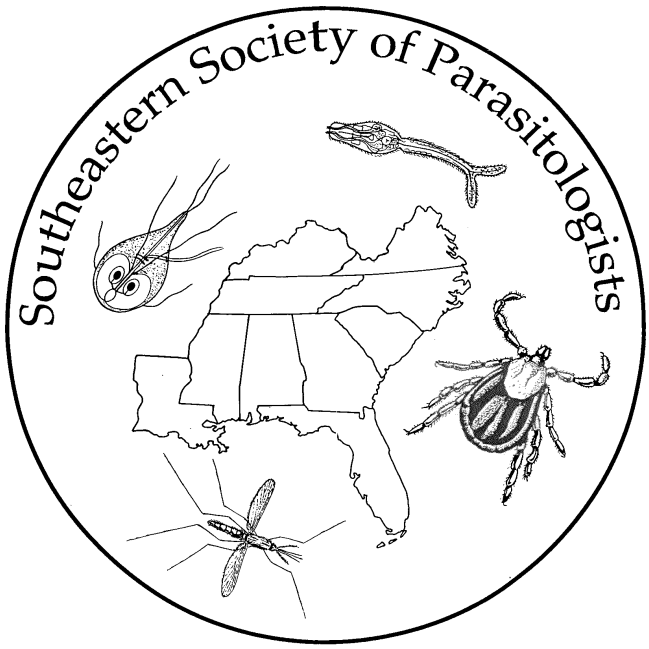
SOUTHEASTERN SOCIETY OF PARASITOLOGISTS

(Affiliate of The American Society of Parasitologists)

PROGRAM AND ABSTRACTS



April 7 – 9, 2010

Hosted by:

Western Carolina University, Asheville, NC

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Southeastern Society of Parasitologists
2010 Program Summary

Meeting Registration/Check In
Wednesday, 7 April 2010, 8:00 a.m. – 8:00 p.m.
Location: Crowne Plaza Lobby

SSP Executive Committee
Wednesday, April 7, 2010, 3:00 – 5:00 p.m.
Location: Magnolia

SSP Presidential Symposium
Wednesday, April 7, 2010, 6:00 – 8:00 p.m.
Location: Mitchell

Food and Water-borne Zoonotic Diseases

Presiding: Dr. Alexa Rosypal, Department of Natural Sciences and Mathematics, Johnson C. Smith University, Charlotte NC

6:00 1 **DAVID S. LINDSAY[1] AND GEORGE FLICK[2].** [1]Department of Biomedical Sciences and Pathobiology, Virginia-Maryland Regional College of Veterinary Medicine, Virginia Tech, [2]Department of Food Science and Technology, Virginia Tech – High hydrostatic pressure processing as a means to control zoonotic parasites in food and water.

6:30 2 **SHAADI ELSWAIFI[1] AND JAMES PALMIERI[1].** Edward Via Virginia College of Osteopathic Medicine – Human Trichinellosis as a public health risk within the European Union: the emerging role of horses in disease transmission.

7:00 3 **DWIGHT D. BOWMAN[1].** [1]College of Veterinary Medicine, Cornell University – You get what you eat and drink!

Thursday Morning, April 8, 2010, 8:15 a.m. – 12:00 p.m.

Byrd-Dunn Student Paper Competition
Southeastern Society of Parasitologists I
Location - Dogwood
*Presenting Author
†Byrd-Dunn Student Paper Competitor

Presiding: Dr. Sheila Mitchell, Scynexis Inc., Research Triangle Park NC

8:15 4† ***FLAVIA GIRAO[1], ANDREA VARELA-STOKES[1], JEROME GODDARD[2].** Department of Basic Sciences, Mississippi State University[1], Department of Entomology and Plant Pathology, Mississippi State University[2] - Detection of *Rickettsia parkeri* in the Gulf Coast tick, *Amblyomma maculatum* Koch, in Mississippi.

8:30 5† ***BARBARA C. SHOCK[1,2], STACI M. MURPHY[1], LAURA L. PATTON[3], PHILIP M. SHOCK[4], COLLEEN OLFENBUTTEL[5], JEFF BERINGER[6], SUZANNE PRANGE[7], DANIEL M. GROVE[8], MATT PEEK[9], JAY BUTFILOSKI[10], DAYMOND W. HUGHES[11], MITCH LOCKHART[12], VICTOR F. NETTLES[1], HOLLY M. BROWN[2], DAVID S. PETERSON[2], AND MICHAEL J. YABSLEY[1,2].** Southeastern Cooperative Wildlife Disease Study[1], University of Georgia[2], Kentucky Department of Fish and Wildlife Resources[3], West Virginia Division of Natural Resources[4], North Carolina Wildlife Resources Commission[5], Missouri Department of Conservation[6], Ohio Department of Natural Resources[7], North Dakota Game and Fish Department[8], Kansas Department of Wildlife and Parks[9], South Carolina Department of Natural Resources[10], USDA Wildlife Services[11], Valdosta State University[12] - Distribution and intraspecific variation of *Cytauxzoon felis* in wild felid populations.

8:45 6† ***ALICE E. HOUK[1], DAVID GOODWIN[1], ANNE M. ZAJAC[1], STEPHEN BARR[2], AND DAVID S. LINDSAY [1]**Department of Biomedical Sciences and Pathobiology, Virginia-Maryland Regional College of Veterinary Medicine, Virginia Tech, Blacksburg, Virginia[1], Department of Small Animal Clinical Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY[2] - Prevalence of IgG antibodies to *Trypanosoma cruzi*, *Toxoplasma gondii*, and *Neospora caninum* in opossums (*Didelphis vriginiana*) from Louisiana.

9:00 7† ***DAVID G. GOODWIN[1], TERRY HRUBEC[1,2], ANNE M. ZAJAC[1], JEANNINE STROBL[2], BRAD KLEIN[1], AND DAVID S. LINDSAY [1]** Department of Biomedical Sciences and Pathobiology, Virginia-Maryland Regional College of Veterinary Medicine, Virginia Tech, Blacksburg, Virginia[1]. Edward Via Virginia College of Osteopathic Medicine, Blacksburg Virginia[2] - Evaluation of interferon-gamma treatment of dams on the behavior of their offspring congenitally infected with *Toxoplasma gondii*.

9:15 8† ***JENNIFER PATONAY[1] AND CHRIS A. HALL[1].** Department of Biology, Berry College[1], Mount Berry, GA - Evidence for an enhanced infectivity of a Type IIa strain of *Trypanosoma cruzi* for placental syncytial trophoblast cells.

9:30 9† ***LORI LOLLIS [1], RICHARD GERHOLD [1,2] , ELIZABETH LYNN[1], LARRY MCDOUGALD[1], ROBERT BECKSTEAD[1].** Poultry Science Department[1], College of Agriculture and Environmental Sciences, University of Georgia, Athens GA. Department of Veterinary Pathology[2], College of Veterinary Medicine, University of Georgia, Athens GA - Molecular characterization of the ITS-1, 5.8s, and ITS-2 rRNA regions of *Histomonas meleagridis.*

9:45 10† ***MATTHEW S. TUCKER[1], LUCIA GERENA[2], KATHERINE SORBER[3], MICHELLE DIMON[3], AZLIYATI AZIZAN[1], ZHINNING WANG[2], QIN CHENG[4], JOE DERISI[3], AND DENNIS E. KYLE[1].** University of South Florida[1], Walter Reed Army Institute of Research[2], University of California-San Francisco[3], Australian Army Malaria Institute[4] - Molecular characterization of resistance to artemisinin drugs in *Plasmodium falciparum.*

10:00 11† *** RICHARD W. GERHOLD[1,2], LORI A. LOLLIS[1], AND LARRY R. MCDOUGALD[1]**. Department of Poultry Science, The University of Georgia[1], Department of Veterinary Pathology, The University of Georgia[2] – Immunization of Northern Bobwhites with a low dose of *Eimeria lettyae* provides protection against a high dose challenge.

10:15 **BREAK: VISIT POSTERS**

10:45 12† **ROXANNE A. CHARLES[1], MICHAEL J. YABSLEY[1,2], ANGELA E. ELLIS[3], ASHLEY M. ROGERS[1], KATHERINE F. SMITH[4].** Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA[1]; Warnell School of Forestry and Natural Resources, University of Georgia, Athens , GA[2]; Veterinary Diagnostic Lab, College of Veterinary Medicine, Athens, GA[3]; Brown University, Providence, RI[4]. A Survey of Parasites of Wild Caught Tokay Geckos (*Gekko gecko*), from Java, Indonesia.

