. Infection of *T. gondii* can occur by ingestion of

microscopic oocysts in contaminated food or water or by ingestion of tissue cysts in undercooked meat. Genotyping has disclosed that *T. gondii* isolates can be divided into six different groups that are associated with varying degrees of virulence with some being highly virulent. *Toxoplasma gondii* infection occurs in many wild birds and mammals; however, genotype data for isolates from these hosts are lacking. Previous studies of isolates from US wildlife suggest that wild species maintain a greater diversity of *T. gondii* genotypes than is found in agricultural animals – suggesting a wild/feral animal diversity model. To further understand the diversity of *T. gondii* in southeastern US wildlife, we screened sera from multiple wild bird and mammal species for *T. gondii* exposure via the modified agglutination test. Heart or tongue from select seropositive animals was digested and inoculated into mice to propagate *T. gondii* tachyzoites. Tachyzoites were genotyped by multiplex multilocus nested PCR-RFLP method employing 10 genetic markers. Of the 204 sampled wild animals, 74 (36.3%) were seropositive. Genotyping results of nine white-tailed deer and one mink disclosed five distinct strains, including the type 12 and type III lineages common in US wildlife, two other previously identified genotypes, and one novel genotype. We conclude that *T. gondii* is prevalent in wildlife from the southeastern US and that further research is needed to understand *T. gondii* diversity, transmission dynamics among wildlife, and the associated potential for human infection with these wild/feral animal genotypes.

25. TYML, TOMÁŠ[1,2], HOLZER, S. ASTRID[2] , McGURK, CHARLES[3], DYKOVÁ, IVA[4], KOSTKA, MARTIN[1,2]. [1]Faculty of Science, University of South Bohemia, Branišovská 31, 370 05, České Budějovice, Czech Republic. [2]Laboratory of Fish Protistology, Institute of Parasitology, Biology Centre ASCR, Branišovská 31, 370 05, České Budějovice, Czech Republic. [3]Scretting Aquaculture Research Centre, Stavanger, Norway. [4]Department of Botany and Zoology, Faculty of Science, Masaryk University, Kotlářská 2, 611 37 Brno, Czech Republic. A severe ciliate infection in the Atlantic salmon gills.

A total of 18 strains of free-living amoebae other than *Neoparamoeba* spp. and 6 strains of scuticociliates were isolated from gills of 36 farmed Atlantic salmon exhibiting gross lesions resembling amoebic gill disease (AGD). Histology and specific PCR did not detect any *Neoparamoeba* sp. in gills of these fish. On histology sections were found a large number of ovoid cells which replaced epithelium between secondary gill lamellae. This infection process was accompanied by hyperplasia of the gill epithelium. Details of cell structure discernible in histological sections stained with protargol tentatively identify the histophagous ciliates with the isolated strains of Scuticociliatida. To the best of our knowledge, this is the first report on histophagous ciliates in farmed Atlantic salmon, pathogenicity of which is confirmed by histological examination.

26. GRIFFIN, MATT J.[1], SYLVIE QUINIOU[2], LEWIS BOGDANOVIC[3], CYNTHIA WARE[1] AND ESTEBAN SOTO[3,4]. [1]Thad Cochran National Warmwater Aquaculture Center, Aquatic Research and Diagnostic Laboratory, College of Veterinary Medicine, Mississippi State University, Stoneville, MS. [2]Thad Cochran National Warmwater Aquaculture Center, Catfish Genetics Research Unit, United States Department of Agriculture, Agricultural Research Service, Stoneville, MS. [3]Department of Pathobiology, School of Veterinary Medicine, Ross University, Basseterre, St. Kitts, West Indies. [4]Marine Research Laboratory, School of Veterinary Medicine, Ross University, Basseterre, St. Kitts, West Indies. Intraspecific rDNA variability of *Kudoa*

sp. isolates from blackfin tuna *(Thunnus atlanticus*) suggests *K. crumena* and *K. thunni* are synonymous.