11:00 13† ***WEATHERLY MEADORS[1], STEPHANIE PALESSE[1,2], ALLAN STRAND[1], WILLIAM A. ROUMILLAT[3], ISAURE DE BURON[1]**. Department of Biology, Grice Marine Laboratory, College of Charleston, Charleston, SC[1], Littoral, Environnement et Sociétés, CNRS, Univ. La Rochelle, 17000 La Rochelle, France[2], Marine Resources Research Institute, South Carolina Department of Natural Resources, Charleston SC[3] - Molecular detection of putative paratenic hosts of the southern flounder philometrid species.

11:15 14† *** VASHA HSU[1], DAVID C. GRANT[2], J. P. DUBEY[3], ANNE M. ZAJAC[1] AND DAVID S. LINDSAY [1]**Department of Biomedical Sciences and Pathobiology, Virginia-Maryland Regional College of Veterinary Medicine, Virginia Tech, Blacksburg, Virginia[1], Department of Small Animal Clinical Sciences, Virginia-Maryland Regional College of Veterinary Medicine, Virginia Tech, Blacksburg, Virginia[2], Animal Parasitic Diseases Laboratory, Agricultural Research Service, United States Department of Agriculture, Animal and Natural Resources Institute, Beltsville, Maryland[3] - Prevalence of IgG antibodies to *Sarcocystis neurona* in cats from Virginia and Pennsylvania.

11:30 15† *** WHITNEY BULLARD, CASEY UNDERHILL, NICOLE ACUFF, AND CHRIS A. HALL**. Department of Biology, Berry College, Mount Berry, GA - Development of an *in vitro* model for the role of complement activation and body temperature in the innate avian resistance to *Trypanosoma cruzi* infection.

11:45 16† ***GAIL MORARU[1], JEROME GODDARD[2], and ANDREA VARELA-STOKES.[1]** Department of Basic Sciences, Mississippi State University[1] , Department of Entomology and Plant Pathology, Mississippi State University[2] - The role of small animals in the natural history of *Rickettsia parkeri*.

12:00 – 1:30 p.m. Lunch Break

Thursday Afternoon, April 8, 2010, 1:30 p.m. – 5:00 p.m.

Byrd-Dunn Student Paper Competition
Southeastern Society of Parasitologists II
Location - Dogwood
*Presenting Author
†Byrd-Dunn Student Paper Competitor

Presiding: Dr. Chris Hall, Department of Biology, Berry College, Mount Berry GA

1:30 17† ***EMILY L. BLIZZARD[1], CHERYL D. DAVIS[2], SCOTT HENKE[3], DAVID B. LONG[4], MARGARET BECK[5], AND MICHAEL J. YABSLEY[1]**, Warnell School of Forestry and Natural Resources and the Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA[1], Western Kentucky University, Bowling Green, KY[2], Caesar Kleberg Wildlife Research Institute, Kingsville, TX[3] USDA-APHIS-Wildlife Services, Kingsville, TX[4], and Goose Creek Wildlife Sanctuary, Tallahassee, FL[5] - Distribution, prevalence and genetic characterization of Baylisascaris procyonis from selected regions of Georgia and Florida.

1:45 18† ***ELIZABETH R. GLEIM[1,2], L. MICHAEL CONNER[3], MICHAEL L. LEVIN[4], AND MICHAEL J. YABSLEY[1,2].** [1]Warnell School of Forestry and Natural Resources and the [2]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA;[3]Joseph W. Jones Ecological Research Center, Newton, GA; [4]Centers for Disease Control and Prevention, Atlanta, GA - Understanding the ecological effects of prescribed fire regimes on the distribution and population dynamics of tick-borne zoonoses: preliminary data.

2:00 19 *** ELIZABETH LYNN[1], RICHARD GERHOLD[2] , LARRY MCDOUGALD[1] , ROBERT BECKSTEAD[1]** Poultry Science Department, College of Agriculture and Environmental Sciences, University of Georgia, Athens GA[1]. Department of Veterinary Pathology, College of Veterinary Medicine, University of Georgia, Athens GA [2] - Determining Virulence Factors in *Histomonas meleagridis*

2:15 20 ***CHARLES T. FAULKNER[1]**. University of Tennessee College of Veterinary Medicine, Knoxville TN[1] - Prevalence of *Dirofilaria immitis* in wild canids from Knox and surrounding counties in East Tennessee**.**

2:30 21 ***SONIA M. HERNANDEZ[1,2], SUSAN SANCHEZ[3], ROBERT COOPER[1], MICHAEL J. YABSLEY[1,2], C. RON CARROLL[4].** Warnell School of Forestry and Natural Resources[1] and the Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine[2], University of Georgia. Department of Infectious Diseases and Athens Diagnostic Laboratory, College of Veterinary Medicine, University of Georgia[3]. Odum School of Ecology and College of Veterinary Medicine, University of Georgia[4] - Do shade-grown coffee plantations ("Bird-Friendly" coffee) pose a disease risk for Neotropical birds in Costa Rica?

2:45 22 ***DANA NAYDUCH[1] AND KATHRYN CLAIRE HILSINGER[1]**. Dept. of Biology, Georgia Southern University[1] - Host and seasonal effects on the infection dynamics of the parasitic nematode *Skrjabinoptera phrynosoma* in horned lizards (*Phrynosoma platyrhinos)*

3:00 **BREAK: VISIT POSTERS**

3:30 23 ***OSCAR J. PUNG[1], ASHLEY R. BURGER[1], AND PATRICIA A. O'LEARY[1].** Georgia Southern University[1] - Effect of incubation vessel and worm density on the ability of *Microphallus turgidus* (Trematoda: Microphallidae) to produce normal eggs in vitro.

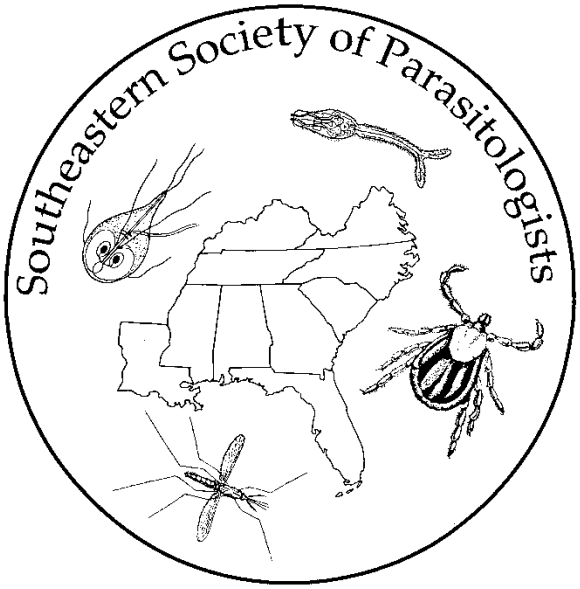
3:45 24 ***J. MICHELLE RIVIERE[1] AND STEPHEN C. LANDERS[1]**. Troy University, Troy AL[1] - Light and electron microscopic analysis of the parasitic ciliated protozoan *Chromidina*.

4:15 25 ***ANURADHA SRIVASTAVA[1] AND DENNIS E. KYLE[1]**. University of South Florida, Tampa, FL[1] - Evaluation of novel Arylimidamides in the hamster model of visceral leishmaniasis.

4:30 26 ***ANDREA VARELA-STOKES[1], ASHLEY CASTELLAW[1], FLAVIA GIRAO[1], GAIL MORARU[1], ERLE CHENNEY[1], AND CLAIRE FELLMAN[1]**. College of Veterinary Medicine, Mississippi State University[1] - Variable membrane protein genes in the tick-borne bacterium, *Borrelia lonestari.*

4:45 27 ***MICHAEL J. YABSLEY[1,2] ELIZABETH HORNE[3], AND NOLA J. PARSONS[4]**. [1]Daniel B. Warnell School of Forestry and Natural Resources, [2]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens Georgia, USA, [3]Penguins Eastern Cape Marine Bird Rehabilitation Center, Cape St Francis, South Africa, [4]Southern African Foundation for the Conservation of Coastal Birds, Cape Town, South Africa - Novel relapsing fever Borrelia detected in African penguins admitted to rehabilitation centers in South Africa.

SSP Business Meeting/ Breakfast
Friday Morning, April 9, 2010, 7:30 a.m - 10:00 a.m.
Location – The Venue
Shuttle service provided


Southeastern Society of Parasitologists

PROGRAM ABSTRACTS

1. DAVID S. LINDSAY [1] and GEORGE FLICK[2] Department of Biomedical Sciences and Pathobiology, Virginia-Maryland Regional College of Veterinary Medicine, Virginia Tech, Blacksburg, VA[1], Department of Food Science and Technology, Virginia Tech, Blacksburg, VA[2]. High hydrostatic pressure processing as a means to control zoonotic parasites in food and water.

High hydrostatic pressure processing (HPP) has been shown to be an effective non-thermal means of eliminating non-spore forming bacteria from a variety of food products. The shelf life of the products is extended and the sensory features of the food are not or only minimally affected by HPP. Other advantages of HPP over traditional thermal processing include reduced processing times, minimal heat damage problems, retention of freshness, flavor, texture, and color; no vitamin C loss, no undesirable changes in food during pressure-shift freezing due to reduced crystal size and multiple ice-phase forms, and minimal undesirable functionality alterations. Only recently have parasitologists began examining the effects of HPP on eliminating zoonotic metazoan and protozoon parasites from food. Pressures of greater than 200 MPa (1 MPa = 10 atm = 147 psi) kill *Trichinella spiralis* larvae in pork and similar pressures will kill larvae of *Anisakis simplex* in king salmon and arrowtooth flounder. Tissue cysts of *Toxoplasma gondii* in ground pork are inactivated by exposure to 300 MPa and the infectivity of sporulated *T. gondii* oocysts on raspberries is eliminated by treatment with 340 MPa. The infectivity of oocysts of *Cryptosporidium parvum* from experimentally exposed oysters for neonatal mice is greatly reduced by treatment with 550 MPa. Treatment of liquids with HPP has been shown to render spores of *Encephalitozoon cuniculi* and sporulated oocysts of *T. gondii* non-infective for cell cultures and mice, respectively. The results of these studies on metazoan and protozoon parasites indicate that HPP has the potential to be a useful tool in protecting the food and water supply.

2. SHAADI ELSWAIFI[1] AND JAMES PALMIERI[1]. Edward Via Virginia College of Osteopathic Medicine[1]. Human Trichinellosis as a public health risk within the European Union: the emerging role of horses in disease transmission.

Trichinellosis is emerging or re-emerging in the European Union (EU). Reservoirs include wild boar, domestic pigs, wolves, rats, meat-eating birds, and horses. Most human trichinellosis is acquired from these animals. Within the EU the number of reported cases started to increase in 2006, indicating reemergence of the disease. From 1975 to 2000 over 3,000 cases of human trichinellosis were reported from consumption of horse meat imported into Italy and France. While considered herbivorous, evidence suggests that horses also eat animals that may host *Trichinella spp.* Feeding horses meats, or waste products containing meat, occurs in Europe. Furthermore, horses have been experimentally infected from pork products. Conversely, while often thought as a primary source of human infection, < 0.01% of wild boar are found to be infected, suggesting that boar is not a primary source of infection for humans, however, the horse is. *T. pseudospiralis* is a non-encapsulated species responsible for a growing number of infections and is causing increased concern. *T. pseudospiralis* is cosmopolitan and reported from mammalian and avian species. The increase in incidence of trichinellosis caused by *T. pseudospiralis* indicates that *T. pseudospiralis* is an emerging parasite that is contributing to the overall prevalence of trichinellosis in the EU and probably increasing trichinellosis worldwide.

3. DWIGHT D. BOWMAN[1]. Department of Microbiology and Immunology, College of Veterinary Medicine, Cornell University, Ithaca, NY[1]. You get what you eat and drink!

This presentation will cover infection of parasites through the ingestion of parasitic stages. This mode of infection involves the ingestion of parasites either in foodstuffs or water that has been contaminated, through the ingestion of microorganisms that serve as intermediate or paratenic hosts of parasites that contaminate food or water, or in the flesh of other animals that are consumed. Ingestion of contaminated food items with stages passed in the feces of humans probably remains as one of the major sources of human infection. Similarly, the drinking of water that contains stages of parasites passed in the feces of others is also a vbery common form of infection. Sometimes the stages in water are simply resistant parasite stages, but in other cases they represent contaminants by nearly invisible hosts that contain parasites. Finally, because people remain carnivorous and piscivorous, they become infected through the ingested of raw or undercooked prey. Ingestion remains as being most likely the major means by which people are infected by pathogens. This mode of transmission is often overshadowed by the horrible manifestations of the few important human vector-borne diseases, e.g., malaria, trypanosomiasis, and leishmaniasis, but it still remains the workhorse of parasite transmission.

4. FLAVIA GIRAO[1], ANDREA VARELA-STOKES[1], JEROME GODDARD[2]. Department of Basic Sciences, Mississippi State University[1], Department of Entomology and Plant Pathology, Mississippi State University[2]. Detection of *Rickettsia parkeri* in the Gulf Coast tick, *Amblyomma maculatum* Koch, in Mississippi.

Amblyomma maculatum Koch is currently reported in most of the southern United States. *A. maculatum* vectors *Rickettsia parkeri*, a recently recognized human pathogen. Reports of *R. parkeri* infection in humans described an eschar at the bite site, fever, fatigue, headaches, muscle pain and generalized rash typically a week after the tick bite. In this study, adult Gulf Coast ticks were collected from nine sites in Mississippi from July to September of 2008 and 2009. The objective was to determine the percent of Gulf Coast ticks carrying *R. parkeri* in Mississippi. We extracted DNA from the 350 ticks collected in 2008 and 194 in 2009, a total of 544 ticks encountered in Mississippi. Segments of the tick mitochondrial 16S ribosomal RNA gene and rickettsial outer-membrane protein A gene were amplified by separate nested PCR assays. Tick mitochondrial 16S rDNA was successfully amplified in 99.7% (349/350) of tick extracts collected in 2008 and 20.34% (71/349) of extracts were positive for *Rickettsia* species. DNA has been extracted from ticks collected in 2009 and PCR analysis is currently in progress. Although this tick may carry a rickettsial endosymbiont, the majority of positive samples are suspected to be *R. parkeri* until sequencing, due to its higher prevalence in these ticks, compared to the endosymbiont. Physicians and health authorities should be aware of *R. parkeri* and include it in differential diagnosis for a patient presenting the above symptoms. Further study is warranted to better understand the ecology and epidemiology of this vector and *R. parkeri*.

5. BARBARA C. SHOCK[1,2], STACI M. MURPHY[1], LAURA L. PATTON[3], PHILIP M. SHOCK[4], COLLEEN OLFENBUTTEL[5], JEFF BERINGER[6], SUZANNE PRANGE[7], DANIEL M. GROVE[8], MATT PEEK[9], JAY BUTFILOSKI[10], DAYMOND W. HUGHES[11], MITCH LOCKHART[12], VICTOR F. NETTLES[1], HOLLY M. BROWN[2], DAVID S. PETERSON[2], AND MICHAEL J. YABSLEY[1,2]. Southeastern Cooperative Wildlife Disease Study[1], University of Georgia[2], Kentucky Department of Fish and Wildlife Resources[3], West Virginia Division of Natural Resources[4], North Carolina Wildlife Resources Commission[5], Missouri Department of Conservation[6], Ohio Department of Natural Resources[7], North Dakota Game and Fish Department[8], Kansas Department of Wildlife and Parks[9], South Carolina Department of Natural Resources[10], USDA Wildlife Services[11], Valdosta State University[12]. *Cytauxzoon felis* in wild felid populations.

Cytauxzoon felis, a protozoan parasite of wild and domestic felids, is the causative agent of cytauxzoonosis in domestic and some exotic felids. *C. felis* is known to be transmitted by two ticks, *Dermacentor variabilis* and *Amblyomma americanum*, which have overlapping distributions throughout the Southern US; however, *D. variabilis* ranges further into northern states. Our objective was to determine the distribution and prevalence of *C. felis* in wild felid populations and to characterize the intraspecific variability. Twelve states were included in the study (Florida, Georgia, Kansas, Kentucky, Louisiana, Missouri, North Carolina, North Dakota, Ohio, Oklahoma, South Carolina, and West Virginia). Blood or spleen samples from hunter/trapper-killed felids (n=623) were tested for *C. felis* by PCR, targeting the ribosomal internal transcribed spacer regions (ITS-1; ITS-2). We detected prevalence rates of 79% in Missouri (39 bobcats [*Lynx rufus*]), 63% in North Carolina (8 bobcats), 60% in Oklahoma (20 bobcats), 57% in South Carolina (7 bobcats), 55% in Kentucky (74 bobcats), 44% in Florida (45 bobcats), 33% in Louisiana (1 bobcat, 1 cougar [*Puma concolor*], 1 serval [*Leptailurus serval*]), and 27% in Kansas (41 bobcats). The prevalences were lower in Georgia (9%, 159 bobcats), North Dakota (2.4%, 124 bobcats, 5 cougars), Ohio (0%, 19 bobcats), and West Virginia (0%, 37 bobcats). We also characterized the ITS-1 and ITS-2 genes and found greater intraspecific variability in wild felids than what has been reported in domestic cats. These data indicate that *C. felis* is widespread and quite diverse in bobcat populations.