Numerous myxozoan cysts (~1 mm) were found in the musculature of blackfin tuna (*Thunnus atlanticus*) harvested off the Caribbean island of St. Kitts. Myxospores were consistent with quadrate members of the Kudoidae, measuring 8.8 (8.2-9.4) µm wide, 7.3 (6.6-8.3) µm thick and 6.2 (5.8-6.9) µm long with 4 uniform drop-like polar capsules measuring 2.7 (2.2-3.2) µm long and 2.0 (1.7-2.2) µm wide. The 18S small-subunit (*SSU*) and 28S large-subunit (*LSU*) ribosomal DNA sequences did not result in 100% matches to any published sequences. The *SSU* sequences (1,786 bp) obtained from 6 individual cysts were identical, demonstrating high homology to *K. crumena* (99.6%) from yellowfin tuna (*Thunnus albacares*) and *K. thunni* (99.0%) from albacore (*Thunnus alalunga*). Alternatively, 33 unique sequences were obtained for the *LSU* (~800 bp), demonstrating 0.1 to 5.0% variability between them, although most (60%) demonstrated high homology (>99%) to *K. crumena* and *K. thunni*. Comparatively, *SSU* and *LSU* sequences of *K. crumena* and *K. thunni* differ by 1.6% and 0.6%, respectively. Morphologically, the case isolate was smaller than published descriptions of *K. thunni* or *K. crumena,* however, rDNA sequence homology suggests this case isolate and *K. thunni* are morphologic and genetic variants of *K. crumena* from different hosts.

27. CURRAN, STEPHEN S.[1], VASYL V. TKACH[2], MICHAEL J. ANDRES[1], ERIC E. PULIS[1], AND THOMAS J. FAYTON[1]. The University of Southern Mississippi, Departmentof Coastal Sciences, 703 East Beach Drive, Ocean Springs, MS. [2]University of North Dakota, Department of Biology, Starcher Hall, 10 Cornell Street, Grand Forks, ND. Molecular phylogeny of some intestinal fish flukes belonging in the Apocreadiidae (Digenea: Lepocreadioidea).

The Apocreadiidae is a family of fish flukes consisting of 3 subfamilies: the Postporinae (1 species) from the Caribbean Sea; the Schistorchiinae (12 species in 5 genera) all from the Indo-Pacific Ocean; and the Apocreadiinae (64 species in 12 genera), which is cosmopolitan, mostly marine in the Atlantic and Indo-Pacific Oceans, with 2 genera (*Crassicutis* and *Homalometron*) also having species in brackish and freshwater in the Americas, and 2 monotypic freshwater genera (1 in South America, 1 in Africa). The family has relatively unspecialized and unremarkable morphology and is distinguished from the rest of the Lepocreadioidea by the absence of a cirrus sac and cirrus, and minor differences in cercarial morphology (based on knowledge of life history stages from 8 freshwater and brackish American apocreadiines). The present study investigates the interrelationships among 25 species in 4 genera of Apocreadiinae, and 2 species in the Schistorchiinae. Partial fragments of the 28S rDNA gene from the investigated species are subjected to phylogenetic analyses rooted by 3 species in the Cryptogonimidae. Resulting phylograms suggest that 3 of the apocreadiine genera are polyphyletic. The Apocreadiidae as presently classified needs revision. New and existing life history data from representative species in 2 of these genera from freshwater and brackish habitats in the southeastern United States are found to be helpful for reevaluating the classification of the Apocreadiinae. This material is based on work supported by the National Science Foundation no. 0529684, RAPID 1055071, USDC-NOAA award no. NA08NOS4730322, and Mississippi Department of Marine Resources Sub-Grant S-11-USM-GCRL.

28. CARLETON, RENEÉ E. Berry College, Mount Berry, GA. Parasitology goes viral - a review of parasitology on the world wide web.

What would we do without the internet nowadays? Parasitology is online, in the cloud, tweeted, chatted, and blogged. A Google search for “parasitology” yielded over 5 million hits. What's useful? What's just plain cool? What's a waste of time? Getting the most out of the SSP website and other web-based parasitology resources is easy and fun. A visual guide to our website, a review of other resources, and ideas for the future of parasitology on the net and beyond is presented.

NOTES

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