6. ALICE E. HOUK[1], DAVID GOODWIN[1], ANNE M. ZAJAC[1], STEPHEN BARR[2], AND DAVID S. LINDSAY [11]Department of Biomedical Sciences and Pathobiology, Virginia-Maryland Regional College of Veterinary Medicine, Virginia Tech, Blacksburg,Virginia,[2]Department of Small Animal Clinical Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY. Prevalence of IgG antibodies to *Trypanosoma cruzi*, *Toxoplasma gondii*, and *Neospora caninum* in opossums (*Didelphis vriginiana*) from Louisiana.

We examined the prevalence of antibodies to zoonotic protozoan parasites (*Trypanosoma cruzi* and *Toxoplasma gondii*) and protozoan's of veterinary importance (*Neospora caninum*) in a population of opossums (*Didelphis vriginiana*) from Louisiana. Samples from 30 opossums were collected as part of a hemaculture survey for *T. cruzi* in Louisiana opossums. Frozen sera from these opossums were examined using an indirect immunofluorescent antibody test (IFAT) at the Virginia-Maryland Regional College of Veterinary Medicine (VAMDRCM), Virginia Tech, Blacksburg, VA. Parasite stages used for antigen were grown in vitro in our laboratory. Briefly, epimastigotes of the Brazil strain of *T. cruzi* were grown in Grace's insect medium supplemented with 30% (V/V) fetal calf serum and antibiotics, tachyzoites of the RH strain of *To. gondii* and NC-1 strain of *N. caninum* were grown in human fibroblast cells. Parasite stages were air dried onto wells of Teflon coated IFAT slides and used as antigen. Test opossum sera were incubated with antigens for 30 minutes and the slides washed in phosphate buffered saline

(PBS). Next, rabbit anti-opossum sera were incubated with the antigens on IFAT slides for 30 minutes then the slides washed in PBS. Finally, fluorescence labeled goat anti-rabbit sera were incubated with the antigens on IFAT slides for 30 minutes and washed in PBS. Slides were examined using an epifluorescent microscope. The prevalence of reactive IFAT samples were as follows: 60% for *T. cruzi*, 47% for *To. gondiii*, and 3% for *N. caninum*. Hemaculture revealed that 16 (53%) of the 30 samples were positive for *T. cruzi* compared to 18 of 30 (60%) by IFA. Supported in part by grant 117797 from the Office of Research and Graduate Studies VAMDRCM to DSL.

7. DAVID G. GOODWIN[1], TERRY HRUBEC[1,2], ANNE M. ZAJAC[1], JEANNINE STROBL[2], BRAD KLEIN[1], AND DAVID S. LINDSAY [1 1]Department of Biomedical Sciences and Pathobiology, Virginia-Maryland Regional College of Veterinary Medicine, Virginia Tech, Blacksburg, Virginia. [2]Edward Via Virginia College of Osteopathic Medicine, Blacksburg Virginia. Evaluation of interferon-gamma treatment of dams on the behavior of their offspring congenitally infected with *Toxoplasma gondii*.

Toxoplasma gondii can cause congenital infection in humans. Approximately 85-90% percent of women in the U.S population are at risk of developing congenital infection. Pregnancy brings about a state of immunosuppression making women more susceptible to infectious agents. Administering immune stimulation to pregnant individuals is a way to negate some of the deleterious effects caused by diseases. Chronic infection with *T. gondii* has been shown to result in decreased motor function, increased open field activity and decreased memory in mice. Our experiments used immune stimulation of the pregnant dam with interferon-gamma (INF-g) prior to inoculation with *T. gondii*. Our goal was to examine the role immune stimulation plays in limiting the negative behavioral effects as a result of congenital toxoplasmosis. The Barnes maze test is used to look at spatial memory, rate of learning, memory acquisition, open field activity, and motor function to a minor extent. We used 4 treatment groups; 1) uninfected not given INF-g or *T. gondii*, 2) immune stimulated with INF-g not given *T. gondii*, 3) immune stimulated with INF-g and *T. gondii* infected, and 4) *T. gondii* infected not given INF-g. The offspring used in the experiment were switched to surrogate dams at birth to negate the effects of toxoplasmosis on the dams. One week after weaning (4 weeks of age), the pups were tested using the Barnes maze test. Different mice from the same litter were tested again at 8 weeks of age using the Barnes maze test. By testing at two age points we aim to gain an understanding of how congenital infections may alter mouse behavior both pre or post sexual maturity, and also determine if maternal immune stimulation can prevent any of the observed behavioral changes.

8. Jennifer Patonay and Chris A. Hall. Department of Biology, Berry College, Mount Berry, GA. Evidence for an enhanced infectivity of a Type IIa strain of *Trypanosoma cruzi* for placental syncytial trophoblast cells.

Trypanosoma cruzi represents a genotypically diverse family of organisms with documented differences in tissue tropism and pathogenicity. Previous breeding experiments comparing the relative abilities of Type I and Type IIa strains of T. cruzi to be congenitally transferred in mice suggests that the Type IIa may have adaptations increasing its rate of transmission through the placenta. In this study we sought to determine whether the Type IIa strain has an enhanced ability to infect BeWo cells, an *in vitro* model for the placental syncytial trophoblast interface. Cultures of BeWo cells were exposed to North American isolates of either the Type I or Type IIa strains of T. cruzi. At 48, 72, and 96 hours post-exposure cells were fixed, stained, and microscopically assessed for both the percentage of cells infected and average number of intracellular amastigotes. BeWo cultures exposed to the Type IIa isolate had significantly higher percentages of infected cells, as well as a higher average number of intracellular amastigotes, at all time points tested. Control cultures carried out in DH-82 canine macrophages showed that in these cells the two isolates invaded and reproduced similarly, supporting an enhanced tropism of the Type IIa isolate for the placental cells. These results confirm that significant differences exist in the ability of these two isolates to invade and replicate in placental syncytial trophoblast cells. This provides additional support to the hypothesis that the Type IIa strain may possess adaptations to facilitate placental transmission.

9. Lori Lollis [1], Richard Gerhold [1,2] , Elizabeth Lynn[1], Larry McDougald[1], Robert Beckstead[1.] Poultry Science Department[1], College of Agriculture and Environmental Sciences, University of Georgia, Athens GA. Department of Veterinary Pathology[2], College of Veterinary Medicine, University of Georgia, Athens GA - Molecular characterization of the ITS-1, 5.8s, and ITS-2 rRNA regions of *Histomonas meleagridis*

Histomonosis, caused by *Histomonas meleagridis*, is a major disease of gallinaceous birds and causes significant economic losses to the poultry industry. Although it is known that there are differences in virulence and tropism of *H. meleagridis*, genetic analysis of the parasite has not been conducted to determine if there are genotypic variations responsible for these differences. *Histomonas* DNA was extracted from paraffin embedded tissues of domestic poultry cases previously diagnosed as histomonosis. The ITS1, 5.8S, and ITS2 rRNA regions were amplified by PCR using the primers ITSF and ITSR and sequenced. Nucleotide sequences of approximately thirty amplicons were compared to each other as well as a single *H. meleagridis* sequence, and other closely related protozoan sequences available from GenBank. The results of the sequence analysis suggest that there are at least two different genotypes within the *H. meleagridis* morphologic complex. One group is closely related to the *H. meleagridis* sequence available from GenBank, while the other group of our sequences has a higher nucleotide identity to *Dientamoeba fragilis* (70%) than to *H. meleagridis* (65%) and had at least thirty-eight nucleotide polymorphisms compared to the *H. meleagridis* sequence from GenBank.

10. MATTHEW S. TUCKER[1], LUCIA GERENA[2], KATHERINE SORBER[3], MICHELLE DIMON[3], AZLIYATI AZIZAN[1], ZHINNING WANG[2], QIN CHENG[4], JOE DERISI[3], AND DENNIS E. KYLE[1]. University of South Florida[1], Walter Reed Army Institute of Research[2], University of California-San Francisco[3], Australian Army Malaria Institute[4]. Molecular characterization of resistance to artemisinin drugs in *Plasmodium falciparum.*

Artemisinin (QHS) and its derivatives are effective against all stages of *Plasmodium* spp. and they provide faster clearance of parasitemia than any other drugs. Discontinuous exposure to artelinic acid (AL) or QHS *in vitro* produced AL and QHS resistant progeny of *P. falciparum* lines W2, D6, and TM91c235. Using this method, we produced parasites that could tolerate 340ng/ml of QHS (D6), 200ng/ml QHS (W2), and 280ng/ml of AL (TM91c235). After exposing D6 and D6.QHS340 to concentrations of QHS ranging from 28.2-2400ng/ml, we found D6 could tolerate up to 1500ng/ml QHS, and D6.QHS340 tolerated 2400ng/ml QHS. In vitro susceptibility testing with various antimalarial drugs found resistant D6 and W2 lines were less susceptible to some drugs, but not all. In regard to artemisinin drugs, resistant parasites exhibited similar susceptibility as parental strains, with a few exceptions. Prior microarray and real-time PCR performed on drug selected progeny of W2 and TM91c235 identified differentially expressed genes and increases in *pfmdr1* copy number and/or expression. We conducted similar analyses and employed other molecular methods to dissect resistance using the most drug selected lines. Whole genome sequencing of D6 and D6.QHS2400 identified single nucleotide polymorphisms (SNPs) that may be involved in resistance as well as a 76 kb amplification event. Proteomic analyses found proteins that may be differentially expressed in D6 vs. D6.QHS2400 and W2 vs. W2.QHS200. Future research will focus on further dissecting whole genome sequence and proteomic data of parental and resistant parasites.

11. Richard W. Gerhold[1,2], Lori A. Lollis[1], and Larry R. McDougald[1]. Department of Poultry Science, The University of Georgia[1], Department of Veterinary Pathology, The University of Georgia[2] – Immunization of Northern Bobwhites with a low dose of *Eimeria lettyae* provides protection against a high dose challenge.

To determine if Northern Bobwhite quail (*Colinus virginianus*) can be immunized against *Eimeria lettyae* by a low dose inoculation of oocysts, we inoculated sixty birds with either 100 or 1,000 oocysts within the first week of life. Four weeks following the immunization, the immunized birds were challenged with 1 X 10^6 oocysts of *E. lettyae*. Eight days following the challenge, birds were killed, weighed, and intestines examined for gross lesions. Parameters used to determine effectiveness of the immunization in the immunized challenged quail included percent weight gain, intestinal lesions, severity of diarrhea, feed conversion ratio, and oocysts production compared to the unimmunized unchallenged as well as unimmunized challenged quail. Immunized birds gained an average of 33.3 gm; whereas unimmunized challenged birds gained 11.5 gm. Immunized quail produced 99.7% fewer oocysts, contained minimal gross intestinal lesions, had minimal diarrhea, and had a 50% lower feed conversion ratio compared to unimmunized challenged controls. Our findings indicate that immunization not only aids in suppression of weight loss, but it also leads to the production of significantly fewer oocysts. These findings indicate that vaccination is a viable option for controlling coccidiosis in quail and that research aimed at creating vaccine strains is warranted.

12. ROXANNE A. CHARLES[1], MICHAEL J. YABSLEY[1,2], ANGELA E. ELLIS[3], ASHLEY M. ROGERS[1], KATHERINE F. SMITH[4]. [1]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA; [2]Warnell School of Forestry and Natural Resources, University of Georgia, Athens , GA; [3]Veterinary Diagnostic Lab, College of Veterinary Medicine, Athens, GA; [4]Brown University, Providence, RI. A Survey of Parasites of Wild Caught Tokay Geckos (*Gekko gecko*), from Java, Indonesia.

In the current study we surveyed 81 wild-caught Tokay Geckos (*Gekko gecko*) from the island of Java, Indonesia for endo- and ecto-parasites. Based on necropsy and fecal examination, 94% of geckos were infected with at least one parasite, including at least six helminth species, one pentastomid species, and two species of coccidia. No ectoparasites were detected on any gecko. At necropsy, we identified *Paradistomum geckonum* in the bile duct (prevalence (P)=1.2%, mean infection intensity (MII) = 7.0), *Oochoristica* sp*.* in the small intestine (1.2%, 1.0), larval acanthocephalans and nematodes in the coelomic cavity (13.5%, 2.0 and 1.2%, 1 respectively), *Physalopteroides* sp. in the stomach (11.1%, 2.3), several species of pinworms in the family Pharyngodonidae in the large intestine (54.3%, 29.0), and *Raillietiella affinis* (40.7%, 8.7) in the lungs. Histological examination of stomachs indicated that at least 4.9% of geckos were infected with *Cryptosporidium* spp. In addition, an unidentified trematode was observed in the pancreas of two geckos and endogenous stages of *Eimeria tokae* were detected in the small intestine of numerous animals. At necropsy, a fecal sample was examined for ova and oocysts. We found eggs morphologically consistent with *Paradistomum geckonum* (P=2.6%), *Oochoristica* sp*.* (P=1.3%), *Physalopteroides* sp. (P=9.2%), pinworms (P=50%), and an unidentified trematode (P=5.3%). Oocysts of *E. tokae* were found in 67.1% of geckos. These data indicate that wild-caught geckos from Indonesia are infected with several species of parasites, some of which might be zoonotic (e.g., *Cryptosporidium*).

13. Weatherly Meadors[1], Stephanie Palesse[1,2], Allan Strand[1], William A. Roumillat[3], Isaure de Buron[1]. [1]Department of Biology, Grice Marine Laboratory, College of Charleston, Charleston 29412, [2]Littoral, Environnement et Sociétés, CNRS, Univ. La Rochelle, 17000 La Rochelle, France, [3]Marine Resources Research Institute, South Carolina Department of Natural Resources, Charleston SC 29412. Molecular detection of putative paratenic hosts of the southern flounder philometrid species.

The southern flounder, *Paralichthys lethostigma,* is infected by two species of philometrids, *Philometra overstreeti* and *Philometroides paralichthydis*, which are composed of four genetic clades corresponding to their respective habitat in the host: “fin muscles”, “buccal bones”, “teeth”, and “gill arches”. Population dynamics data showed that these clades have a different ecology and rarely infect all habitats simultaneously. We hypothesized that individuals belonging to these clades have life cycles that involve different fish paratenic host species reflecting potential sequential infection by the various clades. Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (RFLP-PCR) technique was used to identify species and clades of philometrids. Part of the Cytochrome Oxydase I (COI) gene was amplified with taxon-specific primers. Amplicons were digested with six selected endonucleases, *Mse I, Alu I, BsaW I, CviA II, HpyCH4 V* and *Bda I*. Restriction profiles were obtained for each clade of *P. overstreeti* and *P. paralichthydis* and for *Philometra carolinensis* that parasitizes the spotted seatrout, *Cynoscion nebulosus*, which is sympatric to the southern flounder. Mesenteries of 8 fish species known to be preyed upon by southern flounder and infected with nematode larval stages were analyzed. Out of 228 fish dissected, 32 were infected by nematodes, of which 14 were found to be infected by philometrids using PCR. RFLP analysis showed several results: the presence of the “gill arch” clade in the mesentery of one mummichog, *Fundulus heteroclitus*

and one freshwater goby, *Ctenogobius shufeldti*, the presence of *P. carolinensis* in three freshwater gobies, and the presence of 12 unknown profiles in various other fishes. The other three clades ("teeth", "fin muscle", and "buccal bones") were not encountered in any of the fish studied. Although this study demonstrated the usefulness of PRC-RFLP technique to distinguish between philometrids species, the occurrence of several unknown profiles showed its limitation when in the presence of unknown species as is clearly our case. Direct sequencing of a portion of the COI gene is currently being used to differentiate between individuals that could not be positively identified by RFLP.

14. VASHA HSU[1], DAVID C. GRANT[2], J. P. DUBEY[3], ANNE M. ZAJAC[1] AND DAVID S. LINDSAY [11]Department of Biomedical Sciences and Pathobiology, Virginia-Maryland Regional College of Veterinary Medicine, Virginia Tech, Blacksburg, Virginia, [2]Department of Small Animal Clinical Sciences, Virginia-Maryland Regional College of Veterinary Medicine, Virginia Tech, Blacksburg, Virginia, [3]Animal Parasitic Diseases Laboratory, Agricultural Research Service, United States Department of Agriculture, Animal and Natural Resources Institute, Beltsville, Maryland. Prevalence of IgG antibodies to *Sarcocystis neurona* in cats from Virginia and Pennsylvania.

Sarcocystis neurona is best known as the causative agent of equine protozoal myeloencephalitis of horses in the Americas. Domestic cats (*Felis domesticus*) were the first animals described as an intermediate host for *S. neurona*. *Sarcocystis neurona* associated encephalitis has been reported in naturally infected cats in the United States. Thus, cats can be implicated in the life cycle of *S. neurona* as natural intermediate hosts. The present study examined the seroprevalence of IgG antibodies to merozoites of *S. neurona* in populations of domestic cats from Virginia and Pennsylvania. Overall, sera or plasma from 448 cats (Virginia = 239; Pennsylvania = 209) were tested by an indirect immunofluorescent assay at a 1:50 dilution. Antibodies to *S. neurona* were found in 32 (7%) of 448 cats. Of which, 22 (9%) of the 239 cats from Virginia and 10 (5%) of the 209 cats from Pennsylvania were positive for antibodies to *S. neurona.* Because of the low seroprevalence of antibodies to *S. neurona* in cats, the role of domestic cats as intermediate hosts in perpetuating the life cycle of *S. neurona* is probably minimal compared to that of other natural intermediate hosts such as raccoons and skunks that have a much higher seroprevalence.

15. Whitney Bullard, Casey Underhill, Nicole Acuff, and Chris A. Hall. Department of Biology, Berry College, Mount Berry, GA 30149. Development of an *in vitro* model for the role of complement activation and body temperature in the innate avian resistance to *Trypanosoma cruzi* infection.

Although numerous mammalian species are known to be permissive hosts for *T. cruzi*, birds possess an innate resistance to infection. Evidence suggests that modifications in the alternative pathway for complement (APC) activation are largely responsible for this protection. The specific mechanisms involved in the activation of the avian APC against *T. cruzi* are unknown. To facilitate future investigations into these mechanisms we sought to develop a reliable *in vitro* model for the complement mediated lysis of *T. cruzi*. To ensure the fidelity of the system, comparisons to the complement systems of both humans and raccoons were also performed. To assess complement function, separate cultures of blood stream form trypomastigotes (cBSF) and epimastigotes (EMs) were exposed to pooled normal or heat inactivated sera from chickens, humans, or raccoons. Cultures were incubated at 25, 37, or 40^{O}C for 1, 60 or 120 minutes and subsequently evaluated by hemocytometer counting for parasite attrition. Results showed that significant numbers of epimastigotes were lysed upon exposure to both normal and heat inactivated serum from humans and chickens, suggesting a complement independent mechanism of lysis against this stage. When cBSF parasites were exposed to the normal and heat inactivated serum of humans and raccoons, little attrition was observed at 25^{0} and 37^{0}C across all the time points measured. Culturing of cBSFs in the presence of normal chicken serum resulted in significant decreases in parasite concentration, with heat inactivation rendering the chicken serum. Interestingly, all cBSF cultures, including serum free controls, showed sharp decreases after 120 minutes of exposure to 40^{0}C. This suggests that physiological body temperature may contribute to the innate resistance in birds.

16. GAIL MORARU[1], JEROME GODDARD[2], and ANDREA VARELA-STOKES.[1] Department of Basic Sciences, Mississippi State University[1] , Department of Entomology and Plant Pathology, Mississippi State University[2]. The role of small animals in the natural history of *Rickettsia parkeri*.

The Gulf Coast tick, *Amblyomma maculatum*, is the vector of the pathogenic bacterium, *Rickettsia parkeri*; however, the natural history of *R. parkeri* in the Gulf Coast tick is poorly understood. In a study of *A. maculatum* host preference, larvae or nymphs were given a choice of host, among anoles, cotton rats, and quail; we recorded the number of engorged ticks from each host. To evaluate feeding success, we placed ticks directly on each animal and allowed them to feed until engorged. We recorded the number that engorged, successfully molted, and weights of engorged nymphs. To study *R. parkeri* infection, four quail and four rats were injected with organism; one of each species received uninfected media as a control. We collected blood samples during the study to test for antibodies and rickettsial DNA; we also put larvae and later, nymphs on the animals to evaluate acquisition of organism by ticks. Because the number of recovered ticks was low, no significant difference in host preference between quail and rats could be seen. More engorged ticks were recovered from quail in the feeding success study, but those from rats weighed significantly more. We found no ticks that fed successfully on anoles, thus, anoles were not used in the infection study. Both quail and rats exposed to *R. parkeri* seroconverted by day post-infection 11, but none became rickettsemic. These results support a role for quail and rats in the natural history of *R. parkeri,* but the true extent of their role is still unclear.

17. EMILY L. BLIZZARD[1], CHERYL D. DAVIS[2], SCOTT HENKE[3], DAVID B. LONG[4], MARGARET BECK[5], AND MICHAEL J. YABSLEY[1], [1]Warnell School of Forestry and Natural Resources and the Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA, [2]Western Kentucky University, Bowling Green, KY, [3]Caesar Kleberg Wildlife Research Institute, Kingsville, TX [4]USDA-APHIS-Wildlife Services, Kingsville, TX, and [5]Goose Creek Wildlife Sanctuary, Tallahassee, FL. Distribution, prevalence and genetic characterization of Baylisascaris procyonis from selected regions of Georgia and Florida.

Baylisascaris procyonis, a parasitic intestinal nematode commonly found in raccoons (*Procyon lotor*), has historically been absent from the southeastern United States. In 2002, the parasite was first documented in Atlanta, Georgia. The goal of this study was to investigate distribution in Georgia and northern Florida. Intestinal tracts of 207 raccoons from six Georgia counties and 53 raccoons from three northwestern Florida counties were examined for B. procyonis. In Georgia, 12 of 116 (10.3%) raccoons from Clarke County were infected with B. procyonis. A single immature worm from a Florida raccoon was confirmed to be B. procyonis by PCR. No other raccoons were infected. To try and identify a source population for the parasites, we amplified and sequenced regions of the rRNA genes from worms from various locations. To date, ITS-1 sequences have been successfully obtained from 18 worms from Georgia (n=6), Kansas (1), Florida (1), Kentucky (4), and Texas (6). Although numerous polymorphic bases were observed among the samples, none were associated with a particular geographic location. Sequences from the 18S, 5.8S, and ITS-2 regions from six samples from Georgia, Kentucky, and Texas were 100% identical. These data indicate that the distribution of B. procyonis within Georgia is increasing and that limited genetic variation in the rRNA and ITS gene regions is present among widely distributed populations of B. procyonis. In addition, this is the first report of B. procyonis in Florida and increases the distribution of this important zoonotic parasite.

18. ELIZABETH R. GLEIM[1,2], L. MICHAEL CONNER[3], MICHAEL L. LEVIN[4], AND MICHAEL J. YABSLEY[1,2]. [1]Warnell School of Forestry and Natural Resources and the [2]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA;[3]Joseph W. Jones Ecological Research Center, Newton, GA; [4]Centers for Disease Control and Prevention, Atlanta, GA. Understanding the ecological effects of prescribed fire regimes on the distribution and population dynamics of tick-borne zoonoses: preliminary data.

Prescribed fire has become a common forest management tool, particularly in the southeastern United States. As land-use changes are being implicated in the spread and emergence of disease and vectors around the world, it is critical that we understand the impact that land management practices have on wildlife and human diseases and identify practices which may prevent the spread of disease. To better understand the effects of long-term prescribed fire on tick and tick-borne pathogen dynamics, ten sites in southwestern Georgia with variable prescribed fire regimes (none, intermittent, or frequent burns) were sampled for ticks which were subsequently tested for tick-borne pathogens. During initial field work in summer 2009, 40 adult Amblyomma americanum, 154 nymphal A. americanum, 56 adult A. maculatum, 4,268 larval Amblyomma, 21 adult Dermacentor variabilis, and four adult Ixodes were collected. A. americanum adult and nymphal activity peaked in mid- to late July and A. maculatum adult activity peaked in early to mid-July (no A. maculatum larvae or nymphs were captured). Fewer ticks were collected in burned sites (both intermittent and frequent) compared to unburned sites. Furthermore, distinct differences in tick species composition were observed, with Amblyomma maculatum dominating burned sites, while A. americanum dominated unburned sites. These findings have highlighted a new public health threat in southwestern Georgia, as A. maculatum

transmits the causative agent of Rickettsia parkeri rickettsiosis (Rickettsia parkeri). Molecular analysis of ticks for tick-borne pathogens (Ehrlichia, Borrelia, and Rickettsia spp.) is underway.

19. Elizabeth Lynn[1] , Richard Gerhold[2] , Larry McDougald[1] , Robert Beckstead[1]
[1] Poultry Science Department, College of Agriculture and Environmental Sciences, University of Georgia, Athens GA. [2] Department of Veterinary Pathology, College of Veterinary Medicine, University of Georgia, Athens GA. Determining Virulence Factors in *Histomonas meleagridis*

Histomoniasis (blackhead disease) often causes high mortality in turkeys (50-100%) and morbidity in broiler breeder pullets. However, there is considerable variation in the severity of outbreaks. A national study of *H. meleagridis* strains is needed to find associations of variants with expression of virulence factors. By understanding the molecular basis of strain variation, virulence factors can be found and new targets for immunization identified. Using sequence information for virulence genes found in *Entamoeba histolytica* and *Trichomonas vaginalis,* we have generated degenerate PCR primers and amplified and cloned two cysteine proteases genes from *H. meleagridis.* Additionally, we are using RNA subtractive hybridization screens to identify differentially expressed genes found in virulent strains but not expressed in attenuated strains of *Histomonas*. Real-time PCR will be used to determine the expression level of these genes in virulent and attenuated strains. Putative virulence genes will also be expressed alone or in combination in attenuated strains of *Histomonas* and tested for their ability to confer virulence. To accomplish this, we are identifying the promoters of housekeeping genes in *Histomonas* through Splinkerette PCR technology and testing their ability to drive GFP expression in transfected Histomonads.

20. CHARLES T. FAULKNER..University of Tennessee College of Veterinary Medicine, Knoxville TN 37996. Prevalence of *Dirofilaria immitis* in wild canids from Knox and surrounding counties in East Tennessee.

The canine heart worm *Dirofilaria immitis* is an insidious disease producing agent in the companion animal population. The apparent increased incidence of heartworm infection in endemic areas and its occurrence in previously undocumented localities has prompted concern among veterinarians and the pet owning public to better understand the epidemiology of infective reservoirs and the importance of following effective prophylactic programs for its prevention in companion animals. Carcasses of live-trapped nuisance coyotes, gray, and red foxes from Knox and surrounding counties in East Tennessee were examined to estimate the prevalence of heartworm infection in the wild canine population. To date the prevalence of heartworm in coyotes is 50% while none of the gray and red fox examined were infected.

21. SONIA M. HERNANDEZ[1,2], SUSAN SANCHEZ[3], ROBERT COOPER[1], MICHAEL J. YABSLEY[1,2], C. RON CARROLL[4]. Warnell School of Forestry and Natural Resources[1] and the Southeastern Cooperative Wildlife Disease Study, College of Veterinary Medicine[2], University of Georgia. Department of Infectious Diseases and Athens Diagnostic Laboratory, College of Veterinary Medicine, University of Georgia[3]. Odum School of Ecology and College of Veterinary Medicine, University of Georgia[4]. Do shade-grown coffee plantations ("Bird-Friendly" coffee) pose a disease risk for Neotropical birds in Costa Rica?

Habitat loss and fragmentation has reached unprecedented proportions and is now the leading cause of wildlife species extinction. The resulting increased "edge effect" and smaller habitat patch area poses a variety of threats to biodiversity, including**:** 1) promoting biological impoverishment, 2) creating favorable conditions for the persistence of invasive exotic species, 3) favoring the abundance of generalists species and 4) potentially creating points of artificial aggregation or concentration of wildlife. Disease is one of the most understudied factors affecting wildlife populations. Shade-grown coffee is heavily promoted in the Neotropics as a sustainable agricultural alternative that maintains a diverse and abundant avifauna. However, we hypothesized that the shade-grown coffee plantations, because they are biologically impoverished, promote the persistence of exotic species, favor generalist species in high abundance and are small areas that artificially concentrate wild birds, might serve as disease risks for Neotropical birds. We measured various parameters to estimate health, pathogen prevalence and diversity across 3 replicates of 2 habitat types (shade coffee vs. nearby forest patches). From 2005-2008, we captured 1,550 birds and examined them for body condition, parasite and pathogen prevalence and diversity. Our results were mixed, with some trends indicating that parasite diversity is highest in birds living in shade-grown coffee and wild birds inhabiting these plantations have a higher prevalence of one directly-transmitted disease. Whereby this is unlikely to cause visible mortality, fitness trade-off from investment in immunity are likely to have ripple effects on reproductive output, which can have more subtle, yet important population effects.

22. DANA NAYDUCH AND KATHRYN CLAIRE HILSINGER. Dept. of Biology, Georgia Southern University. Host and seasonal effects on the infection dynamics of the parasitic nematode *Skrjabinoptera phrynosoma* in horned lizards (*Phrynosoma platyrhinos)*

Skrjabinoptera phrynosoma is a common parasitic nematode of horned lizards whose unique life cycle has received little attention. We assessed the effect of season and host characteristics on the infection dynamics in *Phrynosoma platyrhinos*. Nematodes were collected via stomach and cloaca flushes, and fecal pellets during three collection periods in the active season of 2008. Parasite load variables (sex, number, length, and total worm burden (∑L) within lizards) were analyzed both within collection period and across season. Additionally, the relationships between parasite variables and host characteristics (sex, size) were determined. The number of both non-gravid female and juvenile nematodes from lizards' stomachs decreased significantly between early and late collection periods. The number of male nematodes did not change across season; however, their length increased significantly between early, middle and late periods. Host SVL was positively correlated with non-gravid female and juvenile nematode lengths during the early collection period. In late season, there was a negative relationship between lizard SVL and number of gravid female nematodes. Nematodes retrieved from cloacal sampling were exclusively gravid females, with highest prevalence mid-season. We propose that, in lizards with stable male nematode populations, newly-establishing juvenile nematodes develop into non-gravid females, which then mate and become gravid female nematodes, exiting mid-season. Further, in larger lizards, these events may occur more

rapidly due to the added space and/or resources available in larger hosts. The observed seasonal and host effects on infection dynamics this system most likely reflect the importance of timing in this unique parasite life cycle.

23. OSCAR J. PUNG, ASHLEY R. BURGER, AND PATRICIA A. O'LEARY. Georgia Southern University. Effect of incubation vessel and worm density on the ability of *Microphallus turgidus* (Trematoda: Microphallidae) to produce normal eggs in vitro.

Most attempts to culture adult digeneans have been unsuccessful. However, metacercariae of *Microphallus turgidus* cultured in our laboratory mature into adults and secrete eggs infective to the hydrobiid snail *Spurwinkia salsa*. The goal of the present study was to determine if the successful in vitro growth of *M. turgidus* is due to some peculiarity of our culture procedures. In our standard protocol, excysted *M. turgidus* metacercariae (n > 50 worms) from grass shrimp (*Palaemonetes pugio*) are incubated overnight at 37 C in a 50 ml conical bottom centrifuge tube containing Hank's balanced salt solution. On the next day the worms are transferred to 24 well, flat-bottom plates (containing 2 ml RPMI-1640 plus 20% horse serum, gas phase = air, 41 C) for cultivation. Worms cultured using this protocol secrete significantly more eggs and a higher percentage of normal eggs than worms put into 24 well flat-bottom culture plates immediately after excystation. Furthermore, we observed sperm in the seminal receptacle and uterus of ~50% of worms incubated overnight in a conical bottom tube but not in worms put into culture plates immediately after excystation. We hypothesize that overnight incubation in a conical bottom tube facilitates copulation and subsequent fertilization of oocytes. An experiment is now in progress to compare the infectivity of eggs secreted under both conditions.

24. J. MICHELLE RIVIERE AND STEPHEN C. LANDERS. Troy University, Troy AL. Light and electron microscopic analysis of the parasitic ciliated protozoan *Chromidina*.

The ciliate *Chromidina* is a relatively unstudied parasite from the renal organs of cephalopods. This report examines the structure of the trophotomont stage using light microscopy and transmission electron microscopy. The ciliates were obtained from the renal organs of the short-finned squid *Illex coindetii*, collected in the Northeastern Gulf of Mexico on the NOAA ship Gordon Gunter. Whole mount and sectioned material examined by light microscopy revealed details of the cell's unique structure. The cell is covered with spiralling ciliary rows, is elongated (approx. >1500 µm X 32 µm), and has a bulbous anterior attachment end. The most distinctive structure within the cell is the macronucleus, which forms a reticulum that extends throughout the parasite. Numerous vacuoles and mitochondria fill the cytoplasm. Under the pellicle there are darkly stained structures associated with the ciliary rows that are shown by TEM to be kinetodesmal fibers. These fibers are stacked and extend into folds of the outer pellicle on the bulbous anterior end of the ciliate. The specialized structure of the pellicular folds and the kinetodesmal fibers at the anterior end may be used by the ciliate for attachment to the host renal tissue. Further structural details of this specialized cell will be presented. We thank NOAA and the NMFS, SEFSC Mississippi Laboratory for providing ship time and sample collection on the R/V Gordon Gunter.

25. ANURADHA SRIVASTAVA AND DENNIS E. KYLE. University of South Florida, Tampa, FL. Evaluation of novel Arylimidamides in the hamster model of visceral leishmaniasis.

Leishmaniasis, a neglected tropical disease, is caused by parasitic protozoa of the genus *Leishmania*, including 20 species pathogenic for humans. The current drugs of choice for treatment of visceral leishmaniasis (VL) suffer from well documented limitations, including emergence of resistance, toxicity, parenteral administration, long courses and cost. Arylamidamides (AIAs) have been identified as promising VL candidates in the anti leishmanial drug discovery pathway implemented by Consortium for Parasitic Drug Development (CPDD). Submicromolar IC_{50} values were obtained in the axenic *L.mexicana* amastigote, and infected macrophage assay with beta lactamase transfected *L.amazoenensis* and *L.donovani*. Based upon excellent *in vitro* activity, and promising *in vivo* oral efficacy in BALB/C mice VL model, the AIAs DB745, DB766, DB1960, DB1955 were evaluated for efficacy in liver, spleen and bone marrow in Syrian hamsters in our laboratory. The hamster model of VL represents a surrogate of disease progression similar to that seen in humans. A modified Hanson 11 day model of VL in hamster has been established and validated in our laboratory. Till now, most reports are for acute (short term) studies to screen drugs and do not take in account the chronic manifestations of the model that mimic human infections. Therefore, we established a severe infection model (39 days) and all the above mentioned AIA's have been evaluated in both the models. Significant oral activity was observed with all the compounds at 50mg/kg and 100 mg/kg doses. The data also confirmed bioavailability of the compounds. We will report test results of all the compounds.

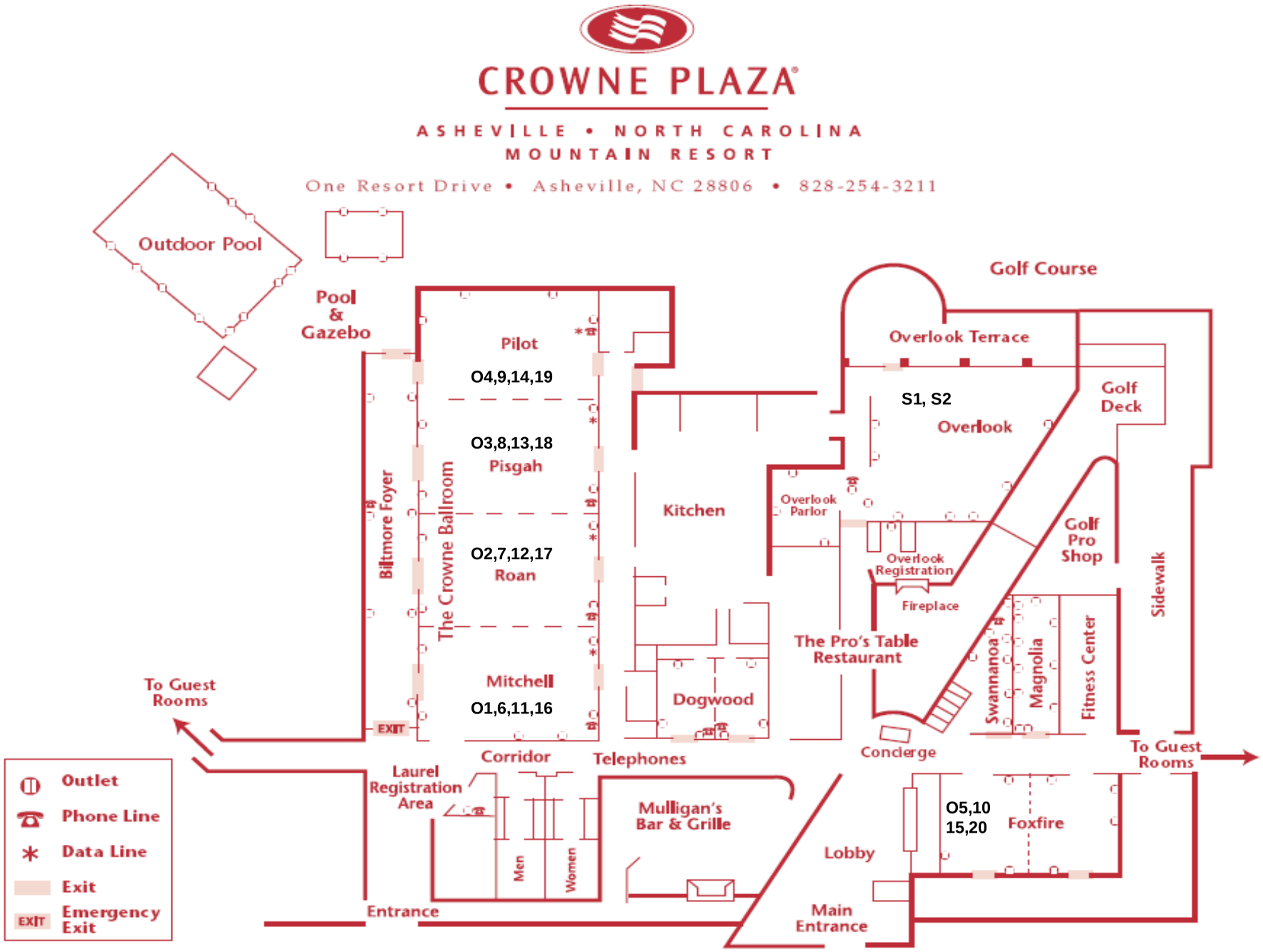
26. ANDREA VARELA-STOKES, ASHLEY CASTELLAW, FLAVIA GIRAO, GAIL MORARU, ERLE CHENNEY, AND CLAIRE FELLMAN. College of Veterinary Medicine, Mississippi State University. Variable membrane protein genes in the tick-borne bacterium, *Borrelia lonestari.*

Borrelia lonestari is a spirochete vectored by the lone star tick, *Amblyomma americanum*. Although it was associated with one case of "southern tick-associated rash illness" (STARI), there has been no further evidence supporting its role as the causative agent. Thus, unfortunately, its potential role in human and animal disease remains unclear and its natural history is only beginning to be understood. Because *B. lonestari* is more closely related to relapsing fever spirochetes, we hypothesized that the genes responsible for causing relapses would be present in *B. lonestari* and that the expression of these genes would change during infection. The variable membrane proteins (vmps) are responsible for mediating antigenic variation in the relapsing fever spirochete, *Borrelia hermsii*, and are divided into the vlp and vsp families. We found evidence of three of four vlp subfamilies (vlpα, vlpβ, vlpγ) and the vsp family, using family and sub-family specific primers, in *B. lonestari* (LS-1 strain). For the infection study, we transmitted *B. lonestari* to white-tailed deer via feeding infected ticks; three exposed deer became infected as demonstrated by PCR. Our studies to identify the expressed variable membrane protein are underway, however in a previous study using *B. lonestari*-infected deer, we were able to detect presence of a variable membrane protein gene at the expression site using primers specific for that site. We anticipate that results of this study will be able shed light on the potential for *B. lonestari* to evade the immune system and possibly its role in human and animal disease.

27. MICHAEL J. YABSLEY[1,2] ELIZABETH HORNE[3], AND NOLA J. PARSONS[4]. [1]Daniel B. Warnell School of Forestry and Natural Resources, [2]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens Georgia, USA, [3]Penguins Eastern Cape Marine Bird Rehabilitation Center, Cape St Francis, South Africa, [4]Southern African Foundation for the Conservation of Coastal Birds, Cape Town, South Africa. Novel relapsing fever Borrelia detected in African penguins admitted to rehabilitation centers in South Africa.

The African penguin, Spheniscus demersus is the only penguin species that breeds in Africa, The population of African penguins is about 10% of that at the start of the 20th century when it was estimated at over 1.45 million adult birds. African penguins are classified as vulnerable and current threats include oil spills, guano and egg collection, reduced food availability, and diseases (aspergillosis, babesiosis, and malaria). From 2002 – 2009, spirochetes morphologically consistent with Borrelia were observed on blood smears from 31 of 4,026 (0.77%) African penguins admitted to two rehabilitation centers in South Africa. Infections were detected in penguins from both coasts with 6 of 650 (0.92%) penguins from the east coast being positive 25 of 3,376 (0.74%) penguins from the western coast being positive. The majority of infections were detected in the summer (Oct-Feb, 28/31 positives) and in younger birds (14 chicks, 13 blues, and four adults). Three of the infected penguins died of suspected borreliosis, one of which had spenomegaly, splenic reticuloendothelial hyperplasia with hemosiderosis, edematous lungs, and moderate, subacute, lymphocytic meningoencephalitis. However, the pathogencity is unknown because some penguins did not receive treatment and survived. Analysis of partial flaB gene sequences indicated the spirocheate was a relapsing fever Borrelia most similar to a Borrelia sp. detected in soft ticks from a seabird colony in Japan. This represents the fourth report of a relapsing fever Borrelia sp. in an avian species and suggests that borreliosis might be a concern for African penguins.

NOTES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O1,6,11,16
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